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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and  
uses thereof.

## NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

### 1. TECHNICAL FIELD

4           The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

### 8    2. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel  
12 polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent  
16 "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the  
20 case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for  
24 genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

### 3. SUMMARY OF THE INVENTION

28           The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more  
32 epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.



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The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases.

- 4 The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NOS: 1-13901. The polypeptides sequences are designated SEQ ID NOS: 13902-27802. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, \* corresponds to the stop codon.

- The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-13901 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NOS: 1-13901. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-13901 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

- The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-13901. The sequence information can be a segment of any one of SEQ ID NO: 1-13901 that uniquely identifies or represents the sequence information of SEQ ID NOS: 1-13901.

- A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

- This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

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full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-13901 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-13901 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-13901; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NOS: 1-13901; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NOS: 1-13901. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-13901; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (*e.g.*, SEQ ID NOS: 13902-27802); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (*e.g.* orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-13901; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (*e.g.*, with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (*e.g.* host cells) of the invention.

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The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

4       The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

      The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium  
8       under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

      Polynucleotides according to the invention have numerous applications in a variety of  
12       techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is  
16       largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

      In other exemplary embodiments, the polynucleotides are used in diagnostics as  
20       expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

      The polypeptides according to the invention can be used in a variety of conventional  
24       procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight  
28       markers, and as a food supplement.

      Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a  
32       pharmaceutically acceptable carrier.

      In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

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The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (*i.e.*, increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

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effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

#### 4. DETAILED DESCRIPTION OF THE INVENTION

##### 4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can

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be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOS: 1-13901.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NOS: 1-13901. The sequence information can be a segment of any one of SEQ ID NO: 1-13901 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NOS: 1-13901. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because  $4^{20}$  possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ( $1 \times 4^{25}$ ) times the increased probability for mismatch at each nucleotide position ( $3 \times 25$ ). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

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The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.



The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134-143) and factors released from damaged cells (*e.g.* Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55).

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*, washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

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In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

4 The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether  
8 or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified  
12 using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is  
16 determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.  
20

#### 4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the  
24 nucleotide sequences of SEQ ID NO: 1-13901 ; a polynucleotide encoding any one of the peptide sequences of SEQ ID NOS: 13902-27802; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NOS: 13902-27802. The polynucleotides of the present invention also include, but  
28 are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-13901; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a  
32 polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NOS: 13902-27802. Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in receptor-like polypeptides include ligand-binding,

extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-13901 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-13901 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-13901 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpi, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-13901, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that

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are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO: 1-13901, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-13901 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-13901 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altshul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

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acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression



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of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

- Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

- The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

- In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-13901, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

- A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

- The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-13901 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-13901 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and

promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, 4 pNH18a, pNH46a (Stratagene); pTrec99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXII, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression 8 control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in* 12 *Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol 16 transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine 20 kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* 24 and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is 28 assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired 32 characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

#### 4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-13901, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

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NOS: 13902-27802 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-13901 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-13901), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N<sup>6</sup>-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N<sup>6</sup>-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxycarboxymethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N<sup>6</sup>-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -n-meric nucleic acid molecule. An  $\alpha$ -n-meric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-O-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

#### 4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-13901). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-1124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

#### 4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

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recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3



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cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice

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sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

- 4           The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element.
- 8           Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by
- 12          the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively
- 16          selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the
- 20          Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

          The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to

24          Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

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#### 4.6 POLYPEPTIDES OF THE INVENTION

- The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NOS: 13902-27802 or an
- 32          amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-13901 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-13901 or

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(b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NOS: 13902-27802 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides

4 biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NOS: 13902-27802 or the corresponding full length or mature protein; and "substantial equivalents" thereof (*e.g.*, with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%,

8 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NOS: 13902-27802.

- 12 Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer.*
- 16 *Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

- The present invention also provides both full-length and mature forms (for example,
- 20 without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form
- 24 of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

- 28 Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

- The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.
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A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

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retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

4       The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist  
8       activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

12       In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NOS: 13902-27802.

16       The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

20       The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine  
24       residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the  
28       protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the  
32       importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

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methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBaf™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

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The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, *etc.*, as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

#### 4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., *Nucleic Acids Research* 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., *Nucleic Acids Res.* vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., *J. Comp. Biol.*, Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, *ISMB-97*, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., *Nucleic Acids Res.*, Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (*J. Mol Biol*, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215:403-410 (1990).

#### 4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

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another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for



example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

#### 4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

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the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

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added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultschi et al., each of which is incorporated by reference herein in its entirety.

#### 4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, *e.g.*, homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecci, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

#### 4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

#### 4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

#### 4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

#### 4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

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confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, IIT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- $\gamma$ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### 4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder



layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

4 Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source  
8 of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

12 Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or  
16 genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition,  
20 the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell  
24 types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus  
28 et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as  
32 retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

*In vitro* cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

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sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci., U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

#### 4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

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- Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

#### 16 4.10.6 TISSUE GROWTH ACTIVITY

- A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.
- 20 A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have
- 24 prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.
- 28 A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking
- 32 inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### 4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by *in vivo* animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

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transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., *Science* 257:789-792 (1992) and Turka et al., *Proc. Natl. Acad. Sci. USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial

immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

4 Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the  
8 patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be  
12 capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to  
16 reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and  $\beta_2$  microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II  
20 proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as  
24 the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

28 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D.  
32 H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.



- Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.
- 4 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production,
- 8 Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.
- Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described
- 12 in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512,
- 16 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.
- Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in:
- Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine
- 20 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation
- 24 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.
- Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry
- 28 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.
- 32 Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### 4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

#### 4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells.

- 4 Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

- 8 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margules, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

#### 4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

- A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

Therapeutic compositions of the invention can be used in the following:

- 28 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### 4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy.

- 4 Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

- Cancer treatments promote tumor regression by inhibiting tumor cell proliferation,  
8 inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic  
12 cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal  
16 cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle,  
20 kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma,  
24 hemangiopericytoma and Kaposi's sarcoma.

- Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically  
28 effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

- 32 The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine.

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- Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepe, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguanzone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

- In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

- In vitro* models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

#### 4.10.12 RECEPTOR/LIGAND ACTIVITY

- A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions

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and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenberg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

#### 4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening

utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol.* 1(1):114-19 (1997); Dörner et al., *Bioorg Med Chem.* 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

#### 4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.



#### 4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

#### 4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

#### 4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of

therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including

4 human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with

8 surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord

12 infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease,

16 tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

20

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease,

24 tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or

28 sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or

32 injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, e.g., choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motor-sensory Neuropathy (Charcot-Marie-Tooth Disease).

#### 4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape);

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effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

#### 4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or

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absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, *e.g.*, by an antibody specific to the variant sequence.

#### 4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, *et al.*, 1983, *Science*, 219:56, or by B. Waksman *et al.*, 1963, *Int. Arch. Allergy Appl. Immunol.*, 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed *Mycobacterium tuberculosis* in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed *Mycobacterium tuberculosis* in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of *Mycobacterium* CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

#### 4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

##### 4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1 µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

#### 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth

factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (*e.g.*, heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (*e.g.*, at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other

hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

#### 4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

#### 4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers



comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral

administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other

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sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically

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acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01  $\mu$ g to about 100 mg (preferably about 0.1  $\mu$ g to about 10 mg, more preferably about 0.1  $\mu$ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired

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patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

#### 4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the  $IC_{50}$  as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD<sub>50</sub> (the dose lethal to 50% of the population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD<sub>50</sub> and ED<sub>50</sub>. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED<sub>50</sub> with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

#### 4.12.4 PACKAGING



The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

### 4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$ ,  $F_{ab}'$  and  $F_{(ab)2}$  fragments, and an  $F_{ab}$  expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG<sub>1</sub>, IgG<sub>2</sub>, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 1351), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will

indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety.

Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

### 5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (*The Scientist*, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

### 5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., **133**:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., **107**:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for

example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

### 5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

### 5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

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Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (*Bio/Technology* 10, 779-783 (1992)); Lonberg et al. (*Nature* 368 856-859 (1994)); Morrison (*Nature* 368, 812-13 (1994)); Fishwild et al. (*Nature Biotechnology* 14, 845-51 (1996)); Neuberger (*Nature Biotechnology* 14, 826 (1996)); and Lonberg and Huszar (*Intern. Rev. Immunol.* 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse<sup>TM</sup> as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the

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immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

- 4 An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the
- 8 locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

- 12 A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another
- 16 mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

- In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds
- 20 immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

#### 5.13.4 F<sub>ab</sub> Fragments and Single Chain Antibodies

- 24 According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F<sub>ab</sub> expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of
- 28 monoclonal F<sub>ab</sub> fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F<sub>(ab')<sub>2</sub></sub> fragment produced by pepsin digestion of an antibody molecule; (ii) an F<sub>ab</sub> fragment generated
- 32 by reducing the disulfide bridges of an F<sub>(ab')<sub>2</sub></sub> fragment; (iii) an F<sub>ab</sub> fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F<sub>v</sub> fragments.

#### 5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.* F(ab')<sub>2</sub> bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al.*, *Science* 229:81 (1985) describe a procedure



wherein intact antibodies are proteolytically cleaved to generate  $F(ab')_2$  fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The  $Fab'$  fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the  $Fab'$ -TNB derivatives is then reconverted to the  $Fab'$ -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other  $Fab'$ -TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally,  $Fab'$  fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., *J. Exp. Med.* 175:217-225 (1992) describe the production of a fully humanized bispecific antibody  $F(ab')_2$  molecule. Each  $Fab'$  fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the  $Fab'$  portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain ( $V_H$ ) connected to a light-chain variable domain ( $V_L$ ) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the  $V_H$  and  $V_L$  domains of one fragment are forced to pair with the complementary  $V_L$  and  $V_H$  domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain  $Fv$  (sFv) dimers has also been reported. See, Gruber et al., *J. Immunol.* 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on

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a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc R), such as Fc RI (CD64), Fc RII (CD32) and Fc RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

### 5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/00373; EP 03089). It is contemplated that the antibodies can be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

### 5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*, 3: 219-230 (1989).

### 5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of

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bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, *saponaaria officinalis* inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include  $^{212}\text{Bi}$ ,  $^{131}\text{I}$ ,  $^{131}\text{In}$ ,  $^{90}\text{Y}$ , and  $^{186}\text{Re}$ .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as *N*-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (*p*-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(*p*-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., *Science*, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is in turn conjugated to a cytotoxic agent.

#### 4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled

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artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-13901 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-13901 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored

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therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

#### 4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

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Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

#### 12 4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization,

amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

#### 4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (*e.g.*, where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection).

See, *e.g.*, Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

#### 4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-13901, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to



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activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

#### 4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NOS: 1-13901. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-13901 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

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chromosome spreads has been described, among other places, in Verma *et al* (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

#### 4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) *J. Clin. Microbiol.* 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) *Mol. Cell Probes* 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. Covalink NH is a polystyrene surface grafted with secondary amino groups ( $>NH$ ) that serve as bridge-heads for further covalent coupling. Covalink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to Covalink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) *Anal. Biochem.* 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm<sub>7</sub>), is then added to a final concentration of 10 mM 1-MeIm<sub>7</sub>. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm<sub>7</sub>, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

#### 4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*II, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI\*\*), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI\*\* digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI\*\* restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

#### 4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm<sup>2</sup>, depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

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Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm<sup>2</sup> and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers *e.g.* a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

## 5.0 EXAMPLES

### 5.1 EXAMPLE 1

#### Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems

(ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

## 4           5.2           EXAMPLE 2

### Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-13901 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 3 sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO: 1-13901) of the present invention, and their corresponding nucleotide locations to each of SEQ ID NO: 1-13901. Table 3 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-13901 were obtained by a BLASTP version 2.0a1 19MP-WashU search against Genpept release 120 and Geneseq database release 200101 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest



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homologue for SEQ ID NOS: 1-13901. The nearest neighbor results for SEQ ID NO: 1-13901 are shown in Table 2 below.

Tables 1, 2 and 3 follow. Table 1 shows the various tissue sources of SEQ ID NOS: 1-13901. Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homologue with an identifiable function for each assemblage. Table 3 contains the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 3 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO. in USSN 09/515,126

TABLE 1

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	83 544 597-598 600-607 616 841 1004 1148 1346 1493 1974 2138 2141 2143 2161 2266 2345 2363 2511 2569 2876 2880 3001 3099-3101 3105-3106 3110-3111 3115-3117 3199 3272 3282 3284 3356 3425 3537 3634 3689 3709 3797 3810 3839 3899 4006 4021-4022 4025 4043 4194 4201 4253 4277 4297 4388 4399 4410 4667 4671 4742 4747-4748 4750 4755 4767 4845 4865 4940 5037 5075 5093 5118 5163 5171-5172 5268 5481 5523 5553 5656 5724 5894 5902 5938 6052 6170-6173 6176 6214 6307 6336 6369 6374 6793 6894-6897 6979 7058 7169 7455 7492-7493 7495-7499 7501 7504 7577 7586 7761 7792 7864 7870 8035 8065 8085 8110 8120 8140 8224 8226 8298 8372 8427 8452 8456 8535 8648 8672 8674-8679 8681-8684 8816 8838-8839 8870 8898 9012 9041 9079 9128 9257 9264 9304 9217 9460 9503 9517 9567 9623 9734 9781 9792-9798 9929 9964 9999 10296 10330 10469-10470 10578 10679 10778 10786 10895 10984-10986 11032 11052 11069 11130 11145 11239 11289 11402 11818 11862 11870-11876 11878-11881 12017 12037 12127 12160 12294 12363 12375 12405 12424 12438 12467 12539 12570 12590 12615-12616 12618 12685 12688 12712 12739 12748 12830 12913 12916 12948-12950 13002 13064 13073 13083 13141 13150 13153 13164-13166 13257 13391 13456 13479 13489 13492 13494 13499 13501 13503 13560 13595-13596 13627 13645 13679 13782 13795 13861 13866 13869 13882
adult brain	GIBCO	ABD003	67 83 142 443 587 598 608-609 611 613-624 633 731 734 737-742 760 799-800 809 1148 1152 1167-1184 1193 1346 1433 1516 1552 1575 1671 1756 1774 1833 1974 2138 2145 2176-2178 2237 2266 2299-2301 2303-2306 2343 2363 2412 2444 2449 2511 2516 2555 2569 2576 2614 2716 2809 2876 2911 2926 3001 3093 3114 3119 3121-3124 3126 3128-3130 3234 3254-3256 3258-3263 3265-3267 3270-3274 3276-3277 3280-3281 3284 3286 3348 3356 3378 3435 3459 3484 3537 3548 3595 3605 3625 3627 3634 3686-3697 3700 3702 3709 3711 3720 3722 3737 3757 3797 3804 3810 3839 3856 4006 4019 4025 4040 4055 4057-4058 4060 4078 4194 4201 4246 4253 4277 4282 4390 4405 4412 4431 4620 4622 4641 4689 4751-4764 4791 4808 4837 4845 4847-4849 4852-4858 4860-4862 4864-4869 4940 4957 4962 4972 4998 5021 5031 5037-5038 5040 5076 5093 5108 5118 5167 5169 5171-5172 5251-5261 5263-5265 5270 5364 5401 5481 5492 5521 5523 5535 5656 5674 5693 5776 5788 5817 5906-5909 5938 6005 6027 6057 6064 6147 6178 6180-6182 6189 6214 6229-6233 6254 6272 6369 6371 6421-6426 6555 6595 6598 6601 6799 6803 6825 6836 6886 6894 6913 6972 6995 7058 7104 7130 7133 7148 7164 7169 7339 7347 7386 7426 7455 7494 7502 7507 7509 7511-7512 7516 7520 7584-7587 7590-7596 7598-7601 7603-7604 7608 7632 7677 7743 7748 7761 7768 7792 7797 7807 7815 7839 7849-7861 7864 7870 7930 7937 8035 8065 8067 8080 8087 8095 8110 8120 8139-8140 8209 8224 8226 8235 8246 8262 8285 8298 8320 8323 8336 8354 8361 8365 8370 8375 8387 8452 8456 8535 8556 8576-8577 8603 8630 8648 8674 8685-8686 8688-8690 8693 8695 8702 8712 8742 8760-8761 8763-8764 8766-8769 8813 8815-8816 8830 8834 8838-8839 8848 8863 8870 8898 8921 8943-8944 8951 8989 9010 9041 9050-9056 9058-9064 9076 9079 9092 9097 9128 9144-9145 9257 9264 9271 9278-9279 9304 9315 9317 9455 9466 9472 9475 9480 9503 9511 9517 9525 9539 9689 9734 9773 9781 9791 9799-9802 9847 9852 9873 9928-9929 9964 9999-

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			10001 10003-10004 10053 10175 10267 10276 10330 10349 10434 10449 10466 10471-10474 10492 10496 10509 10566 10578 10597-10599 10645 10679 10788 10891 10948 10988- 10990 11032 11039 11041-11043 11052 11065 11069 11105 11108 11130 11145 11167 11196 11203-1207 11209 11239 11399 11401-11402 11406 11459 11470 11604 11606 11642 11761 11818 11862 11877 11882-11884 11886 11889-11893 11944-11946 11981 11988 12016 12019 12022 12037 12083 12127 12143 12164-12165 12168-12171 12178 12195 12236 12265 12305 12327 12363 12375 12405 12423-12424 12430 12438 12546 12570 12590 12594 12612 12615-12618 12630 12670 12674 12685 12688 12693 12704 12706-12707 12748 12772 12830 12885 12904 12913 12916 12923 12933 12951 12956 12993 13001 13020-13021 13038 13047 13064 13072- 13073 13084-13085 13092 13117 13142 13167-13171 13191 13254 13257 13260 13295 13390-13391 13394 13456 13479 13483 13489 13497 13501 13503 13505-13507 13512 13516 13546 13551 13555 13575 13590 13592 13597 13613-13614 13645 13649 13659 13711 13782 13795 13838 13861 13869 13875 13882 13884-13885 13888 13892 13896
adult brain	Clontech	ABR001	142 858 1542 2174 2407 2483 2652 3272 3287 3460 3492 3535 3595 3737 3839 4005 4060 4282 4434 4791 4972 5040 5293 5523 5530 5535 5788 5906 6082 6601 6799 6980 7373 7577 7587 7759 7788 7851 8081-8082 8110 9167 9455 9466 9781 9928 10422 10774 10791 11069 11401 11406 11459 11604 11607 11791 11818 11865 11961 11979 12022 12122 12160 12327 12442 12594 12615 12640 12670 12705 12935 12957 12985 13047 13197 13257 13456 13511-13512 13546 13554 13646 13793 13885 13889 13893
adult brain	Clontech	ABR006	6 67 1004 1908 3272 3286 3548 4011 4282 4998 5923 5928 6374 6730 6815 6867 6890 7067 8365 9264 9729 9780 10776 11587 11618 12596 12601 12605 12704 12749 12754 12951 13047 13051 13090 13479 13488 13498-13499 13503 13512 13575 13882
adult brain	Clontech	ABR008	6 11 21 41 51 88 142 364 376 579 598 651 736 800 1050 1148 1184 1251-1265 1291 1346 1404 1479 1529 1543 1671-1674 1697 1699-1710 1820 1830 1832-1838 1840 1848-1849 1908 1914 1919 1927 1957 1964 1974 1976 1978-1979 2005-2006 2050 2081 2090 2110-2111 2129 2150 2174 2200 2310 2327 2342 2408-2410 2420 2444 2449 2461-2467 2484 2490 2499- 2506 2511 2553 2574 2576 2611 2652 2809 2827 2866 2894 3032 3207 3535 3591 3610 3634 3715 3722 3737 3766-3770 3819 4006-4007 4011 4025 4032 4060 4078 4095 4109 4128 4143-4155 4182 4194 4247-4257 4277 4282 4294 4296 4310 4330 4348 4355 4360 4381 4395 4399 4411 4431 4543 4641 4662 4694 4698 4767 4781 4791 4808 4833 4837 4985 5001 5022 5040 5075 5094 5108 5163 5303-5306 5308-5314 5320 5380 5523 5553 5615 5625-5626 5634 5638-5644 5701 5706 5711 5727-5742 5766 5772 5775 5783 5801 5814 5817 5820- 5821 5829 5837 5851 5855 5858 5864 5867 5874 5885 5890 5897 5901 5906 5923 6057 6125 6214 6223 6288 6302 6456- 6464 6545 6598 6601-6602 6624 6676-6685 6699 6726 6728 6746-6749 6765 6799 6805 6834 6860 6893-6894 7004-7007 7049 7076 7078 7081-7083 7105 7117 7119 7133 7153 7166 7431 7579 7708 7768 7849 7900-7905 8018 8083-8084 8095 8110 8196-8208 8262 8288 8312 8320 8331 8336 8356 8375 8452 8482 8633 8681 8710 8739 8777 8815 8817 8830 8839 8963 8965 8983 9010 9097 9100 9102-9108 9111 9128 9142 9257 9264 9313 9364 9378-9384 9401 9454-9455 9458 9460- 9464 9503 9509 9511 9515-9516 9522 9528-9529 9533 9539 9542 9544 9573 9577 9646 9773 9780 9924 10000 10025-

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			10029 10097 10148 10209 10218-10223 10225-10229 10267 10275-10276 10284 10292 10296 10303 10313 10326 10329- 10331 10333-10334 10343 10346 10393 10430 10494 10496 10513 10542 10557 10613-10616 10679 10688 10691 10719- 10721 10729 10743 10758 10760 10776 10782 10786 10795 10895 11100 11114 11132 11195 11240 11242-11254 11401 11406 11437 11454 11459 11462 11466-11473 11475-11476 11519 11532-11535 11550 11553 11555-11556 11559 11588- 11589 11606 11615 11618 11621 11627-11628 11633 11761 11791 11807 11818 11932 11955 12006 12039 12041 12092 12212-12224 12231 12236 12305 12363 12368 12396-12399 12405 12424 12439 12442 12465-12466 12468 12477 12479- 12482 12490 12521 12546 12552-12553 12576-12577 12579 12582 12585 12590 12601 12609 12617-12618 12636 12658 12707 12725 12735-12736 12749 12754 12776-12779 12859 12868 12894 12905 12909 12940 12955 12959 12977 12980 12990 13002 13004-13005 13020 13035 13038 13042-13044 13047 13051-13052 13056 13062 13073 13082-13083 13196 13249 13280 13311-13312 13336 13387 13417 13421-13426 13436 13445 13456 13458 13479-13482 13488 13490 13494- 13495 13497-13500 13503 13507 13512 13516 13533 13546 13554-13555 13590 13613 13630 13649 13659 13670 13678 13713 13724 13769 13793-13794 13808 13827-13828 13838 13861 13867-13868 13875 13882 13884-13885 13888-13889 13893 13896 13898
adult brain	Clontech	ABR011	1006 1257 3797 4006 4025 5535 6057 7169 7870 8262 8937 8966 9257 10778 12736 13394 13679 13793 13861
adult brain	BioChain	ABR012	88 398 1007 1134 2597 3557 3590 3627 3797 4006 4192 4246 4282 4391 4940 5523 5535 6288 6338 7138 8110 8898 9076 9401 9455 9476 10772 11061 11114 12989 13394 13511 13866
adult brain	Invitrogen	ABR013	598 2614 3191 4355 4391 5523 5788 8085 8486 11513 12521 12989 13861
adult brain	Invitrogen	ABT004	40 51 598 1050-1057 1148 1777-1778 1947 1976 2270-2272 2327 2490 2617 3050 3600-3602 3722 3987 4390-4391 4434 4543 4689 5031 5157-5159 5167 5169 5466 5505 5682-5683 5701 5766 5778 5794 5902 6147 6367-6371 6459 6545 6709 6728 6783 6801 6971 7104 7175 7815 7839 7864 8139 8342 8345 8355 8363 8372 8452 8633 8963 8975-8976 9012 9133 9423-9424 9511 9515 9517 9528 9556 9827 9949 10260 10267 10275 10570-10571 10733 10767 11132 11159 11406 11459 11932 12009 12092 12109-12111 12127 12283 12428 12511 12579 12605 12725 12747 12830 12885-12886 12910 12913 12954 12987-12989 13051 13054 13062 13073 13090 13249- 13253 13438 13445 13456 13489 13500 13512 13516 13533 13546 13590 13622 13649 13683-13684 13713 13803 13838 13861 13866 13896
cultured preadipocytes	Stratagene	ADP001	1134 1346 2343 2614 3272 3426 3610 3720 3839 3885 4011 4277 4282 4297 4346 4388 4391 4405 4434 4641 4833 4940 4985 5018 5030 5040 5163 5167 5523 5581 5778 5788 5794 5895 5951 6082 6147 6272 6607 7067 7141 8093 8235 8285 8312 8363 8629 8648 8830 8839 9290 9401 9466 9503 9781 10346 10470 10776 10795 10971 11108 11170 11513 11818 12034 12037 12046 12093 12375 12387 12405 12424 12570 12636 12670 12674 12688 12735 12749 12913 12940 13126 13163 13295 13489 13494 13497 13499 13511 13516 13575 13652-13653 13866 13888-13889
adrenal gland	Clontech	ADR002	8 83 142 225 351 443 551 569 731 864 1134 1266-1271 1273- 1274 1276-1292 1294-1295 1381 1391 1544-1545 1658 1671 1908 1959 1983 2010 2023 2145 2175 2283 2310 2328-2334 2343 2444 2449 2510 2522 2576 3032 3069 3153 3166 3272

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			<p>7516 7520 7544 7561 7584 7587 7599 7601-7604 7635 7638-7643 7645-7649 7651-7655 7657 7659-7662 7733 7735 7743 7748 7783-7796 7815 7852 7857 7862-7863 7865-7870 7930 7933 7983 8062-8065 8067 8087-8088 8093 8095 8110 8116 8120 8139-8140 8224 8226 8235 8262 8298 8336 8344-8345 8354 8356 8363 8368 8372 8378 8387 8410 8427 8452 8456 8531-8532 8534-8535 8563-8569 8572 8576-8577 8592-8593 8597 8603 8606 8610 8613-8614 8616-8617 8646 8648 8670 8681 8691 8698-8699 8702 8712 8742 8756 8760 8763 8795 8807-8809 8811-8814 8816-8819 8821-8833 8835-8839 8858 8863 8870 8898 8921 8927 8936 8939 8943 8946 8950-8951 8956 8988-8992 8994-8995 9010 9049 9059 9065-9067 9070-9072 9076 9097-9098 9167 9190 9257-9260 9262 9269 9281 9287 9301 9304 9315 9317 9401 9454-9455 9466 9476 9480 9484 9556 9577 9612 9689 9698 9720-9721 9734 9741-9743 9747-9750 9758 9781 9791 9804 9871-9882 9884-9885 9928 9939 9942 9954-9960 9999-10000 10005 10175 10179 10275 10284 10292 10296 10329-10331 10346 10400 10422 10430-10431 10437 10442 10444-10447 10475 10511-10512 10514-10521 10557 10576-10577 10616 10645 10679 10691 10729 10742 10744 10772 10774 10777-10778 10782 10788 10839 10891 10894-10895 10902 10917-10920 10937 10942 10946 10948 10969-10970 10992 11032 11044-11045 11061 11066-11074 11108 11114 11132 11145 11153 11165-11170 11173 11205 11208 11210-11215 11283 11289 11386 11388 11401-11402 11406 11462 11559 11565 11576 11596 11606 11615 11620 11744 11788-11789 11793 11818 11823-11825 11831-11832 11869 11894 11947 11961 11982-11989 12000 12006 12009 12011 12019-12020 12028 12037 12044 12078 12081 12093 12119-12122 12143 12160 12166 12172-12175 12177-12179 12197 12205 12335 12363 12375-12376 12383 12387 12400 12402 12405 12424 12428 12438 12479 12521 12523 12546 12560 12564 12570 12590 12599 12601 12605 12609 12611 12616-12618 12653 12662-12663 12670 12674 12688 12717-12720 12734 12752 12754 12772 12905 12907 12914 12916-12917 12923 12925 12940 12961 12963-12965 12989 12991 12993 13020-13021 13033 13035 13072-13073 13082-13083 13104 13117 13126 13132 13136 13141-13142 13148 13169 13203-13210 13212 13260-13261 13293 13295 13326 13377 13394 13413 13442 13456 13477 13480 13488 13490 13494-13496 13501-13503 13506-13507 13511 13516 13533 13568 13570-13571 13575 13582 13592 13613 13624-13630 13632 13644 13646 13659-13660 13678-13679 13689 13701 13711-13713 13775 13782 13795 13797 13866-13869 13872 13882 13884-13885 13893</p>
adult kidney	GIBCO	AKD001	<p>49 67 83-84 142 354 405-407 415-429 431-432 445 460 462 479-484 486 488 492-493 524 548-549 598 616 631-638 744 787 809 841 1004 1068 1086 1160 1163-1166 1171 1184 1193 1346 1359 1449 1479 1516 1552 1556 1671 1724 1727 1774 1826 1858 1914 1974 1976 1978-1979 2081 2097-2099 2111-2113 2117-2118 2129-2130 2138 2145 2148-2150 2161 2186 2218 2266 2268 2302 2310 2327 2343 2363 2409 2412 2444 2449 2468 2483 2523 2569 2576 2614 2617 2827 2845 2876 2910 2915 2926-2931 2933-2934 2938-2943 2945-2947 2955-2956 2976 2981 2983-2984 3001-3016 3018 3053 3109 3114 3140 3142-3146 3149-3150 3199 3254 3265 3272 3283-3284 3286 3333 3350 3356 3378 3406 3435 3445 3460 3492 3503 3535 3537 3544 3548 3590-3591 3598 3625 3627 3634 3676-3677 3679-3685 3689 3697 3709 3711 3720 3722 3737 3757 3797 3808 3810 3839 3885 3989 4005-4006 4011 4019 4022 4025 4040 4043 4054-4055 4060 4078 4109 4192 4194 4201</p>

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			<p>4246 4253 4269 4277 4341 4354 4387-4388 4390 4398 4402</p> <p>4405 4410 4434 4473 4540 4543 4583 4591-4592 4607 4637</p> <p>4640-4641 4649 4654 4665 4668 4676-4677 4680-4685 4688-</p> <p>4689 4711-4712 4751 4758 4766-4768 4783 4808 4833 4836-</p> <p>4837 4845 4874 4904 4940 4957 4962-4963 4972 4983 4991</p> <p>4998 5022 5037 5040 5076 5093 5118 5143 5163 5171-5172</p> <p>5246-5249 5281 5362 5364 5380 5422 5481 5521 5523 5526-</p> <p>5527 5535 5656 5693 5726 5740 5766 5769 5778 5788 5794</p> <p>5894 5902 5908 5911 5916-5917 5923 5928 5938 5990 6005</p> <p>6049-6051 6057 6078 6082 6086 6088 6105-6107 6112-6117</p> <p>6120-6122 6147 6159 6186-6189 6215 6257 6272 6288 6369</p> <p>6418 6423 6430 6555 6595 6598 6738 6743 6765 6767 6793</p> <p>6799 6805 6815 6836 6857 6867-6870 6872-6873 6878 6884</p> <p>6886 6893 6899-6900 6931 6947 6976 6979 6988 7024 7045</p> <p>7058 7104 7118 7155 7275 7281 7306 7312 7338 7347-7348</p> <p>7351-7352 7355 7357 7359-7363 7366 7369 7371-7373 7381</p> <p>7383 7386 7400 7402 7404-7406 7408 7420 7422 7424 7426-</p> <p>7428 7430-7431 7433-7435 7439 7455 7465-7468 7494 7502</p> <p>7506 7517-7521 7579 7587 7604 7634 7639 7642 7733 7735</p> <p>7743 7748 7792 7797 7839 7842-7846 7848 7852 7857 7862</p> <p>7864 7870 7930 7933 8065 8077 8084 8087 8093 8095 8105</p> <p>8110 8116 8120 8139-8140 8156 8224 8226 8235 8262 8320</p> <p>8336 8345 8351 8354 8359 8364 8368 8370 8372 8375 8377</p> <p>8387 8427 8452 8456 8461 8486 8518 8520 8527 8535 8563-</p> <p>8564 8566 8572-8573 8575-8577 8580-8583 8585 8588-8589</p> <p>8597 8603 8618-8621 8623 8625-8626 8628 8630 8634 8647-</p> <p>8650 8664 8674 8677-8678 8691 8694 8701-8704 8706 8711</p> <p>8722 8740 8742 8763 8792 8798 8806 8812-8813 8816 8830</p> <p>8838-8839 8848 8853 8863 8876 8898 8921 8935 8943-8944</p> <p>8948 8951 8966 8989 9012 9041 9047-9049 9076 9092 9128</p> <p>9137 9167 9218 9244 9249 9257 9264 9287 9304 9315 9317</p> <p>9424 9455-9457 9466 9472 9475 9484 9503 9511 9517 9529</p> <p>9536 9542 9544 9558 9612 9683 9699 9703 9722-9723 9725</p> <p>9734 9744 9752-9755 9758 9772-9773 9780-9781 9805-9807</p> <p>9841 9843 9927-9929 9939 9942 9969 9998-10000 10007</p> <p>10175 10275 10284 10287 10292 10319 10346 10376 10423-</p> <p>10424 10431 10442 10446 10448 10450 10475 10480 10496</p> <p>10542 10557 10645 10679 10774 10778 10782 10788 10895</p> <p>10921-10928 10947 10949-10953 10986 10994-10996 11032</p> <p>11052 11061 11069 11114 11130 11132 11143 11145 11197-</p> <p>11202 11205 11208 11212 11239 11289 11401-11402 11406</p> <p>11459 11513 11586 11596 11604 11607 11618 11620 11695</p> <p>11711 11759 11761 11790-11791 11793-11794 11818 11820-</p> <p>11822 11834-11836 11857 11865 11869 11895-11899 11950</p> <p>11970 12006 12022 12041 12078 12143 12159-12160 12178</p> <p>12195 12197 12256 12265 12305 12327 12359 12363 12375</p> <p>12387 12405 12424 12428 12438 12442 12467 12511 12521</p> <p>12523 12535 12539 12546 12564 12570 12590 12599 12601</p> <p>12609-12611 12616 12618 12630 12653 12656 12664 12666-</p> <p>12667 12670 12674 12688-12689 12691 12739 12754 12830</p> <p>12834 12904 12913-12914 12916-12917 12923 12940-12941</p> <p>12951-12952 12956 12972 12976-12977 12993 12999 13002</p> <p>13052 13062 13064 13066 13072-13073 13082-13083 13095</p> <p>13104 13127 13131 13133 13136 13141 13143-13146 13148</p> <p>13154-13155 13169 13172 13184 13195-13196 13249 13254</p> <p>13260 13263 13280 13295 13307 13319 13394 13442 13456</p> <p>13477 13479-13480 13488-13490 13492 13494-13495 13497-</p> <p>13503 13506-13507 13512 13515-13516 13546 13551 13554-</p> <p>13556 13572-13574 13590 13592 13613 13627 13631 13644-</p> <p>13645 13656 13659-13660 13665 13670 13710 13713 13776</p> <p>13782 13795 13859-13860 13864 13866-13868 13872 13882-</p>

PCT/US01/04927

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			13885 13888 13891-13892
adult kidney	Invitrogen	AKT002	679 1450-552 598 639-641 1004 1015 1493 1516 1947 2215 2299 2343 2353 2449 2618 3054-3055 3152-3153 3155-3157 3434 3535 3590 3709 3797 3808 3839 3885 4011 4022 4025 4040 4253 4277 4391 4405 4671 4759 4767 4769 4837 4949 4972 5001 5035 5037 5052 5108 5526 5581 5615 5726 5788 5895 6062 6139 6190-6191 6803 6900 6947 6975 7468-7469 7473 7733 8095 8110 8139 8262 8323 8361 8363 8375 8520 8539 8648 8711 8798 8912 8950 8966 8983 9076 9264 9368 9510 9517 9665 9703 9734 10175 10476 10791 10989 10997 11132 11618 11745 11900 12006 12039 12160 12363 12375 12405 12424 12585 12702 12707 12904 13035 13060 13104 13136 13295 13394 13456 13488 13495 13501 13512 13533 13554 13583 13644 13670 13679 13696 13713 13795 13866 13888 13891
adult lung	GIBCO	ALG001	83-84 553 598 642-644 650 747 975 1004 1009 1015-1022 1449 1516 1816 2161 2186 2215 2343 2444 2968 3056 3158 3160-3162 3345 3466 3503 3519 3566 3568-3573 3595 3709 3797 3810 3839 3885 4025 4039 4059 4194 4405 4622 4755 4767 4770 4797 4865 4940 4949 4963 4972 4987 4991 4998 5001 5117-5129 5171-5172 5233 5401 5481 5581 5724 5788 5938 5960 6123 6125 6140 6215 6322 6336 6343-6348 6371 6886 6966-6967 7024 7143 7275 7441 7444 7502 7522-7523 7749-7752 8093 8110 8140 8336 8345 8375 8378 8449 8535 8612 8622 8635 8648 8651 8674 8702 8707-8708 8838-8839 8898 8941-8942 8944 8948 8951 9076 9128 9457 9466 9475 9497 9503 9544 9567 9703 9756 9758 9808-9810 9843 9873 9926 9999 10161 10175 10275 10329 10344 10400 10458 10554-10555 10796 10998 11032 11046 11069 11132 11144- 11145 11483 11627 11818 11837 11901 12006 12028 12039 12041 12087-12092 12146 12363 12375 12424 12438 12539 12570 12601 12617 12661 12670 12674 12688 12738 12749 12754 12904 12940 12974 13062 13173 13195 13232 13234 13260 13295 13307 13456 13472 13477 13490 13494 13497- 13498 13569 13584 13592 13660 13663-13666 13670 13743 13776 13882 13885 13889 13891
lymph node	Clontech	ALN001	83 142 364 487 495-497 554 629 645-646 648-650 716 938-951 953-962 1134 1516 1549 1671 1774 1976 2138 2225-2232 2234-2235 2340 2879 3019-3020 3057 3103 3163-3165 3272 3356 3498-3505 3507-3513 3515-3516 3538 3548 3628 3697 4194 4201 4253 4405 4641 4687-4688 4771-4772 4783 4808 4845 4963 4972 4987 4998 5042-5065 5076 5163 5504 5523 5835 5895 5917 6027 6142 6192 6272 6288 6308-6311 6313- 6314 6765 6805 6871 6949-6951 7700-7705 7707-7709 8085 8088 8091 8110 8235 8375 8387 8432 8629 8631 8633 8648 8677 8709 8713-8715 8830 8863 8887-8889 8891-8896 8943- 8944 8966 9010 9076 9111 9128 9142 9222 9455 9472 9520 9549 9734 9774 9780 9811 9905-9907 9928 9939 9999 10027 10129 10296 10439 10452 10501 10543-10545 10679 10777- 10778 10788 10891 10999-11000 11111-11113 11115 11130 11145 11344 11406 11513 11584 11885 12006 12028 12050- 12056 12143 12256 12363 12405 12442 12570 12674 12690 12913 12917 12940 12968-12970 13173 13220-13221 13394 13400 13492 13503 13511 13533 13630 13642 13645 13713 13868 13885 13889 13891
young liver	GIBCO	ALV001	211 498 598 651-653 1008-1014 1193 1264 1575 1976-1977 2131 2161 2254-2255 2269 2363 2568 2617 2627 2633 2636 2961 3021 3059 3093 3166 3215 3272 3356 3378 3426 3479 3559-3565 3590 3597 3627 3634 3673 3709 3797 3810 3885 3993 4006 4011 4019 4025 4194 4246 4253 4277 4422 4426 4431 4434 4437-4438 4634 4654 4687 4714 4722 4725 4773-



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PCT/US01/04927

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			4774 4808 4957 5001 5037 5052 5113-5115 5163 5167 5171 5508 5510 5526 5581 5616 5693 5726 5757 5772 5788 5928 6125 6141-6142 6193 6288 6340-6342 6589 6765 6815 6886 6901 7024 7118 7141 7442 7524 7735 7747-7748 7792 7852 7870 7924 7930 8066 8110 8120 8262 8375 8378 8518 8520 8648 8652 8691 8702 8716-8718 8816 8838-8839 8938-8940 9097 9119 9263-9264 9301 9317 9424 9454-9455 9544 9689 9703 9734 9758 9775 9925 9947 10393 10477 10769 10774 11001 11132 11140-11142 11173 11208 11318 11406 11587- 11588 11725 11804 11902 12081-12086 12118 12160 12178 12375 12377 12405 12424 12479 12511 12570 12599 12601 12618 12670 12674 12688 12737 12830 12913 12916 12933 12953 12977 12993 13047 13062 13073 13126 13169 13174 13230-13231 13295 13488-13489 13494 13498-13499 13502 13506-13507 13575 13592 13646 13660-13662 13670 13866 13868-13869 13882 13888 13901
adult liver	Invitrogen	ALV002	6 25 60 142 598 1004 1213 1296-1301 1381 1493 1513-1514 1977 2139 2161 2269 2310 2335 2342 2400 2413 2449 2458 2497 2568-2569 2576 2636 2809 2827 2880 2926 3471 3484 3503 3597 3722 3792-3796 3885 3994-3995 4025 4060 4201 4326 4422 4426 4618 4689 4767 4786 4985 4998 5093 5163 5337-5339 5511 5526 5581 5693 5701 5724 5726 5757 5895 5922-5923 5979 6020 6027 6083 6125 6192 6195 6253 6333 6346 6483-6485 6716 6765 6797 6975 7169 7422 7468 7614 7642 7807 7932 8089 8110 8140 8262 8323 8378 8633 8677 8711 8740 8759 8786 8834 8839 8944 9002 9128-9129 9264- 9265 9282 9466 9484-9485 9517 9677 9700 9773 10007 10046- 10047 10135 10616 10669 10777 11032 11114 11132 11142 11194 11271 11389 11462 11502 11560 11587 11602 11818 11980 11989 12086 12160 12195 12253-12254 12316 12327 12363 12378-12379 12411 12424 12511 12570 12630 12693 12706 12788-12789 12840 12863 12913-12914 13047 13062 13072-13073 13090 13242 13256 13378-13379 13389 13479 13487 13489 13497 13555 13734-13738 13859 13864 13889
adult liver	Clontech	ALV003	346 2529 3548 3797 3885 4438 4940 5101 5801 5902 9597 10769 10778 11587 11927 12086
adult ovary	Invitrogen	AOV001	6 13 40 67 83 88 142 196 444 522 555-560 577 579 598 609 654-657 659-665 667-668 708 740 745-749 751-754 756-761 806 841 871 1004 1023 1028-1034 1036-1039 1041-1047 1055 1087-1115 1119 1151-1162 1298 1346 1359 1456 1493 1507 1516 1658 1697 1752 1774 1812 1826 1848 1914 1974 1976- 1977 1979 1983 2099 2111 2138 2153-2155 2161 2175 2180- 2181 2186 2258-2267 2284-2286 2288-2290 2298-2299 2342- 2343 2449 2483 2523 2529 2555 2569 2576 2591 2597 2618 2708 2750 2783 2818 2839 2926 2961-2962 2988 3007 3022 3031 3060-3061 3063 3069 3166-3172 3174-3175 3177-3189 3226 3272 3286 3288-3289 3291-3293 3295-3299 3435 3450 3460 3479 3486 3503 3535 3577-3589 3612 3627 3629 3631- 3643 3673 3675 3720 3722 3737 3797 3806 3810 3812-3813 3839 3885 3985 4006 4012-4014 4023 4025 4040 4043 4060 4078 4133 4192 4194 4201 4246 4269 4277 4282 4341 4362 4381 4383 4385 4388 4390-4391 4396 4399 4402 4405 4410 4434 4465 4473 4515 4543 4582 4610 4654 4689 4694 4715- 4717 4722 4759 4767 4775-4782 4836-4837 4873-4878 4880 4940 4944 4957 4960 4962-4964 4972 4975 4981 4985 4998 5001-5002 5018 5030 5037 5040 5045 5075-5076 5093 5108 5135-5136 5138-5146 5148 5163 5191-5209 5213 5238-5245 5262 5374 5380 5451 5455 5490 5503 5505 5521 5523 5527 5560 5581 5674 5701 5724 5757 5778 5783 5788 5794 5817 5874 5894-5895 5902 5906 5908-5909 5916-5917 5923 5932 5938 5979 5989-5990 6005 6027 6048 6054 6057 6061 6078

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			6082 6086 6125 6140 6143-6144 6165 6171 6192 6194-6200 6215 6235-6239 6241 6270 6288 6307 6333 6336 6354-6360 6362-6364 6374 6385-6392 6410 6412 6415-6417 6458 6461 6508 6555 6583 6595 6598 6604 6607 6624 6626 6629 6708 6765 6767 6793 6797 6799 6801 6805 6825 6860 6870-6871 6873 6886 6888 6900 6902-6904 6915-6917 6947 6969-6970 6975 6980-6987 6998 7054 7058 7104 7109 7118 7133 7137 7141 7155 7166 7169 7171 7191 7204 7281 7386 7408 7431 7443 7468 7471-7472 7494 7507 7525-7528 7604-7609 7614 7642 7687 7716 7729 7762-7763 7765-7767 7769-7771 7773- 7775 7788 7802-7818 7829-7835 7838-7841 7864 7905 7937 7977 8007 8035 8077 8088 8093 8095 8110 8120 8134 8139- 8140 8143 8156 8235 8246 8262 8292 8320 8336 8345 8355 8358 8363 8365 8368 8370 8372 8375 8387 8444 8452 8456 8486 8520 8593 8610 8633-8634 8653 8719-8724 8773-8777 8779 8781-8782 8792 8798 8813 8830 8839 8853 8863 8870 8876 8898 8928 8944 8950 8956-8961 8963-8971 8989 9004- 9007 9009-9019 9042-9046 9055 9076 9097 9128 9134 9185 9264 9283-9284 9291 9313 9358 9424 9445 9454-9455 9457 9460 9466 9471-9472 9475 9480 9511 9517 9533 9539 9542 9544 9553 9565 9577 9586 9612 9626 9677 9694 9703 9722 9734 9757-9758 9773 9776-9778 9791 9812-9819 9827 9838 9843 9848-9853 9922 9927-9940 9942 9962-9970 9989-9992 9994-9997 10007 10027 10097 10149-10152 10249 10252 10275 10298 10333-10334 10346 10349 10351 10383 10386 10417 10438-10439 10452 10459 10470 10478-10480 10493- 10498 10557-10562 10564-10565 10580-10586 10594-10596 10645 10658 10676 10679 10767 10772 10774 10778 10782 10788 10791 10954 10971-10972 11002-11004 11032 11047- 11052 11061 11069 11083 11108 11130 11132 11151-11153 11155 11157-11158 11167 11170 11172-11176 11193-11196 11274 11343 11369 11406 11411 11431 11588 11596 11600 11604 11606-11607 11618 11620-11621 11629 11668 11814 11860 11865 11876 11903-11909 11932 11949-11954 11980 11985 12000 12006 12017 12022 12033 12039 12080 12083 12092-12093 12095-12104 12127-12129 12131-12142 12146 12159-12160 12162-12163 12178 12213 12216 12236 12256 12260 12305 12327 12363 12368 12371 12375 12379 12387 12401-12402 12405 12424 12430 12467 12520 12522 12546 12570 12576 12590 12594 12599 12605 12609 12611 12615 12617-12618 12630 12636 12643 12657-12658 12663 12670 12674 12685 12688 12691 12693 12702 12705-12707 12713 12724 12729 12735 12740-12745 12749 12754-12760 12765- 12770 12777 12842 12848 12875 12904 12906 12910 12913 12916-12917 12935 12940 12955 12957 12963 12972 12977- 12980 12982-12984 12992-12994 12997-13000 13020 13034 13047 13051 13054 13056 13060 13062 13066 13070 13072- 13073 13075 13082 13090 13092-13093 13104 13126 13136 13141 13175-13177 13179-13180 13193-13194 13196-13197 13202 13236-13241 13243 13245 13249 13254 13263-13275 13277 13286-13292 13295 13319 13351 13377 13589-13591 13394 13420 13436 13456 13477 13479 13488 13492 13494- 13495 13497-13499 13502-13503 13506 13512 13516 13533 13546 13549 13554-13555 13575 13590 13597 13600-13601 13613 13616-13620 13627 13631 13644-13645 13649 13659- 13660 13670 13674-13679 13693-13699 13707-13709 13713 13782 13803 13864 13866 13868-13869 13872 13875 13882- 13885 13888-13889 13892
adult placenta	Clontech	APL001	669-671 1006 1134 1184 1551 2053 2090 2156-2158 2342 2490 2716 3001 3064-3065 3190 3272 3625 3670 4019 4055 4194 4201 4246 4641 4718 4720-4721 4783-4786 4957 5523

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PCT/US01/04927

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			5536 5581 5788 5895 6145-6146 6201-6202 6358 6803 7049 7204 7529 8367 8375 8609 8611 8630 8725-8727 9097 9480 9734 9820 10319 10460 10579 10795 10895 11519 11723 11737 11776 11827-11828 11959 12403 12546 12570 12663 12848 12875 12913 13051 13394 13782 13869 13889
placenta	Invitrogen	APL002	142 561 1023 1551 1976 2449 2569 2614 3191 3340 3592 3668 4060 4346 4767 4787-4789 4892 4985 5536 5674 5693 5757 5772 5794 5906 6147 6203 6215 6598 6788 6799 6979 7158 7530-7531 8139 8361 8611 8863 9457 9484 9517 9563 9703 9758 9821 9927 9939 9942 10481 10557 10778 10802 10973 11006-11011 11723 11731 11737 11776 11807 11866 11910- 11916 11959 12379 12403 12590 12685 13020 13054 13392 13489 13533 13554-13555 13867 13882 13888 13891
adult spleen	GIBCO	ASP001	463 499 562-563 598 672 990-993 995 1004 1020 1346 1515- 1516 1556 1774 1877 1914 1977 2159 2161 2215 2248 2257 2363 2529 2569 2614 2617 2812 2827 3093 3192 3195 3199 3272 3286 3350 3356 3434 3470 3503 3537 3544-3546 3548 3604 3634 3689 3709 3720 3722 3796-3798 3812 3839 3885 4006 4011 4022 4025 4043 4194 4201 4246 4253 4277 4388 4391 4396 4405 4434 4641 4689-4690 4781 4957 4987 4998 5001 5017 5030 5037 5052 5076 5118 5512-5513 5523 5526 5701 5740 5778 5788 5796 5801 5895 5938 6005 6064 6125 6140 6147 6192 6204 6272 6329 6458 6551 6590 6607 6873 6886 6931 6958 7018 7058 7109 7118 7133 7171 7233 7506 7532-7533 7561 7586 7733 7736 7807 7842 7845 7933 8065 8085 8095 8095 8110 8116 8139-8140 8226 8235 8262 8323 8359 8363 8365 8368 8372 8456 8535 8648 8702 8792 8816 8838-8839 8858 8863 8865 8876 8923-8928 8943 8950-8951 9128 9257 9264 9317 9455 9457 9466 9474 9544 9560 9773 9781 9919-9920 9927 9939 9942 10000 10048-10049 10155 10175 10267 10275 10296 10331 10549 10566 10774 10777 10828 10944 11032 11061 11108 11113 11132 11173 11272 11401 11406 11620-11621 11804 11818 11861 11917 12006 12039 12041 12073-12074 12078 12118 12127 12236 12327 12375 12387 12402 12405 12424 12426 12511 12546 12560 12570 12601 12617-12618 12670 12674 12734-12735 12749 12772 12790 12913 12916-12917 12972 12977 13002 13021 13066 13082 13084-13085 13169 13228-13229 13256 13260 13295 13316-13317 13394 13456 13488-13489 13494 13497 13512 13516 13546 13645 13649 13651 13659 13679 13739 13776 13864 13866-13867 13888
testis	GIBCO	ATS001	50 142 500-502 564-565 598 673-678 963-968 1193 1346 1556 1671 1826 1968 1977 2160-2161 2236-2237 2555 2590 2597 3024 3093 3196-3202 3284 3378 3517-3522 3524 3720 3797 3839 3885 4006 4025 4055 4109 4253 4354 4377 4388 4405 4434 4473 4480 4543 4688 4792 4940 4957 4962 4964 4975 5001 5018 5030 5037 5067-5072 5076 5118 5171 5481 5525 5535 5740 5757 5788 5907 5924 6125 6147 6257 6316-6322 6324 6607 6886 6952 7058 7141 7288 7445 7484 7534-7540 7677 7710-7711 7713-7717 7735 7792 7815 8087 8110 8120 8262 8368 8370 8375 8535 8577 8648 8655 8702 8729 8838- 8839 8848 8898-8906 8936 8939 8966 9076 9087 9244 9264 9304 9455 9466 9485 9542 9567 9703 9758 9822-9825 9908- 9910 9928 10462 10475 10478 10482 10551 10583 10679 10772 10778 10795 10955 10974 11108 11113 11116 11118- 11120 11132 11173 11239 11425 11606 11620 11629 11695 11807 11862 11918-11919 12000 12006 12017 12033 12057- 12061 12375 12405 12424 12570 12577 12599 12601 12605 12609 12668 12692 12730-12731 12748 12904 12917 12923 12929 12935 12940 12956 12971 13047 13051 13073 13090 13169 13222-13225 13249 13394 13442 13456 13479 13494

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PCT/US01/04927

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			13497 13502-13503 13506 13512 13515 13533 13549 13555 13575 13613 13616 13627 13644-13646 13660 13866 13875 13882 13889
Genomic DNA from BAC 63118	Research Genetics (CITB BAC Library)	BAC001	8711
adult bladder	Invitrogen	BLD001	731 1710 1779-1791 2076 2367 2479-2481 4067 4208-4214 4681 4767 4775 5163 5169 5553 5560 5581 5674 5684-5688 5794 6082 6244 6716 6718-6721 6799 6931 7045 7094-7097 7967 8110 8226 8249-8258 8364 8648 8737 9012 9097 9425- 9428 9430 9626 9703 9928 10007 10261 10557 10734-10735 11459 11504-11506 12000 12212 12512-12513 12515-12517 12670 12735 12914 13085 13439 13512 13687 13838-13841 13866
bone marrow	Clontech	BMD001	11 70 83 85 142 150 162-184 186-198 200-210 230-243 245- 277 279-281 306 370 373-387 389 433-435 438-440 457 483 503-510 566 568-569 595-596 598 609 616 679-683 740 770 843-857 859 861 864 867-876 880-884 886-890 892-893 896 900 902-920 1000 1004 1116-1120 1122-1126 1128-1134 1184 1211 1346 1359 1516 1552-1554 1575 1583 1671 1724 1774 1877 1894 1927 1974 1976 1983 2012-2024 2031 2033-2038 2040 2043-2044 2084-2088 2111 2120-2121 2132-2133 2137- 2138 2161 2163-2164 2186 2189 2199-2200 2202-2203 2205- 2210 2213-2218 2266 2291-2295 2342-2343 2414-2416 2444 2529 2555 2566 2569 2575-2576 2591 2597 2652 2681-2709 2711-2716 2735-2738 2740-2744 2746-2748 2750-2756 2758- 2759 2761-2764 2766-2768 2770 2772-2781 2783-2787 2806 2812-2813 2816 2873 2875 2880-2881 2883-2885 2887-2897 2899 2901 2926 2948 2954 2958 2977 2984 3026-3029 3032 3068-3069 3071 3081 3093 3096-3097 3139 3203-3205 3207 3238 3257 3272 3282-3283 3286 3317 3345 3356 3404-3418 3422-3434 3437-3438 3440 3442 3447 3449-3450 3456-3459 3461-3464 3466-3473 3483 3497 3535 3538 3548 3557 3572 3588 3593 3600 3604-3605 3610 3612 3625-3627 3634 3644- 3647 3649-3651 3653-3657 3709 3711 3722 3725 3727 3737 3797 3804 3808 3810 3839 3899 4005-4006 4011 4015-4019 4023 4025 4040 4043 4058 4060 4129 4132 4192 4194 4201 4246 4253 4277 4282 4367 4403 4466-4472 4474-4477 4479- 4484 4486-4490 4492-4497 4509 4512-4540 4582 4595 4597- 4606 4608-4615 4622 4642 4648 4650 4654 4667 4691-4695 4723 4741-4742 4759 4767 4783 4794-4796 4808 4836 4928- 4929 4931-4934 4938 4940 4942 4944-4948 4950-4953 4955- 4960 4962-4964 4967-4971 4973 4976-4979 4985-4987 4992- 4998 5000 5004-5016 5030 5037 5052 5075-5076 5093 5143 5149-5151 5163 5169 5210-5215 5217-5226 5262 5317 5357 5503 5523 5535 5537-5540 5560 5604 5695 5740 5748 5766 5788 5796 5801 5862 5874 5895 5906 5908 5938 5965-5967 5969-5979 5991-5994 5996-6005 6007-6009 6027 6047 6057 6065 6067-6068 6071-6072 6082 6086 6089-6091 6112 6125- 6127 6148-6152 6195 6214 6233 6257 6269-6276 6278-6280 6282-6283 6285-6289 6292-6300 6321 6374 6393-6403 6508 6555 6605 6607 6722 6730 6788 6815-6822 6826-6832 6836 6859-6861 6867 6870-6871 6873-6874 6905 6915 6929 6933- 6937 6940-6942 6944-6945 6988-6992 7051 7126 7155 7166 7169 7199-7210 7212-7219 7226 7233-7253 7256-7264 7275 7317-7318 7320 7322-7326 7347 7349 7373-7374 7379 7382 7446-7448 7473-7474 7491 7502 7542 7544 7569 7577 7579 7663-7671 7674 7677-7678 7680-7684 7686 7689-7696 7742 7768 7791 7815 7819-7824 7847 7864 7930 7995 8065 8085

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PCT/US01/04927

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			8088 8090-8093 8095 8110 8120 8134 8139 8224 8226 8235 8241 8246 8262 8336 8354 8359 8363 8365 8368 8375 8421- 8427 8429-8440 8444 8452 8456-8460 8463-8465 8467-8476 8478-8489 8538-8539 8542-8551 8563 8566 8577 8593-8595 8597 8603 8633 8635-8637 8648 8656-8657 8671 8677 8679 8701 8792 8796 8817 8830 8840-8845 8847-8849 8852 8855- 8860 8863-8868 8870 8873 8875 8879-8881 8898 8935 8944 8963 8965 8995 9010 9012 9020-9031 9049 9051 9066 9076 9092 9097-9098 9128 9257 9264 9285-9288 9304 9317 9339 9381 9399 9401 9454-9455 9466 9471-9472 9474-9476 9516- 9517 9519 9529 9544 9622 9630-9643 9646 9650-9665 9689 9705-9712 9730 9734 9740 9758 9779-9781 9826 9885-9889 9892-9902 9928-9929 9939 9942 9972-9976 9978-9982 9999- 10000 10068 10153 10175 10249 10275 10277 10284 10287 10296 10319 10321 10343-10344 10346 10364-10374 10379- 10382 10385-10394 10414 10416 10426 10429 10439 10447 10452 10467-10468 10475 10483 10520 10522-10526 10528- 10529 10531-10535 10587-10590 10595 10616 10677-10679 10691 10750 10760 10767 10772 10778 10788 10794-10795 10828 10831-10837 10846-10847 10849-10851 10853-10858 10891 10895 10897 10899-10903 10905-10907 10931-10933 10956-10959 10975-10976 11012 11032 11046 11057 11059 11061 11077-11082 11085-11086 11088-11098 11108 11113 11132 11145 11177-11181 11194 11208 11289 11344 11401- 11402 11513 11618 11620 11631 11673-11675 11677-11690 11695 11697-11704 11706 11708-11715 11736 11742 11762- 11772 11774 11795-11796 11802-11804 11817-11818 11829 11839-11842 11863 11920 11946 11992-12002 12004-12008 12010 12012-12013 12015-12019 12022-12029 12033 12041 12081 12142-12149 12160 12178 12195 12200 12231 12236 12283 12305 12308 12316 12327 12363 12368 12404-12405 12424 12-26 12430 12439 12527 12546 12570 12576 12590 12608 12610 12616 12634-12636 12641-12645 12654-12655 12657-12659 12669-12670 12674 12721-12724 12754 12761 12834 12840 12842 12904-12905 12910-12911 12913 12916- 12917 12922-12923 12925-12928 12933 12938 12956 12966 12977 12989-12990 12993 12995 13020 13033 13047 13060 13062 13064 13066 13095 13098 13103-13105 13107 13111- 13113 13129 13135 13137 13141 13150 13163 13173 13181 13213-13217 13234 13276-13278 13280 13391 13394 13400 13456 13472 13477 13490 13492 13494 13498 13501-13502 13506-13507 13511 13516 13528 13530-13534 13538 13540 13546 13551-13552 13554-13555 13560 13585-13586 13594 13613 13630 13633-13639 13644-13646 13649 13659-13660 13670 13673 13679 13713 13775 13795 13866 13872 13875 13882-13885 13889 13891 13893
bone marrow	Clontech	BMD002	511242 442 654 1004 1134 1841-1904 1908 1927 2023 2107 2215 2342 2408 2507-2529 2576 2597 2806 2866 3286 3434 3722 3736-3737 3817 3823 3839 4060 4246 4258-4290 4389 4396 4411 4618 4641 4828 4836 4957 4987 5030 5037 5052 5108 5163 5526 5711 5743-5772 5774-5804 5813 5895 5939 6131 6236 6266 6287 6306-6307 6333 6655 6675 6728 6730 6750-6762 6764-6769 6788 7049 7106-7117 7137 7156 7738 8068 8085 8134 8156 8290-8297 8299-8305 8307-8312 8323 8368 8482 8499 8858 8863 8865 8928 8935 9076 9111 9128 9465-9502 9626 9700 9703 9923 9928-9929 9942 10277-10280 10282-10284 10286-10297 10396 10434 10515 10551 10645 10675 10691 10744-10753 10772 10778 11057 11098 11108 11132 11232 11252 11519 11536-11553 11606 11620 12033 12039 12146 12260 12305 12387 12402 12405 12500 12554- 12578 12594 12599 12608 12674 12754 12777 12839 12895-

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12904 12916 12923 13020-13021 13043 13057-13064 13169 13249 13446-13454 13479 13492 13494 13513 13533 13555 13659 13713 13775 13803 13863-13875 13877-13887 13889 13891
bone marrow	Clontech	BMD004	2249 2529 3286 3494 3548 3551 3797 3839 4025 4058 4201 4277 4282 5052 5108 6345 6961 8262 8898 9474 10000 11098 11818 13021 13893
bone marrow	Clontech	BMD007	8539 9780 9927 13021
adult colon	Invitrogen	CLN001	319 346 487 731 799 1792 1848 2050 2161 2449 2482-2483 3431 3901 4215-4217 4940 4957 4987 5163 5239 5560 5689-5695 5865 5911 5923 6722 6765 7098 7815 7864 7880 8110 8259-8262 8486 8597 8951 9484 9529 9542 9556 10376 11507-11508 11617 11869 12127 12236 12424 12518-12523 12601 12610 12777 12976 13062 13073 13367 13440 13507 13512 13630 13713 13843-13844 13864 13868-13869 13888
Mixture of 16 tissues - mRNAs*	Various Vendors*	CTL016	6815 10776 12977 13064 13512
Mixture of 16 tissues - mRNAs*	Various Vendors*	CTL021	1671 6738 8432 8648 8863 8944 9511 10769 13021 13062 13064
adult cervix	BioChain	CVX001	50 67 142 158 308 332 346 475 598 654 895 1004 1086 1286 1449 1516 1671 1698 1701 1711-1756 1758-1776 1828 1848 1959 2134 2186 2257 2267 2343 2408 2414 2468-2474 2476-2478 2608 2716 3002 3136 3166 3191 3199 3529 3535 3554 3572 3627 3722 3737 3777 3797 3839 3985 4158-4176 4178-4195 4197 4199-4207 4246 4277 4391 4396 4434 4641 4667 4759 4783 4828 4885 4940 4957 4963 4987 4998 5001 5038 5075 5108 5163 5293-5294 5455 5481 5523 5552 5581 5646-5652 5654-5659 5661-5671 5673-5681 5687 5701 5711 5723 5740 5788 5794 5848 5902 5908 5923-5924 5964 6020 6052 6057 6062 6091 6106 6112 6125 6129 6181 6350 6371 6374 6410 6446 6458 6504 6508 6512 6551 6598 6686-6687 6689-6705 6707-6715 6788 6873 6893 6917 6998 7008 7045 7078 7084-7093 7095 7130 7141 7148 7169 7204 7507 7579 7608 7675 7733 7768 7815 7871 7880 7893 8078 8138 8209-8215 8217-8236 8238-8242 8244-8248 8298 8345 8370 8444 8456 8486 8499 8535 8558 8592 8633 8635 8648 8669 8679 8742 8853 8863 8870 8898 8921 8939 8948 9012 9061 9098 9107 9128 9137 9153 9304 9308 9317-9318 9355 9385-9391 9393-9403 9405-9406 9408-9418 9420-9422 9457 9466 9475 9510 9539 9612 9734 9773 9927-9928 9939 9947 9960 10110 10175 10230-10256 10258-10259 10267 10274 10319 10329 10344 10491 10496 10540 10616 10660 10691 10722-10732 10778 10782 11055 11145 11217 11376 11462 11477-11489 11491-11503 11519 11584 11604 11695 11853 11869 11891 11980 12006 12066 12081 12127 12160 12195 12216 12240 12266 12308 12363 12379 12402 12405 12424 12438 12483-12494 12496-12510 12579 12605 12610-12611 12617-12618 12643 12653 12670 12674 12688 12691 12703 12707 12735 12740 12754 12830 12840 12866 12870-12881 12883-12884 12905

\* The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12913-12914 12917 12923 12951 12955 12957 12965 12989-12990 12993 13002 13020 13035 13045-13050 13062 13064 13072 13092 13136 13141 13174 13197 13254 13283 13307 13391 13428 13430-13437 13442 13473 13479 13492 13494-13495 13497-13498 13502 13532 13554-13555 13575 13590 13597 13613 13616 13627 13644 13679 13713 13775 13829-13837 13866 13868-13869 13872 13884 13888 13891
diaphragm	BioChain	DIA002	731 1346 3548 3711 3885 4282 4654 5895 6873 8120 8931 8936 9455 11132 11818 12405 12609
endothelial cells	Strategene	EDT001	21 51 67 83 332 569 598 609 762 796 1004 1024-1026 1086 1561 1848 1928 1959 1976-1977 1983 2138 2161 2166 2257 2282-2283 2417 2483 2490 2555 2569 2614 2926 3042 3189 3191 3272 3300-3303 3426 3494 3503 3548 3574-3576 3605 3627-3628 3673 3709 3720 3722 3737 3797 3839 3885 4005 4011 4019 4055 4133 4192 4246 4269 4282 4340 4354 4365 4384 4388 4399 4405 4410-4411 4434 4543 4641 4654 4767 4797-4799 4802 4881-4882 4885-4886 4888 4940 4957 4964 4972 4985 4998 5002 5017 5030 5076 5103-5104 5132-5133 5163 5167 5183-5185 5187-5190 5380 5523 5527 5535 5541-5542 5544 5674 5684 5693 5724 5766 5778 5788 5794 5796 5874 5895 5916 5923 5928 5938 6005 6048 6057 6068 6082 6165 6205 6215 6240-6241 6307 6321-6322 6349-6353 6383 6458 6595 6598 6606-6607 6765 6799 6805 6815 6860 6871 6873 6890 6918 6968 6972 6976 6979-6980 6998 7058 7067 7104 7113 7116 7137 7139 7169 7275 7468 7613 7716 7755-7757 7759-7760 7797 7799-7801 7930 8077 8084 8093-8095 8120 8139 8235 8262 8320 8323 8335-8336 8345 8354 8358 8363-8364 8370 8372 8375 8387 8452 8592 8648 8786 8788 8792 8813 8863 8898 8944-8955 8965 8996-9001 9051 9076 9097 9128 9264 9289-9291 9304 9315 9414 9455-9456 9466 9472-9473 9475 9484 9504 9517 9529 9542 9563 9570 9626 9703 9780-9781 9843 9927 9939 9961 10000 10027 10154 10267 10285 10321 10330-10331 10342 10344 10349 10496 10500 10550 10556-10557 10579 10679 10772 10776 10778 10788 10795 10802 11013 11132 11136 11146-11149 11406 11483 11565 11588 11600 11606-11607 11615 11626 11807 11818 11932 11955 12006 12034 12037 12041 12044 12078 12092-12094 12123-12126 12150 12213 12375 12381 12387 12405 12411 12424 12426 12522 12570 12576 12590 12601 12610 12612 12615 12617-12618 12663 12670 12674 12707 12729 12739 12749 12753-12754 12777 12830 12842 12913-12914 12916-12918 12929 12940 12972 12975-12977 13002 13024 13047 13051 13054 13062 13064 13082-13084 13090 13092 13094 13123 13126 13136 13195 13235 13263 13380 13389 13392 13394 13400 13456 13479 13488-13489 13492 13494-13499 13502 13506-13507 13514 13516 13546 13555 13568 13575 13590 13592 13613 13616 13621 13630 13649 13659-13660 13667-13668 13670-13673 13678-13679 13690-13692 13713 13796-13797 13838 13866-13869 13872 13882 13884 13888 13893
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM001	150 2023 2327 2490 4109 4783 5503 5560 10267 10760 12017 12160 12557 12582 12923 13020 13514
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM003	5560 12017 12146

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
8			
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM004	4783 4798 5560 10817 11926 12017 12160
esophagus	BioChain	ESO002	999-1000 2449 3272 3315 3548 3550 3634 3697 3796 4011 4025 4058 4201 4282 5106 5163 5553 6082 6873 7739 9304 10296 11133 11818 12033 12570 13869
fetal brain	Clontech	FBR001	51 142 1184 3664 4060 4109 4940 5021 5270 5523 5553 6112 6805 6908 7294 8558 9457 10376 11059 11985 12006 12122 12160 12754 13438 13507 13888
fetal brain	Clontech	FBR004	60 2704 3711 4025 4109 4783 5001 6082 7597 9010 9504 9949 11837 12033 12039 12363 12705 12905 13020 13503 13512 13891
fetal brain	Clontech	FBR006	6 60 67 598 800 932 1004 1170 1793-1794 1796-1797 1799-1805 1905-1914 1916-1958 1974 1976 1979 1983 2057 2129 2174 2221 2407 2444 2449 2484-2492 2530-2554 2556-2561 2563 2576 2857 3064 3207 3479 3556 3673 3709 3722 4060 4078 4157 4218-4221 4223-4224 4277 4291-4334 4338 4355 4364 4369 4431 4957 5001 5109 5270 5380 5553 5634 5696-5706 5711 5724 5766 5788 5794 5801 5805-5833 5834-5879 5882-5901 5936 5990 6057 6723-6732 6765 6770-6791 6797 6805 6894 7049-7050 7100-7102 7105 7118-7123 7125 7127 7169 7905 8263-8265 8267-8273 8294 8312-8333 8359 8361 8375 8452 8633 8664 8740 8757 8884 9010 9111 9432-9436 9503-9516 9518-9545 9547-9551 9556 9570 9577 9780 9895 9923-9924 9928 9942 10007 10027 10202 10263-10268 10276 10284 10298-10310 10329 10331 10496 10542 10595 10621 10736-10737 10755-10761 10772 10774 10795 11108 11132 11406 11483 11509-11523 11555-11582 11589-11590 11600 11606 11621 11713 11729 11807 11837 12006 12039 12044 12092 12113 12218 12231 12236 12327 12363 12398 12405 12465 12511 12524-12530 12576-12577 12579-12601 12729 12735 12754 12863 12869 12889 12906-12910 12914 12954 12973 13020-13021 13051-13052 13054 13065 13082-13083 13427 13445 13455-13470 13488 13490 13496 13498-13501 13507 13516 13560 13613 13630 13649 13708 13713 13769 13831 13845-13855 13868 13872 13882 13884 13888-13894 13896-13900
fetal brain	Clontech	FBRs03	1005 4405 5111 6337 6964 7742 13084 13864 13891
fetal brain	Invitrogen	FBT002	51 83 142 321 430 746 932 1054 1058-1065 1493 1833 1947 2273-2275 2299 2444 2449 2926 3479 3492 3885 4347 4534 4391 4405 4410 4434 4530 4804 4985 4998 5075 5160-5169 5380 5428 5466 5750 5788 5801 5895 6132 6215 6371-6374 6458 6598 6973-6974 7067 7096 7716-7778 7780-7782 7937 8143 8323 8361 8364 8372 8377 8452 8633 8977-8984 8986 9010 9142 9264 9332 9457 9474 9503 9511 9517 9539 9582 9827 9848 9927 9950-9953 10027 10161 10329 10430 10492 10573-10575 11014 11160-11164 11406 11628 11742 11814 11830 11985 12092 12112-12114 12116-12117 12127 12424 12511 12521 12570 12576 12643 12696 12735 12748-12751 12754 12830 12835 12913 12957 12977 12990 13002 13020 13062 13072 13083 13117 13254-13259 13377 13486 13489 13496 13499 13507 13590 13649 13685-13688 13713 13867 13888 13891 13893
fetal heart	Invitrogen	FHR001	1001 1004 2250 4025 6334 6765 7740 8933 8935 9457 9544 10000 11132 12599 12609 13021 13568 13656 13866
fetal kidney	Clontech	FKD001	142 346 364 511-517 570-572 574 598 685-690 969-970 972-



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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			981 983-987 1134 1346 2123 2167-2169 2238-2246 2342 2444 2483 2516 2555 2617 2728 2843 2876 3032 3049 3072 3206 3208 3282-3283 3525-3531 3533-3543 3548 3591 3709 3722 3797 3839 3878 4015 4019 4043 4246 4277 4367 4405 4696- 4698 4725 4767 4805-4810 4940 4947 4957 4986 4998 5037 5056 5073-5080 5082-5091 5099-5100 5108 5258 5504 5523 5560 5923 6005 6207-6208 6225 6272 6288 6325-6332 6478 6603 6702 6793 6815 6906 6953-6959 7045 7058 7204 7355 7426 7449-7450 7520 7543-7546 7561 7587 7718-7732 7930 8077 8097 8262 8375 8387 8452 8520 8638 8658 8736-8737 8834 8863 8898 8907-8918 8922 8950 9010 9134 9257 9401 9457 9544 9597 9760 9781 9791 9828-9830 9912 9914-9918 10296 10440 10484 10546-10548 10772 11108 11121-11129 11131-11132 11170 11513 11638 11695 11923-11924 12006 12033 12062-12070 12072 12160 12405 12522 12570 12594 12599 12605 12626 12663 12670 12732-12733 12749 12848 12904 12914 12940-12941 12990 13020 13083 13188 13226- 13227 13234 13263 13277 13280 13351 13391 13394 13491 13501 13512 13590 13644 13647-13650 13713 13782 13867- 13868 13872 13875
fetal kidney	Clontech	FKD002	3286 5030 5037 5105 11108 12033 12490 12570 13494 13866
fetal kidney	Invitrogen	FKD007	3272 3806 4025 4253 4277 4654 5112 5535 5788 5801 8863 8935 9401 9466 10553 11628 11818 13494 13646 13866
fetal lung	Clontech	FLG001	79 2367 2395 3010 3460 3885 4828 4948 4962 5001 5723 5748 5902 5908 6186 6738 7051 7067 7677 7759 9264 9553 9700 10007 10478 11098 12017 12383 12417 12424 12749 12917 19020 19169 13472 13554 13644 13782 13835
fetal lung	Invitrogen	FLG003	142 319 364 629 1671 1806-1814 1816-1819 1877 2129 2161 2169 2367 2449 2493 2529 3191 3503 3610 4109 4225-4234 4367 4434 4957 5108 5380 5421 5581 5707-5710 5712 5714 5788 5801 6057 6733-6741 7034 7103 8274-8278 8365 8597 8948 9264 9327 9437-9442 9444 9466 9510 9525 9530 9539 9677 9773 9841 10007 10190 10198 10269-10271 10329 11519 11524-11527 11927 12531-12539 12848 12890 12904 13021 13072 13249 13445 13472 13489 13551 13575 13649 13670 13679 13856-13857
fetal lung	Clontech	FLG004	1003-1004 2597 5110 6963 9924 10552 11138-11139 12080 12990 13659
fetal liver-spleen	Columbia University	FLS001	-2-4 14 16-22 24 26 28-31 33-46 48-49 51-61 63-68 71-91 93- 102 104-110 112-124 126-156 158-162 282-283 285-290 292- 299 301-304 307-312 314-326 328-338 340-344 346-353 355- 365 369 390-400 402 436 441 483 557 567 575-585 595 598 629 673 678 691-699 701-702 708 731 736 763-767 769-776 778-786 788-791 793-794 796 925 975 1004 1015 1023 1038 1068 1104 1134 1144 1184 1192 1216 1264 1298 1346 1482 1493 1516 1518-1521 1551 1556 1575 1583 1594 1636 1641 1707 1724 1774 1826-1829 1841 1858 1927 1959 1962-1965 1967-1972 1974-1979 1981-1998 2000-2009 2011 2045-2051 2053-2055 2057-2058 2060-2063 2065-2083 2089-2094 2100- 2101 2161 2170 2174 2184-2194 2215 2222 2269 2290 2310 2342 2409 2411 2414 2444 2449 2458 2483 2490 2497-2498 2510 2516 2523 2529 2555 2562 2566-2576 2578-2586 2588- 2591 2593-2601 2604 2607-2608 2611-2612 2614-2618 2620 2622-2642 2644 2646-2653 2655-2664 2666 2668 2670-2680 2696 2750 2788-2793 2795-2811 2814-2826 2828-2835 2837- 2842 2844 2846-2848 2851-2858 2860 2862-2871 2876 2878 2893 2900-2905 2907-2909 2926 2929 2949 2952-2953 2959- 2960 2984 2992 3032 3058 3069 3073-3076 3078-3080 3082 3093 3166 3194 3196 3207 3210-3211 3213-3214 3217-3225 3249 3257 3272 3282 3286-3287 3304-3307 3310-3311 3314-

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			3317 3319 3321-3332 3334-3346 3356 3419 3426 3434 3446 3450 3455 3468 3470 3479 3484 3494 3503 3535 3537 3548 3552 3557 3572 3590 3594 3597 3604-3605 3610 3612 3625 3627 3634 3668 3670 3709 3711 3720 3722 3729 3737 3777 3797 3806 3808 3810 3813 3839 3885 3926 3990 3996-3997 4006 4009 4011 4019-4022 4025 4040 4043 4060 4078 4095 4109 4129 4192 4194 4201 4245-4246 4253 4261 4277 4282 4297 4335-4338 4340-4357 4359-4361 4364 4366-4367 4370- 4372 4374-4377 4379-4382 4384-4386 4388-4392 4395-4396 4398-4414 4417-4424 4426-4455 4457-4458 4460-4465 4542- 4543 4545 4547-4553 4555-4562 4565-4575 4577 4579 4581- 4582 4585-4588 4593 4596 4607 4616-4629 4644-4645 4647 4654 4671 4676 4687 4689 4694 4721 4726-4729 4759 4767 4775 4783-4784 4788 4790-4791 4811-4819 4830 4837 4845 4862 4874 4889-4902 4930 4940 4948-4949 4957 4962-4965 4972 4985 4998 5022 5029-5030 5037 5040 5075-5076 5092 5108 5132 5152 5163 5167 5171-5172 5335 5380 5398 5473 5503 5514 5516 5523 5526-5527 5535-5536 5553 5581 5598 5604 5616 5674 5684 5691 5693 5711 5715 5724 5726 5748 5750 5757 5778 5788 5794 5801 5817 5865 5874 5894-5895 5902-5914 5916-5919 5921-5928 5930-5949 5951-5954 5956- 5964 5966 5979 6005 6010 6013-6015 6017-6018 6020-6022 6024-6025 6028-6032 6034-6048 6052-6062 6064 6068 6073- 6081 6086 6092-6094 6104 6112 6125 6135 6140 6147 6149 6153-6157 6165 6186 6195 6209-6211 6240-6241 6243-6248 6250-6253 6272 6276 6287-6288 6307 6313 6338 6371 6374 6419 6430 6446 6451 6458 6478 6496 6508 6545 6579 6595 6598 6607 6611 6624 6629 6642 6658 6695 6726 6728 6730 6738 6745 6754 6765 6767 6788 6793-6797 6799-6808 6810- 6815 6833-6843 6845-6847 6850-6856 6858 6860 6862-6865 6870-6871 6875 6877 6891 6893-6894 6900 6907-6908 6917 6919-6925 6950 6979 7049 7058 7067 7077 7096 7109 7116 7118 7128-7131 7133-7135 7137-7141 7144-7147 7149-7150 7152-7153 7155-7179 7181-7192 7194-7198 7265-7271 7273- 7280 7282-7305 7307-7312 7316 7327-7336 7375-7376 7383 7386 7451 7455 7468 7473 7475-7477 7479 7484 7548-7553 7555-7558 7561 7608 7617-7618 7620-7631 7642 7675 7687 7695 7716 7768 7809 7811 7839 7842 7864 7883 7933 7977 8069 8093 8095 8105 8110 8116 8139 8224 8226 8235 8241 8262 8323 8334-8340 8342-8350 8352-8355 8357-8359 8361- 8408 8410-8411 8414-8419 8452 8456 8490-8498 8500-8502 8504-8526 8529-8530 8537 8540-8541 8553-8560 8563 8566 8568 8577 8592 8611 8639 8648 8659-8661 8664 8668-8669 8710 8738-8739 8741 8777 8792-8804 8830 8834 8839 8853 8858 8863 8865 8876 8898 8926 8935 8939 8950-8951 8957 8963 9010 9012 9076 9092 9097 9112 9119 9128 9257 9264 9266 9284 9291 9301 9304 9313 9318 9352 9375 9399 9414 9424 9445 9455 9457 9466 9473-9474 9476 9480 9484-9485 9511 9517 9528-9529 9536 9539 9542 9544 9552-9557 9559 9561-9564 9566-9572 9574-9577 9579-9630 9646 9655 9666- 9667 9669-9671 9673 9675-9697 9700-9701 9703-9704 9713- 9715 9718-9719 9722 9726-9729 9734 9752 9758 9761 9777 9780-9784 9813 9831 9854-9867 9869 9906 9927 9929 9939 9942-9943 9969 9983 10000 10007 10205 10267 10284 10296 10305 10311 10313-10316 10318-10325 10327 10329-10331 10333-10354 10356-10363 10395-10397 10400-10403 10405- 10410 10413 10417-10422 10427 10446-10447 10463 10470 10485 10496 10502-10507 10515 10542 10557 10565-10566 10645 10679 10688 10691 10729 10750 10760 10762 10764- 10769 10772-10774 10776-10782 10784 10786-10795 10797- 10815 10817-10830 10859 10861-10869 10871-10879 10881-

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			10893 10908-10916 10929 10934 10943 10948 10968 10971 10975 10977-10983 11005 11009 11011 11015-11018 11028 11031 11054-11063 11094 11108 11114 11132 11136 11142 11194 11208 11213 11246 11390-11391 11401 11406 11411 11414 11459 11462 11483 11508 11513 11521 11534 11559- 11560 11565 11573 11585-11603 11606-11610 11612-11616 11618-11638 11640 11642-11657 11659-11667 11669-11670 11672 11699 11716-11718 11720-11722 11724-11741 11743- 11758 11760-11761 11775-11787 11797 11799-11801 11818 11830 11862 11864-11866 11869 11876 11889 11911 11925- 11928 11958-11961 11963-11976 11979-11980 12000 12006 12017 12019 12028 12033-12034 12041 12078 12086 12092 12122 12127 12159-12160 12178 12216 12218 12236 12245 12256 12260 12289 12303 12305 12308 12327 12330 12363 12375 12382 12387 12402-12405 12424 12426 12439 12442 12465 12470 12476 12511 12522-12523 12546 12551 12560 12570 12576 12590 12601-12602 12604-12619 12621-12633 12636 12639 12646-12653 12670-12671 12674 12682-12683 12688 12693 12696 12706 12709-12715 12735 12749-12750 12772 12790 12823 12830-12832 12835 12842 12849 12855 12863 12904-12905 12910-12911 12913-12916 12918-12924 12929 12931-12932 12934-12937 12939-12940 12954-12955 12965 12973 12976-12977 12989-12990 12993 12999 13020- 13021 13035 13051 13054-13055 13060 13062 13066-13067 13069-13087 13089-13095 13097-13102 13114-13117 13119- 13120 13122-13126 13134-13136 13141 13147 13156 13174 13193 13195-13196 13198-13201 13254 13260 13264 13277 13280 13295 13351 13368 13377 13391 13394 13400 13409 13412 13420 13456 13472-13477 13479-13484 13486-13492 13494-13496 13498-13499 13501-13510 13512-13516 13518- 13527 13533 13541-13544 13546-13551 13553-13555 13560 13575 13587-13589 13597 13603-13604 13613 13616 13622- 13623 13630-13631 13644-13646 13649 13659 13670 13679 13713 13743 13748 13769 13775 13782 13793 13803 13808 13818-13819 13858-13860 13864 13866-13869 13872 13882 13884 13888-13889 13891 13893 13901
fetal liver-spleen	Columbia University	FLS002	6 16 24 30-31 63 67 81 83 89 95 103 115 117 126 140 142 147 150-151 158 162 211 225 287 308 332 356 358 390-391 438- 439 483 551 556 641 654 694 701 708 731 788 997 1006 1012 1047 1082 1151 1154 1178 1184 1208 1212 1356 1480 1507 1551 1556 1623-1647 1649-1667 1669-1671 1675 1677-1698 1828-1829 1858 1877 1885 1889 1914 1927 1947 1961 1997 1999 2028 2057 2070 2092 2098 2138-2139 2154 2161 2174- 2175 2189 2191 2257 2282 2327 2342 2363 2399 2403 2409 2440-2441 2443-2450 2452-2459 2490 2498 2522-2523 2544 2555 2568 2575-2576 2592 2597 2605 2619 2623 2659 2806 2809 2812 2860 2869 2879 2903 2926 2932 2988 3031 3066 3075 3089 3188-3189 3286-3287 3319 3343-3344 3356 3426 3535 3548 3552 3554-3555 3583 3591 3610 3625 3634 3673 3709 3711 3720 3722 3839 3899 3926 3985 4005-4006 4011 4020 4025 4055 4058 4060 4078 4091-4116 4118-4126 4128- 4142 4172 4194 4201 4253 4277 4282 4347 4350 4353-4355 4362 4367 4374 4379 4386 4391 4394 4396 4402 4426 4431 4435 4437-4439 4512 4553 4578 4586 4607 4622 4644 4654 4671 4758 4767 4783 4798 4836 4845 4899 4940 4948 4962- 4963 4985 4991 4998 5001 5037 5108 5167 5171 5177 5198 5237 5293-5294 5380 5400 5523 5535-5536 5581-5591 5593- 5599 5601-5613 5615-5624 5627-5637 5653 5674 5691 5693 5711 5724 5726 5733 5748 5757 5772 5778 5794 5817 5874 5894 5902 5904 5906-5907 5909 5911 5916-5919 5923-5924 5927 5929 5932 5938 5941 5948 5957 5959-5960 5962 5964

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PCT/US01/04927

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			5979 6005 6020 6027 6037-6038 6052 6054 6057 6060-6062 6064 6068 6112 6140 6195 6225 6246 6287-6288 6306-6307 6336 6354 6371 6374 6423 6430 6451 6458 6461 6469 6478 6496 6508 6538 6545 6563 6580 6583 6595 6598 6607 6629 6638 6641-6643 6645-6675 6709 6726 6730 6765-6766 6788 6792-6793 6795 6797-6798 6800-6801 6808 6812 6836 6843 6850-6851 6855 6860 6864 6870 6875 6888 6908 6924 6950 6958 6968 6998 7003 7018 7045 7049 7056 7071-7079 7095- 7096 7109 7116 7118 7126 7133 7135 7137-7139 7155-7156 7166-7167 7169 7175 7178 7275 7291 7294 7329 7422 7426 7478 7608 7627 7687 7695 7716 7815 7839 7871 7893 7914 7937 7977 8022 8095 8120 8133-8134 8148-8149 8151-8167 8169-8182 8184 8186-8192 8194-8196 8241 8246 8276 8289 8298 8336 8339 8343 8345 8349 8355-8356 8361 8363 8365 8367-8368 8370 8373 8375-8378 8385 8388 8417 8496 8518 8520 8543 8558 8561 8563 8646 8667 8710 8738-8740 8786 8803 8813 8865 8926 8946 8948 8963 8970 9010 9049 9119 9128 9142 9164 9222 9264 9289 9296 9301 9317-9318 9320 9322 9335-9341 9343-9362 9365-9368 9370 9372-9373 9375- 9377 9399 9455 9457 9466 9472 9475 9480 9483 9495 9526 9533 9536 9553 9556 9558 9560 9563 9567 9570 9582 9597 9601 9630 9646 9655 9671 9683 9695 9700 9703 9715 9722 9729 9733 9752 9758 9783 9843 9848 9855 9880 9936 9942 9983 10007 10027 10103 10142 10186-10217 10274 10284 10287 10296 10313-10314 10329 10331 10349 10352 10354 10400 10405 10430 10439 10496 10500 10507 10542 10621 10709-10710 10712-10717 10750 10760 10776-10779 10782 10794 10809 10816 10837 10885 10891 10895 10913 10960 10971 10975 11057 11071 11098 11142-11143 11148 11194 11246 11401 11406 11430-11453 11455-11464 11483 11504 11508 11556 11560 11589 11596 11615 11618 11626 11631 11714 11729 11830 11833 11865 11988 12000 12006 12017 12019-12020 12041 12044 12081 12092 12178 12195 12245 12256 12277 12297 12327 12363 12383 12402-12403 12405 12426-12427 12444-12455 12457-12465 12467-12473 12475- 12476 12520 12546 12576 12599 12607 12611 12614-12615 12617-12618 12622 12627 12630-12632 12636 12647-12648 12650 12685 12688 12691 12693 12696 12703 12739-12740 12743 12763 12808 12830 12834 12842 12849-12858 12860- 12866 12885 12895 12906 12910 12913 12915 12917 12920 12922 12929 12933 12940-12941 12954-12955 12957 12965 12977 12990 12993 12999 13021 13039-13040 13047 13051 13054-13055 13060 13062 13072-13073 13077 13082-13083 13085 13092-13095 13098 13117 13123 13136 13173 13195- 13197 13202 13249 13254 13362 13377 13391 13394 13406- 13409 13411-13415 13417-13420 13456 13473-13474 13477 13480 13484 13486 13488-13489 13496-13498 13500 13502 13504 13506-13507 13511-13512 13515 13521 13546 13551 13554-13555 13560 13575 13590 13597 13613 13616-13617 13622 13630 13659-13660 13670 13678-13679 13695-13696 13701 13708 13713 13726 13748 13775 13795-13796 13815- 13826 13835 13838 13859-13860 13864 13867 13869 13872 13882-13885 13888-13889 13891 13893
fetal liver-spleen	Columbia University	FLS003	525 2269 2529 2627 2636 3552 3554-3555 3597 4201 4246 4253 4422 4426 4434 4438 5536 5801 8935 9536 11136 11142 11519 11626 11927 12028 12077-12079 12086 12305 12403 12424 13021 13472
fetal liver	Invitrogen	FLV001	40 51 60 598 731 1023 1048-1049 1820 19762111 2268-2269 2449 2483 2529 2568 2576 2614 2809 3207 3220 3468 3595- 3599 3885 4020 4346 4390 4422 4434 4543 4615 4767 4833 5092 5152-5155 5270 5305 5526 5553 5581 5715 5724 5726

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			5750 5766 5788 5794 5801 5902 6125 6147 6458 6598 6624 6645 6765 6799 6805 6862 7104 7856 8070 8156 8359 8361 8432 8740 8928 8935 8972-8974 9012 9041 9128 9264 9445 9474 9485 9511 9536 9593 9597 9703 9780 9927 9943 9945-9946 9948 10007 10137 10275 10334 10529 10537 10566-10569 10776 10828 11142 11560 11587 11618 11927 12070 12086 12105-12108 12127 12218 12236 12327 12424 12511 12541-12542 12605 12746 12916 12977 12985-12986 13020-13021 13060 13064 13135 13246-13247 13472 13479 13488-13489 13497 13533 13554 13590 13659 13680-13682 13859-13860 13882 13888-13889
fetal liver	Clontech	FLV002	360 996 1134 3226 5102 9401
fetal liver	Clontech	FLV004	998 1927 2449 2627 4025 4043 4426 4438 4834 5030 5726 6730 9474 9942 10769 11142 11587 12590 12608 13889
fetal muscle	Invitrogen	FMS001	40 150 731 894 1264 1555 1613 1821-1822 1883 1959 2161 2343 2494-2496 2555 3203 4235-4237 4434 4671 4694 4783 4885 4940 4985 5037 5045 5481 5716-5718 5724 5788 5902 5932 6624 6742-6743 6825 7054 7104 7141 7632 7800 8279-8281 8863 893 9204 9264 9446-9449 9451 9474 9511 9536 9556 9722 9780-9781 10097 10273-10274 10330 10738-10739 10750 11098 11406 11528-11530 11560 12305 12544-12546 12590 12609 12618 12663 12670 12702 12735 12891-12892 12916 13051 13053 13195 13441-13442 13479 13613 13782
fetal muscle	Invitrogen	FMS002	3378 4348 4434 8932 11132 12033 12570 13782
fetal skin	Invitrogen	FSK001	60 142 235 319 641 683 800 1015 1050 1346 1774 1823-1825 2044 2099 2111 2161 2215 2223 2280 2367 2401 2408 2513 2516 2614 2812 2871 2926 3207 3356 3468 3490 3503 3548 3599 3720 3722 3885 4020 4032 4060 4109 4238 4240-4244 4246 4253 4277 4340 4353 4355 4388-4389 4391 4405 4434 4543 4562 4568 4654 4667 4671 4767 4940 4944 4947 5030 5037 5075 5163 5198 5296 5380 5481 5514 5581 5656 5674 5691 5719-5724 5748 5757 5801 5894 5902 5923 6057 6076 6078 6125 6147 6215 6336 6374 6409 6437-6438 6551 6563 6744 6783 6803 6805 6815 6873 6900 6908 6917 6985 6987 7037 7054 7058 7067 7075 7275 7355 7431 7484 7507 7587 7627 7642 7653 7687 7871 7977 8110 8134 8186 8226 8235 8251 8262 8282-8287 8298 8356 8365 8368 8452 8455-8456 8539 8597 8648 8679 8813 8863 8898 8921 8935 8939 8948 8951 8957 8983 9002 9041 9061 9122 9128 9257 9285 9414 9452-9453 9466 9474 9484 9503 9517 9529 9553 9563 9671 9677 9703 9714 9781 9841 9927 10007 10175 10296 10343 10491 10741-10742 10778 10795 10907 10948 11239 11513 11531 11573 11606 11626 11807 11869 11952 12000 12006 12160 12190 12218 12256 12327 12363 12371 12375 12378 12426 12438 12465 12470 12488 12549-12550 12570 12604 12615 12617 12663 12670 12735 12749 12754 12830 12893 12904 12910 12916-12917 12976-12977 13038 13084 13090 13116 13249 13254 13367 13389 13391 13443-13445 13456 13472 13479-13480 13494 13496 13499 13505 13512 13516 13551 13554-13555 13575 13590 13613 13630-13631 13644 13670 13713 13782 13784 13793 13803 13858 13866 13869 13882 13891
fetal skin	Invitrogen	FSK002	1004 3544 4834 5523 9922 9942 11134-11135 12570 13495 13499 13793 13884 13889
fetal spleen	BioChain	FSP001	997 5030 9466 11108 12033 12749 13590
umbilical cord	BioChain	FUC001	60 83 89 142 166 567 609 760 997 1302-1304 1306-1307 1309 1671 1697 1724 1848 1917 1978 2111 2154 2161 2207 2215 2315 2343 2444 2569 2576 2591 2597 2652 2866 2926 3468 3526 3599 3602 3625 3697 3722 3799-3805 3813 3839 3885 4025 4060 4173 4197 4246 4277 4340 4364 4387 4391 4395-

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			4396 4405 4410 4434 4543 4589 4667 4694 4767 4834 4865 4940 4957 4963 4985 5030 5093 5096 5108 5163 5171 5213 5313 5340 5342-5344 5380 5481 5521 5526 5627 5656 5674 5714 5743 5750 5757 5801 5895 5902 5912 5938 6027 6061 6082 6125 6186 6195 6218 6241 6313 6321 6410 6458 6486 6495 6595 6607-6608 6668 6745 6825 6860 6870 6979 7054 7141 7260-7261 7275 7329 7355 7373 7383 7444 7579 7586 7677 7716 7807 7930 7935-7936 7995 8077 8093 8226 8246 8262 8298 8343 8345 8358 8387 8452 8535 8563 8635 8669 8711 8819 8858 8863 8921 8935 8943-8944 8948 8963 9001- 9002 9012 9097 9130 9132 9134-9138 9264 9303-9304 9313 9332 9401 9424 9466 9472 9474 9544 9597 9665 9677 9700 9722 9734 9758 9834 9841 9848 10050 10175 10183 10267 10277 10311 10337 10446 10470 10508 10529 10566 10691 10772 10828 10961 11108 11132 11145 11239 11241 11273- 11276 11293 11408 11484 11513 11596 11604 11607 11620 11695 11823 11909 11927 11942 12000 12077 12160 12245 12255-12256 12292 12305 12308 12363 12383 12404-12405 12426 12438 12511 12570 12601 12605 12630 12700 12706 12754 12875 12913 12916 12935 12957 12993 13002 13009 13020-13021 13062 13135-13136 13141 13254 13283 13318- 13319 13336 13394 13400 13472 13479 13481 13488-13489 13495-13496 13499 13507 13511-13512 13516 13551 13555 13568 13575 13590 13613 13630 13644 13713 13740-13742 13866-13867 13882 13884 13888
fetal brain	GIBCO	HFB001	51 70 211-213 215-222 224-229 445 586-588 598 608 703-710 712-716 1068 1148 1178 1184 1193 1308 1516 1556 1774 1778 1957 1974 1976-1977 2010 2025-2029 2134-2135 2145 2161 2171 2174 2220 2223 2257 2266 2283 2444 2449 2510 2555 2563 2569 2590 2597 2614 2617 2717 2719-2723 2726 2729- 2734 2809 2997 3002 3081 3083 3086 3109 3226-3237 3239 3257 3272 3278 3282-3283 3286 3356 3419 3460 3479 3492 3495 3544 3548 3557 3590 3604-3605 3625 3627 3634 3673 3689 3697 3709 3722 3797 3810 3839 3885 4006 4011 4019 4022 4025 4040 4054 4059 4095 4194 4201 4253 4277 4282 4355 4364 4383 4399 4405 4410 4412 4434 4473 4480 4498- 4504 4507-4508 4517 4543 4654 4689 4694 4730-4733 4735 4755 4783 4820-4823 4825-4830 4845 4885 4940 4949 4957 4962 4972 4985 5017 5019 5022 5031 5037 5108 5132 5167 5171-5172 5262 5380 5481 5521 5523 5527 5553 5616 5656 5711 5740 5788 5801 5894 5902 5906 5908 5923 5938 5979- 5989 6057 6082 6096 6125 6147 6159 6161-6163 6165 6207 6212-6213 6215-6222 6241 6257 6288 6336 6369 6374 6419 6422 6512 6551 6555 6595 6598 6607 6711 6767 6788 6823- 6825 6860 6871 6879 6892-6894 6900 6909-6910 7058 7118- 7119 7169 7220 7222 7224-7225 7228-7229 7231-7233 7275 7426 7431 7444 7481-7483 7485-7488 7560-7567 7569 7608 7743 7768 7792 7814 7845 7864 7930 7977 7995 8093 8095 8110 8140 8226 8235 8262 8345 8358 8361 8370 8372 8387 8441-8443 8445 8447 8450-8455 8520 8535 8558 8597 8603 8648 8663-8666 8677 8702 8742-8749 8811 8838-8839 8943 8951 9010 9092 9134 9137 9257 9287 9304 9317 9455 9457 9466 9472 9475 9484 9510 9515 9533 9553 9567 9644-9645 9647-9649 9734 9758 9781 9785-9786 9791 9832-9837 9927- 9928 9939 9942 9970 10053 10175 10275 10277 10296 10329 10375-10378 10434 10464 10486 10496 10645 10679 10691 10778 10782 10791 10838-10844 10928 11019-11025 11027 11032 11055 11061 11108 11132 11145 11153 11208 11239 11343 11483 11513 11588 11596 11604 11606 11620-11621 11668 11691-11695 11818 11867 11869 11929-11930 12006 12033 12039 12041 12044 12047 12066 12078 12197 12218

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12327 12375 12405 12411 12424 12438 12521-12522 12564 12570 12576 12582 12590 12599 12601 12604 12611 12626 12630 12637-12640 12670 12674 12688 12694-12695 12703 12734 12748 12754 12785 12835 12840 12913 12916-12917 12929-12930 12935 12940 12946 12959 12989 12993 13020 13051-13052 13054 13073 13083 13090 13108-13110 13117 13131 13136 13148 13158 13160 13169 13184-13186 13254 13263 13277 13295 13389 13394 13438 13456 13477 13479- 13481 13489-13490 13494-13500 13502-13503 13506 13512 13516 13535-13536 13555 13575 13590 13592 13605-13606 13613 13616 13627 13630 13644-13645 13660 13670 13679 13687 13713 13793 13803 13838 13861 13866 13868-13869 13875 13888 13891 13896
macrophage	Invitrogen	HMP001	1002 2253 3548 4011 4058 4201 4246 4282 5526 8093 8262 11137 12039 12426 12511 12521 13888
infant brain	Columbia University	IB2002	6 89 142 211 276 307 518 589-590 598 644 717-718 720-721 773 841 921-924 926-932 937 1023 1091 1147-1150 1289 1493 1522-1525 1557-1564 1724 1778 1928 1947 1976 1978 2097 2111 2138 2172 2218-2223 2257 2283 2401 2418-2419 2444 2449 2516 2555 2563 2569 2575 2597 2627 2809 2818 2880 2932 3087 3166 3226 3241-3245 3272 3435 3474 3476-3477 3481 3483-3486 3488-3489 3492 3494-3495 3497 3538 3544 3548 3572 3595 3597 3669 3671-3672 3709 3720 3722 3737 3797 3817 3885 3985 3997-3999 4006 4011 4022-4031 4040 4095 4201 4246 4253 4277 4297 4355 4405 4410 4434 4676 4689 4767 4775 4831-4834 4837 4885 4962 4983 4998 5017- 5019 5021-5031 5035-5037 5040 5095 5143 5164 5167 5169 5233-5236 5380 5505 5517-5519 5523 5536 5546-5548 5691 5695 5724 5750 5766 5788 5801 5895 6027 6048 6082 6095 6111 6119 6132 6135 6147 6223 6301-6303 6305-6307 6374 6411 6459 6555 6563 6591-6595 6601 6606-6607 6609-6611 6613-6614 6624 6711 6767 6799 6805 6909 6946 7018 7052 7067 7118 7133 7166 7168-7169 7386 7464 7469 7473 7571- 7573 7697-7698 7716 7814 7827-7828 7905 7934 7977 8071- 8073 8084 8098-8104 8235 8320 8331 8351 8354-8356 8364- 8365 8370 8372 8376 8452 8520 8572 8667-8668 8750-8752 8813 8830 8863 8883-8885 8950 8958 8963 9040-9041 9251 9257 9267 9293-9298 9313 9424 9454 9456-9457 9466 9510 9514-9515 9533 9542 9556 9576-9577 9597 9626 9646 9722 9758 9787 9903-9904 9988 10027 10138-10139 10155-10160 10284 10296 10319 10346 10496 10536-10542 10557 10670- 10672 10680 10682 10778 10791 10897 10971 11028-11030 11052 11100-11109 11122 11132 11192 11392 11403-11404 11447 11513 11568 11595 11606 11626 11638 11818 11927 11931-11933 12028 12030-12031 12033-12034 12036-12039 12041 12047 12049 12146 12155-12157 12160 12327 12344 12363 12383-12385 12402 12405-12408 12424 12439 12521- 12522 12570 12590 12601 12611 12615-12616 12626 12639 12684-12685 12688 12696-12697 12707 12725-12727 12729 12748-12749 12754 12763-12764 12830 12904 12913 12916- 12917 12923 12929 12959 12977 12990 12996 13000 13047 13051 13054 13062 13073 13082-13084 13117 13141 13187- 13188 13196 13218-13219 13249 13257 13277 13284-13285 13351 13389 13394-13395 13456 13458 13479-13481 13488 13494-13495 13499 13503 13512 13516 13530 13535 13575 13607-13608 13613 13616 13641 13649 13659 13679 13705- 13706 13708 13713 13793 13798-13801 13803 13861 13869 13872 13875 13883-13884 13888 13891-13893 13896
infant brain	Columbia University	IB2003	6 46 746 1914 1947 1959 1994 2111 2220 2257 2516 2962 3166 3226 3272 3435 3572 3885 4277 4377 4410 4833 4837 5029-5030 5040 5147 5259 5851 6147 6423 6595 6598 6611

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			7145 7169 7716 8262 8354-8355 8364 8452 8865 9264 9457 9515 9556 9577 9626 9646 9715 9781 9928 9970 10027 10329 10376 10557 10791 11083 11289 11406 11459 11513 11663 11933 12039 12405 12546 12570 12601 12616 12685 12754 12913 12916 12954 12977 12990 13000 13056 13062 13195 13257 13392 13456 13458 13480-13481 13488 13497 13499 13506-13507 13511-13512 13514 13516 13549 13616-13617 13649 13793 13861 13884 13888 13891 13896
infant brain	Columbia University	IBM002	1564-1565 1976 2218 2420 3166 4343 4378 6147 6302 10329 11108 11513 12039 12729 12830 13062 13257 13512 13617 13803 13859 13861
infant brain	Columbia University	IBS001	927 931 1564 2915 3166 3737 3885 5029 5044 5095 5143 5701 5894-5895 6135 6307 7018 8452 8963 9424 9556 9626 10296 10542 11083 11100 11108 11167 12383 12611 12785 13257 13280 13479 13495 13506 13617 13679 13713 13896
lung, fibroblast	Stratagene	LFB001	67 235 552 641 746 1346 2090 2186 2343 2770 2812 2871 3203 3537 3548 3634 3812 3839 4073 4253 4434 4654 4783 4786 4821 4940 4957 4963 4985 5163 5172 5492 5523 5788 5911 5938 6027 6048 6057 6223 6272 6322 6599 6873 6886 6997 7204 7759 7815 7933 7977 8226 8235 8262 8354 8452 8648 8742 8791 8830 8863 8898 8944 8948 8951 9000 9076 9097 9128 9290 9304 9414 9455 9466 9472 9476 9503 9544 9563 9671 10000 10050 10342 10376 10434 10447 10679 10760 10857 11055 11094 11289 11402 11607 11818 11837 12000 12006 12178 12363 12405 12462 12582 12617 12636 12670 12754 12913 12916 12917 12925 12940 13126 13377 13394 13446 13456 13494 13497 13499 13502 13575 13613 13670 13679 13691 13795 13797 13867-13868 13882
lung tumor	Invitrogen	LGT002	51 69 88 142 158 211 444 598 608 722-723 733 795-797 799 1004 1023 1135-1145 1308 1338 1346 1493 1526-1533 1535 1566-1569 1626 1654 1816 1841 1848 1860 1976 1983 2090 2150 2161 2173 2223 2257 2266 2296-2297 2342 2402 2449 2483 2555 2569 2576 2591 2611 2623 2724 2809 2868 2880 2926 3088 3166 3272 3347 3571 3658-3666 3673 3722 3737 3797 3839 3885 4000-4002 4006 4011 4025 4032-4034 4060 4133 4201 4246 4253 4277 4282 4340-4341 4384 4388 4391 4399 4402 4405 4434 4543 4622 4671 4686 4767 4783 4791 4833-4834 4836 4885 4903 4940 4957 4987 4998 5001 5017- 5018 5030 5037 5052 5108 5163 5210 5227-5232 5422 5451 5520-5528 5581 5627 5637 5674 5693 5713 5724 5748 5766 5772 5788 5894-5895 5902 5907 5917 5938 5990 6005 6020 6094 6129 6147 6171 6224-6225 6239 6241 6253 6322 6336 6404-6410 6461 6508 6595-6598 6624 6765 6793 6798 6851 6870 6873 6994 7003 7008 7045-7047 7053-7055 7067 7085 7109 7116 7139 7141 7158 7169 7187 7468 7517 7524 7579 7608 7676 7687 7716 7761 7825-7826 8074-8078 8105-8106 8139 8235 8298 8323 8335 8345 8354 8359 8363 8365 8370 8372 8375 8456 8563 8633 8648 8678 8741 8792 8798 8805 8831 8863 8870 8989 9002 9010 9012 9032-9037 9039 9051 9076 9080 9092 9128 9257 9269-9271 9273-9274 9276 9299- 9301 9399 9414 9424 9457 9466 9472 9480 9484-9485 9517 9533 9536 9539 9544 9567 9612 9626 9665 9677 9689 9700 9703 9758 9773 9784 9788 9838-9841 9870 9928-9929 9942 9970 9983-9986 10140-10143 10149 10161 10175 10275 10296 10319 10330 10346 10349 10386 10496 10508 10561 10591- 10593 10673-10674 10742 10774 10778 10782 10788 10802 10836 10971 11031-11033 11064 11108 11132 11182-11191 11393-11395 11406 11459 11462 11560 11565 11588 11596 11604 11606-11607 11615 11618 11629 11821 11823 11845 11869 11932 11934 11961 11978-11980 12000 12006 12017 12022 12033 12078 12080 12127 12150-12154 12178 12236



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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12327 12363 12371 12379 12386-12393 12409 12424 12521 12570 12590 12616-12618 12630 12637 12674 12691 12693 12698-12699 12716 12749 12754 12760 12762 12830 12832- 12833 12842 12904 12907 12913 12917 12923 12993 13020 13031-13032 13035 13060 13062 13064 13072 13083 13090 13136 13150 13193 13197 13202 13234 13277 13279 13281- 13282 13295-13296 13381-13383 13385-13386 13394 13400 13456 13477 13479-13480 13484 13488-13489 13492 13494 13496-13497 13499 13503 13506-13507 13511 13554 13575 13597 13616 13630 13646 13649 13659-13660 13670 13701- 13704 13713 13743 13782 13788-13789 13791-13792 13802- 13803 13864 13867-13868 13872 13882-13884 13888 13892
lymphocytes	ATCC	LPC001	142 316 1034 1977 2161 2342 2367 2483 2513 2529 2952 2962 3272 3711 3722 3839 4006 4277 4282 4405 4434 4836 4970 5037 5239 5451 5706 5796 5924 5941 6048 6147 6301 6765 6793 6805 6815 7133 7171 7275 7320 7687 7815 8033 8093 8095 8105 8110 8246 8262 8345 8365 8368 8370 8535 8664 8674 8722 8834 8858 8898 8919 8963 9012 9257 9456-9457 9484 9539 9544 9560 9758 9928 9939 10175 10201 10284 10333 10496 10520 10529 10679 10744 10766 11032 11108 11508 11513 11519 11853 11862 12033 12160 12363 12387 12402 12424 12438 12520 12560 12570 12663 12830 12913 12923 12968 13021 13066 13072 13085 13140 13147-13148 13394 13479 13488 13495 13499 13507 13575 13867 13869 13888
leukocyte	GiBCO	LUC001	21 49 51 67 83 88 94 142 211 316 326 340 368 371 403 438 443-455 464 485 518-523 525-530 532-535 591-592 616 724- 726 744 800 841 889 943 1004 1346 1556 1570-1572 1826 1914 1916 1927 1959 1976-1977 2095 2103-2107 2124-2127 2134 2138 2145 2161 2163 2175 2215 2223 2237 2266 2343 2363 2412 2421 2449 2483 2529 2555 2569 2575 2597 2617- 2618 2695-2696 2827 2876-2877 2899 2903 2961 2965-2975 3002 3035-3038 3040-3046 3109 3132 3166 3199 3203 3207 3246-3251 3265 3272 3286-3287 3312 3344 3356 3361 3378 3400 3434 3451 3468 3479 3484 3494 3503 3552 3590 3610 3627 3634 3704 3709 3720 3722 3725 3757 3797 3804 3810 3839 3885 3985 3996 4006 4009-4011 4019 4022-4023 4025 4035-4037 4058 4060 4194 4253 4269 4277 4297 4341 4362 4388 4390-4391 4396 4399-4400 4402 4405 4410 4412 4431 4434 4534 4543 4594 4615 4630 4641 4651-4663 4670 4688- 4689 4694 4699-4706 4736 4755 4758-4759 4767 4775 4783 4791 4798 4828 4835-4840 4845 4865 4930 4940 4947-4948 4957 4962 4964 4972 4976 4985 4991 4998 5001 5003 5017 5022 5030 5037 5040 5075-5076 5108 5118 5143 5163 5171- 5172 5313 5481 5503 5505 5521 5523 5526 5535 5549 5552 5656 5691 5724 5726 5740 5750 5766 5772 5788 5794 5796 5801 5865 5874 5894-5895 5906 5908 5923-5924 5928 5938 5989 6027 6042 6057 6063-6064 6082 6094-6103 6125 6130- 6137 6142 6147 6166-6167 6171 6181 6214 6226 6239 6253 6301 6307 6371 6374 6418 6512 6662 6716 6730 6788 6792 6799 6815 6836 6860 6873 6876-6877 6886-6887 6945 6975 6979 7018 7037 7056 7058 7067 7116 7118 7137 7155 7158 7171 7275 7315 7384-7385 7387-7389 7391-7393 7395-7398 7452-7463 7468 7494 7608 7671 7676 7687 7714 7733 7792 7815 7845 7864 7870 7905 7930 8093 8107 8110 8120 8139- 8140 8224 8226 8262 8276 8320 8363-8365 8368 8375 8387 8432 8452 8456 8520 8535-8536 8539 8562 8563 8577 8579 8597 8599-8601 8603-8605 8608 8640-8646 8648 8664 8669 8674 8677 8691 8702 8722 8753 8755 8798 8815-8816 8830 8838-8839 8858 8863 8870 8876 8898 8943-8944 8948 8951 9001 9010 9012 9061 9076 9092 9097 9128 9257 9304 9454-

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PCT/US01/04927

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			9456 9466 9472-9475 9484 9497 9511 9515 9517 9529 9536 9542 9556 9567 9612 9626 9702-9703 9723 9731-9738 9745 9752 9758 9762-9770 9780-9781 9789 9791 9808 9832 9842 9927-9928 9939 9942 9970 10000 10175 10275 10319 10329- 10331 10333 10345-10346 10412 10428 10430 10433 10435- 10436 10453-10454 10456 10465 10470 10475 10488 10496 10513 10566 10645 10679 10683 10691 10774 10776 10778 10788 10791 10795 10802 10891 10928 10930 10935-10941 10948 10961-10962 10964-10967 11034 11055 11108 11132 11136 11145 11239 11289 11405-11406 11459 11483 11519 11588 11604 11606 11618 11620 11693 11695 11805 11809- 11816 11818 11830 11833 11848 11850-11856 11868 11927 11932 11934-11935 11937-11939 11954 11988 12000 12006 12009 12028 12033 12037 12039 12047 12053 12092 12097 12118 12127 12143 12159-12160 12178 12186 12327 12336 12363 12375 12387 12402 12404-12405 12410 12424 12438 12442 12490 12511 12521-12522 12556 12560 12564 12570 12590 12599 12601 12605 12615-12617 12636 12643 12653 12660 12670 12672-12680 12693 12700-12701 12706-12707 12715 12735 12754 12823 12895 12904 12910 12913 12916- 12918 12923 12925 12935 12945 12947 12955-12956 12972 12977 12993 13002 13020-13021 13051 13062 13066 13072- 13073 13082 13085 13117 13126 13130-13131 13135 13138- 13140 13147-13151 13161 13169 13189 13254 13295 13391 13394 13425 13436 13442 13456 13477 13479 13488-13490 13494-13496 13498-13503 13505-13507 13512 13530 13546 13550-13551 13554 13557-13564 13575-13581 13590 13592- 13593 13609 13613 13616 13627 13630 13645-13646 13660 13679 13713 13782 13803 13864 13866-13869 13872 13883 13885 13888 13893
leukocyte	Clontech	LUC003	536 539 541-543 593 728 1552 1927 1974 3089 3252-3253 3434 3548 3709 3711 3722 3797 4011 4019 4040 4060 4194 4201 4277 4282 4622 4707 4791 4841-4842 4949 4998 5001 5030 5345 5895 6052 6138 6227 6419 6595 6754 6765 6767 6788 6911-6912 7049 7139 7171 7464 7575-7577 8093 8110 8116 8365 8370 8375 8592 8648 8830 8863 8944 9466 9544 9612 9758 9771 9773 9790 9929 10326 10346 10679 10779 10961 11035-11036 11132 11401 11513 11853 11940 12160 12256 12405 12670 12674 12681 12840 12904 12906 13020 13051 13162 13280 13400 13488 13511 13516 13554 13670 13679 13860 13869 13883 13889
melanoma from cell line ATCC#CRL 1424	Clontech	MEL004	83 142 360 447 841 1061 1346 1516 1573 1724 1959 1963 2159 2175 2343 2367 2513 2652 2812 2876 2961 3001 3272 3345 3604 3627 3722 3754 3839-3840 3985 3988 4040 4194 4246 4341 4515 4568 4641 4667 4862 4940 5075 5132 5163 5481 5492 5523 5740 5788 6008 6112 6119 6147 6189 6195 6272 6287 6418 6423 6508 6563 6726 6860 6870 7134 7166 7169 7275 7294 7579 7677 7748 7831 7852 7980 8110 8116 8226 8235 8262 8320 8345 8363 8370 8456 8563-8564 8633 8838 9001-9002 9128 9296 9304 9313 9484 9542 9544 9646 9703 9758 9780-9781 9808 9999 10007 10027 10296 10346 10470 11145 11239 11289 11401 11406 11508 11596 11606 11620 11823 11899 11950 12019 12107 12160 12292 12329 12363 12405 12436 12523 12599 12658 12670 12749 12754 12774 12842 12930 13020 13296 13394 13458 13489 13498 13501 13507 13551 13554 13575 13613 13616 13649 13660 13743 13775 13868
mammary gland	Invitrogen	MMG001	51 67 142 449 594 598 616 708 729-733 1004 1060 1194-1196 1310-1315 1329 1536-1541 1826 1848 1858 1914 1947 1974 1976-1978 2174-2175 2283 2299 2310 2336 2343 2403-2406 2449 2483 2555 2563 2576 2597 2611 2614 2617 2812 2827

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			2926 3191 3207 3490 3503 3673 3714-3715 3722 3737 3777 3796 3807-3819 3885 4003-4004 4060 4330 4346 4355 4391 4399 4434 4543 4671 4767 4791 4836-4837 4843 4940 4964 4975 4985 4998 5001 5017 5019 5022 5052 5108 5155 5163 5168-5169 5269 5345-5347 5466 5526-5527 5529 5581 5615 5724 5772 5778 5788 5794 5894-5895 5902 5907 5911 5917 5923-5924 6048 6057 6064 6094 6109 6125 6147 6156-6157 6215 6228 6321 6430 6458 6496-6499 6545 6579 6598-6599 6607 6711 6765 6780 6793 6797 6799 6805 6880 6931 6979 6987 6996 7012-7013 7048 7054 7057 7104 7141 7158 7169 7517 7578-7581 7583 7872 7937-7940 8110 8139 8156 8224 8262 8292 8298 8336 8359 8363 8365 8372 8452 8619 8628 8646 8648 8722 8758-8759 8782 8813 8815 8863 8882 8939 8963 8983 9012 9097 9111 9139-9141 9143 9157 9164 9264 9313 9327 9347 9466 9484 9511 9517 9544 9553 9563 9577 9646 9700 9703 9734 9746 9780 9791 9844-9846 9927-9928 9942 10006-10007 10051-10055 10144 10146-10147 10162 10285 10330 10346 10439 10490-10491 10496 10542 10557 10600 10628 10645 10691 10729 10772 10796 10983 11038 11108 11132 11216-11217 11277-11279 11396-11397 11406 11459 11513 11596 11606-11607 11626 11628 11823 11830 11833 11902 11941-11943 11979 12000 12009 12037 12047 12078 12093 12146 12160 12181 12258-12263 12281 12327 12371 12383 12387 12395 12424 12426 12438 12442 12484 12511 12564 12570 12590 12594 12601 12605 12609 12615- 12616 12618 12621 12653 12670 12691 12699 12702-12703 12749 12771 12791-12794 12834-12835 12885 12898 12905 12913 12916-12917 12920 12923 12955 12976-12977 13002 13020 13035 13047 13062 13064 13066 13072-13073 13084 13090 13092 13127 13135 13169 13190 13193 13195 13249 13254 13296 13320-13322 13392 13456 13477 13479-13480 13488-13489 13494 13497-13499 13505-13507 13512 13514 13516 13546 13551 13554-13555 13590 13611-13612 13631 13649 13670 13713 13743-13745 13838 13864 13866-13867 13869 13872 13875 13882-13885 13888 13891
induced neuron cells	Stratagene	NTD001	88 1493 1552 1561 2034 2090 2510 2522 2570 2576 2623 3226 3272 3839 4006 4058 4282 4384 4694 4783 4888 5103-5104 5172 5523 5541-5542 5684 5766 5788 5794 5938 6082 6195 6418 6449 6607 6960 6972 7058 7494 7815 7937 8370 8929- 8930 8996 9000 9003 9128 9157 9289-9291 9472 9928 10275 10550 10729 10760 11607 11736 11818 12039 12075 12094 12256 12363 12381 12423 12522 12707 12735 12863 12906 12958-12959 12963 13020 13052 13054 13196 13202 13310 13368 13378 13438 13479 13486 13506-13507 13546 13616 13654 13659 13691 13795 13891
retinoid acid induced neuronal cells	Stratagene	NTR001	1552 3839 3885 4282 4434 5030 9308 9466 11108 11132 12034 12039 12405 12424 12570 12905 13047
neuronal cells	Stratagene	NTU001	88 708 1552 1561 1947 2223 2490 2614 3272 3610 3625 3627 4032 4201 4253 4297 4337 4434 4543 4622 4641 5104 5163 5523 5541 5684 5788 6094 6147 6307 6601 6862 7755 8648 8740 8996 9097 9128 9289 9308 9466 9511 9544 10333 10779 10963 11032 11108 11132 12034 12039 12075 12405 12424 12570 12590 12706 12749 12830 12905 12917 12963 13035 13073 13280 13490 13507 13613 13616
pituitary gland	Clontech	PIT004	1148 5674 6068 6371 7759 8093 10430 12605 12636 12658 12916 13021 13082 13875
placenta	Clontech	PLA003	3885 4025 5030 5536 5711 5923 8349 8367 9921 12033 12076 12403 12511 13655 13885
prostate	Clontech	PRT001	67 83 142 225 235 379 486 572 616 1286 1316-1329 1538

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			2023 2139 2147 2161 2266 2290 2337-2344 2346 2367 2422 2444 2511 2631 2809 3001-3002 3084 3419 3563 3625 3627 3797 3810 3821-3827 3829-3835 4019 4022 4173 4282 4332 4434 4667 4755 4791 4862 4865 4998 5001 5066 5171 5349 5352-5356 5358-5361 5363-5364 5481 5581 5656 5674 5723 5740 5902 6027 6047 6125 6321 6371 6374 6427 6458 6463 6500-6507 6509 6563 6598 6643 6793 6803 6871 7014-7015 7058 7104 7275 7320 7608 7635 7733 7842 7852 7864 7941- 7943 7946-7951 7953-7954 8077 8087 8093 8110 8224 8226 8452 8487 8520 8558 8635 8677 8863 8950 8963 8983 8997 9012 9145-9148 9150-9154 9269 9302 9317 9466 9503 9528 9646 9703 9780 10000 10027 10056-10060 10491 10629 10691 10777 10891 11145 11200 11239 11281 11283-11295 11344 11406 11761 11837 11862 12006 12166 12264-12278 12305 12363 12368 12411-12412 12438 12467 12685 12691 12729 12734 12795-12798 12800 12830 12863 12904 13010-13011 13104 13146 13295 13323-13326 13377 13394 13456 13473 13477 13489 13516 13533 13550 13611 13678-13679 13746 13866-13867 13884 13889
rectum	Invitrogen	REC001	6 67 142 683 731 997 1178 1909 1959 2005 2023 2596 2611 2614 2809 2926 3314 3333 3455 3722 3780 3870 4173 4355 4837 4949 4987 5526 5580 5615 5674 5691 5724 5788 5895 5909 5924 6057 6112 6195 6765 6805 7815 7833 8095 8664 8863 9517 9539 9544 9884 9927 10400 10666 11401 11513 11606 11985 12160 12327 12428 12693 12848 12910 12977 13051 13064 13072 13420 13494 13497 13507 13512 13515- 13516 13866 13869 13884 13888
salivary gland	Clontech	SAL001	67 731 800 997 1054 1914 2267 2395 2529 3136 3595 3627 4011 4192 4246 4330 4434 4641 4957 4987 5040 5052 5163 5451 5481 5706 5723 5788 5895 6219 6621 6801 6900 6975 7045 7733 8110 8372 8535 8563 8635 8830 8951 9000 9010 9051 9313 9472 9475 9671 9724 9758 9927 10027 11145 11695 11725 12017 12284 12363 12424 12427 12570 12609 12670 12674 12693 12977 13035 13307 13554 13617 13867 13872 13889 13891
salivary gland	Clontech	SALs03	1516 1724 1858 5030 6186 13657 13864
skin fibroblast	ATCC	SFB001	2251-2252 5788 6068 12511
skin fibroblast	ATCC	SFB002	6068 8951 12511
skin fibroblast	ATCC	SFB003	4025 5895 7741
small intestine	Clontech	SIN001	142 319 627 654 1034 1063 1197-1198 1330-1338 1340-1359 1575 1646 1774 1814 1978 2161 2347-2354 2409 2876 3046 3419 3460 3605 3716-3718 3737 3797 3837-3839 3841-3843 3845-3857 3885 3986 4060 4201 4301 4351 4385 4568 4689 4694 5076 5163 5270-5273 5304 5326 5365 5367-5372 5374 5503 5550 5701 5772 6064 6094 6171 6288 6427 6430-6432 6438 6510-6522 6598 6615 6793 6815 6997-6998 7016-7018 7054 7058 7072 7309 7450 7604 7769 7811 7873-7876 7955 7957 7959-7962 7964 8120 8298 8350 8452 8830 8863 8950- 8951 8966 9010 9073-9075 9119 9126 9128 9155-9166 9303 9544 9560 9780 9884 9928-9929 10008-10010 10061-10068 10097 10262 10330 10351 10601 10630-10634 10760 10983 11061 11219 11296-11308 11310-11313 11513 11620 11693 12182-12183 12280-12287 12327 12363 12488 12707 12799- 12801 12922 12991 13012-13014 13035 13051 13064 13297 13307 13328-13332 13335 13382 13499 13506 13554 13560 13575 13631 13695 13714 13747-13749 13751 13882 13884
skeletal muscle	Clontech	SKM001	1104 1346 2363 2367 2495 2555 2876 2880 3555 3634 3722 4011 4022 4194 4201 4253 4277 4282 4434 4641 4940 4972 4998 5343 5481 5523 5801 6005 6336 6873 7408 7995 8110 8120 8235 8262 8292 8345 8372 8576 8740 8830 8936 8951

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			9303 9689 10616 10679 11132 11145 11825 11869 11927 12387 12442 12467 12570 12663 12735 12916 13280 13503 13872 13885
skeletal muscle	Clontech	SKM002	8535
skeletal muscle	Clontech	SKMs03	6336 6962 8936
skeletal muscle	Clontech	SKMs04	770 1724 3797 4277 6336 12405 13658
spinal cord	Clontech	SPC001	83 142 390 415 598 668 708 731 1184 1199-1207 1360-1375 1377-1396 1516 1574-1576 1595-1596 1849 1927 2070 2129 2161 2311-2314 2345 2355-2368 2423-2424 2430 2484 2529 2569 2576 2876 3215 3249 3272 3283 3532 3584 3627 3634 3711 3719-3722 3737 3839 3860-3884 4011 4025 4038-4039 4043 4055-4056 4173 4246 4282 4354 4375 4391 4434 4681 4767 4781 4808 4964 4985 4998 5037 5163 5233 5274-5277 5375-5392 5394-5402 5523 5569-5570 5581 5615 5723 5788 5835 5902 5928 5936 6047 6078 6082 6211 6288 6374 6433-6435 6512 6523-6531 6534 6595 6616 6625-6626 6788 6894 6979 6999 7018-7026 7126 7166 7359 7473 7642 7653 7807 7814 7877-7879 7965-7968 7970 7972-7980 8105 8108-8110 8139 8246 8298 8345 8363 8368 8482 8603 8646 8884 8898 8981 9010 9012 9076-9078 9098 9167-9179 9184-9189 9264 9302 9304 9319-9320 9455 9466 9520 9530 9544 9556 9567 9781 9895 9901 9928 9942 9947 9969 9999 10007 10069-10077 10079-10085 10177 10296 10326 10346 10376 10422 10566 10602 10635-10638 10679 10685-10686 10729 10776 11132 11220 11246 11314-11323 11325-11330 11417-11418 11459 11513 11818 12000 12011 12017 12033 12039 12160 12184-12185 12288-12292 12295-12299 12301-12305 12363 12375 12383 12387 12402 12413 12442 12468 12527 12605 12617 12636 12657-12658 12739-12740 12754 12772 12802-12809 12830 12835 12841-12842 12905 12923 12940 12976 13003 13015 13017-13021 13051-13052 13117 13126 13136 13260 13277 13283 13295 13336-13343 13367 13442 13456 13473 13477 13481 13495 13497 13499-13500 13507 13516 13659 13670 13713 13715-13716 13748 13752-13759 13803 13869 13872 13884-13885 13888 13893 13896
adult spleen	Clontech	SPLc01	800 1927 4032 4834 6064 6135 6195 6446 6788 6873 7166 7455 8966 9929 10744 12402 12564 12590 12691 12904 12933 13082 13500 13506-13507 13516 13575 13864 13869 13883 13889
stomach	Clontech	STO001	21 83 142 1004 1208-1215 1217-1219 1397 1399-1405 1671 2315-2316 2345 2369-2373 2375 2575-2576 2809 2846 2984 3136 3166 3537 3610 3698 3723-3725 3839 3885-3897 4057-4059 4173 4277 4410 4480 4667 4791 4808 4940 4987 5262 5278-5281 5283-5284 5403-5405 5407-5424 5481 5656 5674 5796 5904 6418 6436-6440 6535-6540 6563 6627-6629 6765 6940 7000-7001 7027-7030 7064 7135 7509 7604 7880-7885 7981-7990 8087 8110 8120 8143 8226 8452 8535 9010 9079-9081 9191 9193-9196 9304-9306 9313 9317 9321 9715 10007 10011-10013 10086-10093 10178-10179 10603-10605 10640-10642 11069 11167 11221-11222 11331-11337 11339-11343 11419 11513 11818 12186-12190 12307-12314 12327 12363 12425-12427 12438 12617 12773-12774 12810-12811 12834 13082 13103 13298-13299 13344-13349 13592 13630 13670 13717 13760-13764 13782 13888
thalamus	Clontech	THA002	579 598 616 1065 1148 1220-1221 1223-1226 1407-1432 1597 2266 2317-2319 2340 2342 2376-2378 2380 2431 2444 2555 3093 3230 3286 3537 3722 3726-3732 3737 3898-3902 3904-

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			3918 3920 3922 4060-4062 4173 4201 4282 4360 4391 5270 5285-5288 5425-5438 5440-5449 5701 5902 5938 6137 6437 6458 6461 6541-6544 6546-6550 6630 6755 7031 7095 7119 7166 7484 7579 7815 7849 7905 7977 7991-8000 8002-8005 8126-8128 8134 8363 8538 8664 8786 8890 8930 8963 9082- 9085 9128 9197-9199 9201-9216 9251 9264 9308 9503 9515 9556 9646 9703 9928 10014-10017 10027 10094-10100 10102 10267 10496 10606-10608 10643-10650 10696 10891 11145 11223-11225 11344-11355 11406-11407 11420 11513 11604 11695 11791 11950 12022 12107 12191-12199 12315-12331 12363 12375 12405 12428-12430 12688 12706 12735 12748 12754 12812-12813 12815 12835 12914 12959 13020 13023- 13025 13060 13073 13300 13351-13358 13402-13403 13489 13496 13506 13512 13719-13720 13765-13768 13770 13872 13883
thymus	Clontech	THM001	51 142 150 332 346 360 438 546 731 760 895 1004 1104 1227- 1234 1264 1391 1516 1577-1585 1812 1860 1877 2129 2174 2215 2263 2321-2322 2408 2414 2425 2449 2490 2555 2569 2575 2611 2847 2880 3435 3530 3722 3727 3733 3735-3742 3839 3870 4006 4041 4043-4046 4060 4109 4375 4396 4399 4434 4667 4671 4759 4791 4885 4976 4987 5108 5289-5290 5466 5481 5526 5553-5554 5796 5956 5979 6020 6186 6253 6336 6371 6411 6438 6441-6447 6617-6621 6765 6788 6797 6870 6886 6908 6972 6994 7059-7060 7126 7141 7166 7168 7310 7383 7450 7494 7632 7716 7779 7887 7889-7891 8087 8111-8114 8117-8120 8139 8226 8343 8368 8370 8452 8456 8635 8830 8898 8921 8963 9010 9076 9086-9087 9128 9134 9264 9304 9307-9313 9401 9466 9497 9544 9563 9582 9612 9626 9646 9758 9781 9927 9937 9969 10018 10065 10163- 10166 10175 10284 10329 10414 10557 10609-10610 10617 10679 10687-10691 10742 10760 10772 10776 10778 10881 10891 11187 11194 11226-11229 11274 11406 11408-11410 11412 11459 11513 11676 11695 11830 11865 11942 12000 12006 12016 12022 12092 12160 12186 12200-12204 12327 12363 12414-12417 12427 12462 12470 12490 12564 12693 12706 12735 12740 12835 12840 12898 12905 12910 12913- 12914 12916 12977 13020 13036 13051 13062 13111 13126 13141 13295 13301-13305 13326 13351 13391 13396-13397 13456 13484 13498 13505 13507 13512 13516 13546 13713 13803 13805 13808 13866 13869 13885 13888
thymus	Clontech	THMc02	16 27 51 67 142 390 598 1233 1493 1508 1585-1588 1598-1603 1724 1841 1918 1927 1959 1976 1979 1989 2057 2107 2161 2223 2290 2407 2426-2428 2432-2433 2444 2487 2569 2617 3537 3664 3711 3720 3722 3737 3780 3817 4021 4025 4047- 4049 4060 4063-4068 4246 4277 4377 4405 4688 4694 4759 4791 4837 4949 4957 4992 4998 5037 5052 5108 5505 5553 5555-5564 5571-5572 5683 5766 5772 5788 5796 5894 5911 6048 6186 6225 6288 6306 6333 6621 6728 6730 6765 6767 6780 6788 6815 6867 6873 6979 7049 7061-7062 7166 7169 7676 7687 7809 8084 8121 8129-8130 8179 8262 8354 8363 8365 8375 8482 8597 8654 8740 8786 8791 8963 9076 9157 9257 9264 9314 9323-9324 9401 9454 9466 9519 9529 9536 9637 9700 9703 9927-9929 9940 10004 10007 10070 10167 10169-10172 10180 10182 10267 10284 10326 10331 10383 10439 10452 10542 10605 10691 10693-10694 10697 10744 10775 10778 10795 11046 11098 11274 11413-11415 11462 11519 11576 11592 11606 11618 11621 11627-11628 11693 11807 11814 12022 12034 12044 12080-12081 12086 12160 12236 12256 12327 12335 12363 12368 12387 12418-12419 12424 12433 12556 12560 12564 12570 12577 12594 12599 12612 12663 12735 12754 12836-12839 12844 12905 12913

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12955 12977 13020 13035 13037 13051 13062 13072 13087 13193 13280 13295 13398 13404 13456 13488 13499-13500 13503 13507 13516 13533 13535 13546 13611 13613 13630 13646 13649 13659 13670 13678-13679 13713 13769 13775 13803 13806-13808 13810-13811 13869 13872 13882-13883 13885 13888-13889
thyroid gland	Clontech	THR001	49 115 142 360 641 698 800 1004 1134 1193 1233 1235 1237- 1241 1329 1433-1471 1473-1476 1478-1481 1589-1591 1593-1594 1604 1606-1612 1614-1615 1639 1671 1906 1927 1959 1976 1994 2090 2099 2134 2150 2161 2174 2186 2215 2343 2367 2381-2387 2429 2434-2437 2449 2490 2510 2529 2535 2569 2662 2827 2901 2961 2997 3001 3109 3265 3286 3425 3490 3503 3560 3643 3698 3722 3737 3743-3747 3797 3839 3885 3923-3941 3943-3954 3956-3961 4009 4050-4053 4060 4069-4082 4109 4173 4194 4253 4277 4282 4348 4354- 4355 4376 4391 4396 4412 4434 4641 4689 4694 4755 4759 4783 4791 4834 4957 4972 4985 4987 5018 5037 5052 5075- 5076 5108 5147 5163 5171 5270 5292-5294 5317 5380 5450- 5461 5464-5481 5503 5523 5565-5568 5573-5574 5693 5711 5724 5757 5772 5788 5894-5895 5917 5923 5938 5959 5966 6005 6013 6027 6047-6048 6061 6064 6125 6135 6139 6189 6215 6240 6336 6371 6374 6448-6449 6458 6508 6538 6551- 6554 6556-6561 6563-6572 6595 6598 6607 6622-6623 6631- 6636 6793 6803 6815 6873 6899 6955 6958 7032-7038 7040 7043 7063 7066-7067 7079 7116 7155 7233 7275 7455 7669 7743 7792 7839 7845 7857 7892-7893 7910 7930 7989 8006- 8008 8010-8033 8053 8067 8087 8092-8093 8110 8116 8120 8122-8124 8131-8143 8196 8226 8235 8262 8345 8365 8368 8370 8372 8375 8452 8520 8535 8543 8597 8646 8711 8760 8816 8839 8863 8898 8930 8948 8951 8963 8966 9010 9055 9088-9091 9142 9157 9217-9220 9222-9227 9229-9242 9244 9257 9264 9304 9315-9316 9325-9330 9368 9401 9455 9466 9484 9525 9542 9544 9563 9646 9695 9703 9780-9781 9855 9928 9942 9947 10000 10019 10027 10103-10117 10119-10120 10173-10175 10183-10185 10346 10376 10440 10470 10496 10611 10651-10657 10666 10679 10695 10698-10704 10760 10772 10778 10782 10788 10891 11033 11051-11052 11061 11063 11112 11231 11256 11356-11357 11359-11360 11362- 11367 11369-11372 11376 11385 11406 11416 11421-11425 11462 11513 11588 11605-11607 11620 11833 11869 11932 11980 11985 12006 12017 12033 12143 12160 12193 12195 12205 12207-12208 12292 12332-12336 12338-12345 12347 12349-12356 12358-12360 12363 12368 12405 12420 12422 12424 12428 12434-12439 12465 12523 12601 12605 12609- 12611 12617 12636 12645 12670 12691 12707 12740 12749 12754 12768 12775 12777 12817-12824 12830 12840 12845- 12848 12863 12911 12940 12955 12977 13020 13026-13028 13038 13047 13051 13062 13072-13073 13090 13104 13117 13126 13195 13202 13254 13295-13296 13360-13371 13389 13391 13399 13412 13479 13488-13489 13492 13494 13498 13500 13503-13504 13506-13507 13511-13512 13516 13533 13551 13554 13590 13613 13627 13644 13646 13656 13659- 13660 13670 13713 13721 13743 13771-13774 13782 13803 13809 13812-13814 13860 13866-13867 13869 13872 13882 13884-13885 13888 13891 13893
trachea	Clontech	TRC001	83 438 483 858 1006 1034 1242-1245 1359 1483-1494 1616- 1619 1621 1671 2266 2324 2388-2391 2409 2438-2439 2444 2575 3001 3136 3272 3425 3460 3535 3548 3748-3756 3810 3962-3967 4083-4086 4530 4755 4758 4949 4957 4987 5075 5213 5295-5299 5481-5482 5484 5486-5488 5490-5491 5535 5576-5580 5656 5941 6091 6450-6453 6574-6578 6637 6797

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Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			6955 7041-7042 7049 7068 7204 7347 7733 7864 7894 8034-8043 8045 8120 8139 8144 8563 8635 8646 9012 9092-9099 9245-9251 9317 9331 9333 9484 9503 9517 9734 10020-10022 10027 10097 10121-10123 10125-10127 10284 10344 10478 10612 10658-10659 10705 10812 10948 11145 11233-11239 11373-11376 11428-11429 11942 12022 12209-12211 12292 12361-12363 12365-12366 12438 12440-12441 12611 12617 12734-12735 12825-12826 12900 12904-12905 12916 12923 12965 12972 12976 12989 13029-13030 13306-13308 13372-13373 13492 13670 13713 13722 13775-13781 13803 13884
uterus	Clontech	UTR001	1036 1134 1246-1250 1324 1493 1495-1511 1622 1671 1928 2145 2266 2310 2326 2343 2367 2392-2397 2555 3281 3479 3720 3757-3760 3762 3969-3986 4088-4090 4192 4201 4246 4277 4390-4391 4434 4515 4998 5002 5184 5300-5301 5481 5492-5504 5656 5695 5712 5794 5936 6116 6475 6579-6587 6595 6870 7002 7043-7044 7311 7484 7895-7899 8046-8055 8057-8059 8061 8110 8146-8147 8152 8226 8262 8622 8677 9008 9092 9137 9252-9257 9334 9370 9414 9466 9539 9703 10023-10024 10128-10134 10346 10595 10660-10668 10706-10708 11145 11239 11289 11377 11379-11385 11695 11850 12367-12369 12371-12374 12442-12443 12570 12670 12693 12827-12829 12914 13002 13047 13073 13083-13084 13131 13260 13277 13309-13310 13374-13376 13394 13489 13512 13713 13782 13784-13787 13866 13869



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TABLE 2

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1	M36501	Homo sapiens	alpha-2-macroglobulin	118	69
2	AF118090	Homo sapiens	PRO2044	247	59
3	X01683	Homo sapiens	alpha 1-antitrypsin	544	78
4	L27428	Homo sapiens	reverse transcriptase	79	27
5	M22332	Homo sapiens	unknown protein	89	40
6	AF015539	Mytilus edulis	precollagen P	113	33
7	X03325	Homo sapiens	apolipoprotein B fragment	540	83
8	AB019280	Mus musculus	sprouty-4	91	35
9	D88152	Homo sapiens	acetyl-coenzyme A transporter	625	87
10	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	124	58
11	AL049569	Homo sapiens	dJ37C10.5 (K1AA0445)	182	82
12	AJ242540	Volvox carterii f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	85	37
13	L27428	Homo sapiens	reverse transcriptase	135	61
14	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	266	72
15	U93569	Homo sapiens	putative p150	135	37
16	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	132	67
17	X53581	Rattus norvegicus	ORF4	124	34
18	AF183961	Homo sapiens	carbon catabolite repression 4 protein homolog	431	75
19	AJ002190	Homo sapiens	dihydroxyacetone phosphate acyltransferase	551	88
20	Y12713	Mus musculus	Pro-Pol-DTPase polypeptide	127	45
21	AK001269	Homo sapiens	unnamed protein product	1643	99
22	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	275	58
23	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	123	75
24	AF156550	Mus musculus	putative E1-E2 ATPase	168	58
25	AF119856	Homo sapiens	PRO1851	585	83
26	U49974	Homo sapiens	mariner transposase	187	46
27	G00901	Homo sapiens	Human secreted protein, SEQ ID NO: 4982.	86	30
28	AF295773	Homo sapiens	ral guanine nucleotide dissociation stimulator	126	74
29	AF113685	Homo sapiens	PRO0974	92	73
30	U83303	Homo sapiens	line-1 reverse transcriptase	102	50
31	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	279	75
32	AF003535	Homo sapiens	ORF2-like protein	114	47
33	M15386	Homo sapiens	gamma-globin	370	84
34	M19419	Mus musculus	proline-rich salivary protein	110	35
35	AF211943	Homo sapiens	WW domain-containing protein WWOX	585	83
36	X13885	Nicotiana tabacum	extensin (AA 1-620)	103	35
37	U93563	Homo sapiens	putative p150	127	58
38	U93564	Homo sapiens	putative p150	103	77
39	AF069732	Homo sapiens	ADA2-like protein	524	88
40	X61046	Hydra sp.	mini-collagen	101	34
41	AK000322	Homo sapiens	unnamed protein product	566	80
42	G03646	Homo sapiens	Human secreted protein, SEQ ID NO: 103	103	57

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7727.		
43	AF071081	Mycobacterium tuberculosis	proline-rich mucin homolog	104	41
44	AF092135	Homo sapiens	PTD014	228	41
45	Y73353	Homo sapiens	HTRM clone 1870914 protein sequence.	293	56
46	AF118082	Homo sapiens	PRO1902	119	44
47	X78926	Homo sapiens	zinc finger protein	442	52
48	X54326	Homo sapiens	glutamyl-tRNA synthetase	542	81
49	D50645	Homo sapiens	SDF2	321	95
50	M92439	Homo sapiens	leucine-rich protein	344	80
51	U28963	Homo sapiens	Gps2	593	82
52	U41806	Homo sapiens	p60	660	81
53	AF181490	Homo sapiens	prenylcysteine lyase	461	78
54	U93570	Homo sapiens	putative p150	147	36
55	W73499	Homo sapiens	Von Willebrand factor.	529	76
56	AF119851	Homo sapiens	PRO1722	126	57
57	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	115	61
58	AL021939	Homo sapiens	JF352A20.2 (aldehyde dehydrogenase family protein)	422	90
59	L24158	Homo sapiens	integrin alpha 9 protein	117	71
60	Y32157	Homo sapiens	Human SH3D1A protein.	530	91
61	X61296	Rattus norvegicus	open reading frame 2	117	31
62	AK002064	Homo sapiens	unnamed protein product	330	80
63	AB012223	Canis familiaris	ORF2	80	56
64	U93570	Homo sapiens	putative p150	113	37
65	U15647	Mus musculus	reverse transcriptase	152	55
66	G05411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	126	54
67	Y48359	Homo sapiens	Human prostate cancer-associated protein 56.	590	99
68	W74879	Homo sapiens	Human secreted protein encoded by gene 151 clone HTLEF62.	368	98
69	AF104921	Homo sapiens	succinyl-CoA synthetase alpha subunit	604	93
70	AF175265	Homo sapiens	vacuolar sorting protein 35	632	88
71	U93571	Homo sapiens	p40	106	33
72	X15324	Homo sapiens	angiotensinogen	330	84
73	Z98204	Hordeum vulgare	extensin	111	38
74	Y30713	Homo sapiens	Amino acid sequence of a human secreted protein.	232	61
75	AF118092	Homo sapiens	PRO2061	453	79
76	M63175	Homo sapiens	autocrine motility factor receptor	190	85
77	M26361	Mus musculus	LINE/Ig H-chain fusion protein	153	38
78	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	171	58
79	X78926	Homo sapiens	zinc finger protein	199	37
80	M77381	Homo sapiens	acrosin	98	54
81	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	129	44
82	U93569	Homo sapiens	putative p150	94	38
83	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
84	AF255446	Cryptocodium cohnii	Dip1-associated protein C	129	34
85	R59837	Homo sapiens	Sequence of human microtubule-	82	48

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			associated protein tau.		
86	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	157	76
87	AF116712	Homo sapiens	PRO2738	91	58
88	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	77	44
89	Y82742	Homo sapiens	DNA replication and repair associated protein (DRASP).	315	79
90	M16961	Homo sapiens	alpha-2-HS-glycoprotein	138	74
91	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	250	56
92	AF220656	Homo sapiens	apoptosis-associated nuclear protein PHLDA1	62	69
93	U65928	Homo sapiens	Jun activation domain binding protein	188	75
94	U93568	Homo sapiens	putative p150	102	48
95	S80119	Rattus sp.	reverse transcriptase homolog	130	53
96	U93563	Homo sapiens	putative p150	242	50
97	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	105	46
98	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	132	62
99	X74045	Equus caballus	preproalbumin	289	65
100	AF118090	Homo sapiens	PRO2044	269	90
101	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	198	51
102	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	88	53
103	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	225	82
104	AF003535	Homo sapiens	ORF2-like protein	114	47
105	AF130079	Homo sapiens	PRO2852	133	56
106	AF130089	Homo sapiens	PRO2550	107	71
107	M63473	Homo sapiens	alpha-5 type IV collagen	131	45
108	AF116661	Homo sapiens	PRO1438	112	54
109	X92485	Plasmodium vivax	pva1	101	41
110	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	80
111	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	199	69
112	AF194537	Homo sapiens	NAG13	104	44
113	L27428	Homo sapiens	reverse transcriptase	160	34
114	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	137	56
115	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	191	67
116	AF130052	Homo sapiens	PRO0956	163	47
117	L27428	Homo sapiens	reverse transcriptase	117	36
118	U93569	Homo sapiens	putative p150	104	66
119	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	96	66
120	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	81	57
121	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	78	51
122	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	95	80
123	X61296	Rattus norvegicus	open reading frame 2	94	36
124	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	131	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
125	AF119900	Homo sapiens	PRO2822	168	68
126	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	209	58
127	L27428	Homo sapiens	reverse transcriptase	102	35
128	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	99	63
129	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	73
130	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	170	36
131	U93572	Homo sapiens	putative p150	168	38
132	U37263	Homo sapiens	KRAB zinc finger protein; Method: conceptual translation supplied by author	155	57
133	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	137	92
134	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	58	61
135	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	66
136	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	102	38
137	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	230	55
138	AK000496	Homo sapiens	unnamed protein product	127	46
139	X53581	Rattus norvegicus	ORF4	136	38
140	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	158	48
141	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	162	65
142	AF090930	Homo sapiens	PRO0478	127	65
143	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	141	58
144	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	98	65
145	AJ238588	Sciurus vulgaris	cytochrome c oxidase subunit III	417	72
146	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	139	76
147	Y36156	Homo sapiens	Human secreted protein #28.	91	40
148	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	121	70
149	Y76184	Homo sapiens	Human secreted protein encoded by gene 61.	214	85
150	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	95	57
151	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	126	66
152	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	105	51
153	AF119900	Homo sapiens	PRO2822	116	62
154	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	149	66
155	AB009993	Mus musculus	collagen a1(V)	105	36
156	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	155	69
157	V00662	Homo sapiens	URF I (NADH dehydrogenase subunit)	348	71
158	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	146	54
159	AF247705	Oryctolagus cuniculus	alpha 1 type X collagen	102	42

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
160	R95913	Homo sapiens	Neural thread protein.	99	56
161	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	52
162	X71442	Rattus norvegicus	ORF 1; putative	96	47
163	U93570	Homo sapiens	putative p150	118	38
164	U23515	Caenorhabditis elegans	weak similarity to adenylyl cyclase-associated protein (CAP) and to P. chabaudi adami major merozoite surface antigen protein (PIR:A32555). Final exon overlaps gene predicted on other strand.	93	37
165	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	143	66
166	AF130079	Homo sapiens	PRO2852	143	90
167	L27428	Homo sapiens	reverse transcriptase	200	53
168	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	92	51
169	R95913	Homo sapiens	Neural thread protein.	116	54
170	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	324	85
171	U83303	Homo sapiens	line-1 reverse transcriptase	111	50
172	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	111	69
173	AF130089	Homo sapiens	PRO2550	126	59
174	S80119	Rattus sp.	reverse transcriptase homolog	151	46
175	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	113	53
176	U15647	Mus musculus	reverse transcriptase	104	46
177	M24732	Homo sapiens	lamin-like protein	112	42
178	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	137	38
179	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	143	58
180	AF194537	Homo sapiens	NAG13	92	90
181	U93564	Homo sapiens	putative p150	131	53
182	U93574	Homo sapiens	putative p150	86	46
183	Y14166	Gallus gallus	attachment region binding protein	91	40
184	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	104	64
185	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	183	73
186	U93572	Homo sapiens	putative p150	139	64
187	M22332	Homo sapiens	unknown protein	79	41
188	Y87202	Homo sapiens	Human secreted protein sequence SEQ ID NO:241.	75	71
189	U70935	Peromyscus maniculatus	reverse transcriptase	132	37
190	S80119	Rattus sp.	reverse transcriptase homolog	172	43
191	AF194537	Homo sapiens	NAG13	81	75
192	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	112	64
193	X92485	Plasmodium vivax	pva1	96	40
194	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	112	45
195	L27428	Homo sapiens	reverse transcriptase	141	37
196	U93570	Homo sapiens	putative p150	201	41
197	X92485	Plasmodium vivax	pva1	120	48
198	AF130089	Homo sapiens	PRO2550	137	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
199	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	377	84
200	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	119	52
201	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	151	68
202	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	247	78
203	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	126	56
204	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	362	80
205	R59842	Homo sapiens	ApoE4L1 protease.	100	82
206	AF161356	Homo sapiens	HSPC093	78	62
207	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	111	48
208	U83280	Leishmania donovani	39 kDa antigen	121	53
209	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	84	80
210	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	146	72
211	M69197	Homo sapiens	haptoglobin-related protein	344	92
212	AF034611	Homo sapiens	intrinsic factor-B12 receptor precursor; cubilin	123	37
213	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	65
214	V00662	Homo sapiens	cytochrome oxidase I	485	87
215	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	124	80
216	U35312	Mus musculus	nuclear receptor co-repressor	115	47
217	L26953	Homo sapiens	chromosomal protein	143	77
218	U12690	Homo sapiens	cytochrome oxidase subunit II	224	70
219	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	125	75
220	AB018114	Arabidopsis thaliana	RING finger protein-like	111	38
221	D38112	Homo sapiens	ATPase subunit 6	475	84
222	V00662	Homo sapiens	cytochrome B	466	77
223	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	175	85
224	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	125	38
225	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	86	65
226	X77816	Rattus norvegicus	PR-Vbeta1	130	54
227	U09500	Homo sapiens	cytochrome b	274	62
228	AF081104	Mus musculus domesticus	ORF2	111	36
229	AF090942	Homo sapiens	PRO0657	88	57
230	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	76	57
231	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	101	66
232	B12310	Homo sapiens	Human secreted protein encoded by gene 10 clone HDPGP94.	116	54
233	AF010400	Homo sapiens	transaldolase-related protein	253	77
234	AF197913	Helicoverpa armigera nuclear polyhedrosis virus	basic DNA-binding protein BDBP	137	50

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
235	AF090931	Homo sapiens	PRO0483	123	75
236	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	185	86
237	M19503	Homo sapiens	ORF1; putative	99	40
238	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	93	58
239	AF014883	Homo sapiens	NADH dehydrogenase subunit 2	305	65
240	G03102	Homo sapiens	Human secreted protein, SEQ ID NO: 7183.	60	44
241	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	79	50
242	U15647	Mus musculus	reverse transcriptase	117	47
243	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	56
244	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	94	45
245	AK023542	Homo sapiens	unnamed protein product	82	38
246	X55702	Drosophila melanogaster	polycomb protein	84	31
247	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	129	65
248	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	154	70
249	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	142	63
250	Y17832	Human endogenous retrovirus K	env protein	297	71
251	U93568	Homo sapiens	p40	103	46
252	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	201	47
253	AF090895	Homo sapiens	PRO0117	139	60
254	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	185	72
255	L27428	Homo sapiens	reverse transcriptase	156	40
256	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	157	59
257	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	118	70
258	AF194537	Homo sapiens	NAG13	141	38
259	B01372	Homo sapiens	Neuron-associated protein.	115	71
260	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	113	53
261	M22332	Homo sapiens	unknown protein	78	45
262	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	70	78
263	X61296	Rattus norvegicus	open reading frame 2	108	36
264	AF016099	Mus musculus	endonuclease/reverse transcriptase	178	45
265	G03303	Homo sapiens	Human secreted protein, SEQ ID NO: 7384.	81	63
266	Y01154	Homo sapiens	Protein sequence Seq Id 54 from WC0901020.	116	84
267	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	118	52
268	AF119855	Homo sapiens	PRO1847	74	70
269	AF109907	Homo sapiens	S164	85	61
270	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	137	63
271	X92485	Plasmodium vivax	pva1	107	72
272	AF194537	Homo sapiens	NAG13	167	51

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
273	U93564	Homo sapiens	p40	104	40
274	L27428	Homo sapiens	reverse transcriptase	142	56
275	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	150	60
276	X61296	Rattus norvegicus	open reading frame 2	96	48
277	AF090931	Homo sapiens	PRO0483	140	65
278	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	231	66
279	AF130089	Homo sapiens	PRO2550	164	60
280	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	98	58
281	L22548	Homo sapiens	collagen type XVIII alpha 1	92	38
282	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	68
283	AF116715	Homo sapiens	PRO2829	160	75
284	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	111	53
285	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	94	53
286	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	120	53
287	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	147	66
288	U93572	Homo sapiens	putative p150	125	32
289	AL050399	Arabidopsis thaliana	putative proline-rich protein	142	44
290	X92485	Plasmodium vivax	pva1	147	43
291	AB047600	Macaca fascicularis	hypothetical protein	172	66
292	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	108	55
293	D38115	Pongo pygmaeus	NADH dehydrogenase subunit 5	342	71
294	AF090942	Homo sapiens	PKO0657	99	66
295	M61185	Bos taurus	glutamic acid-rich protein	114	44
296	M13100	Rattus norvegicus	unknown protein	107	43
297	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	114	50
298	X92485	Plasmodium vivax	pva1	93	78
299	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	127	75
300	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	115	42
301	L24521	Homo sapiens	transformation-related protein	117	60
302	X83413	Human herpesvirus 6	U88	219	49
303	U93567	Homo sapiens	putative p150	130	48
304	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	72	61
305	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	153	68
306	D38112	Homo sapiens	cytochrome c oxidase subunit 3	532	79
307	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	84	53
308	L27428	Homo sapiens	reverse transcriptase	151	72
309	M69297	Homo sapiens	ORF 3	145	43
310	X92485	Plasmodium vivax	pva1	81	60
311	L27428	Homo sapiens	reverse transcriptase	103	41



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
312	AF130079	Homo sapiens	PRO2852	135	49
313	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	110	58
314	AF090928	Homo sapiens	PRO0470	88	48
315	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	175	64
316	U93568	Homo sapiens	putative p150	148	46
317	AF119855	Homo sapiens	PRO1847	108	84
318	P60839	Homo sapiens	Sequence of human serum albumin (HSA) on plasmid pXL53.	175	50
319	W46424	Homo sapiens	Human macrophage stimulating protein (MSP).	257	69
320	AL049547	Homo sapiens	d34F7.2 (CREB-RP (G13))	247	64
321	G02552	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	110	66
322	AF016099	Mus musculus	endonuclease/reverse transcriptase	102	48
323	AF090930	Homo sapiens	PRO0478	141	72
324	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	126	44
325	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	146	59
326	R59842	Homo sapiens	ApoE4L1 protease.	95	60
327	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	84	61
328	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	123	66
329	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	125	65
330	AF119855	Homo sapiens	PRO1847	121	80
331	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	364	71
332	AK000496	Homo sapiens	unnamed protein product	145	41
333	D00570	Mus musculus	open reading frame (196 AA)	153	53
334	AF119855	Homo sapiens	PRO1847	116	74
335	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	50
336	R13556	Homo sapiens	Protein encoded downstream of hbc_M oncoprotein.	129	56
337	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	107	59
338	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	115	72
339	AL359782	Trypanosoma brucei	possible (hly-6) u1102, variant a dna, complete virion genome.	117	50
340	AK022217	Homo sapiens	unnamed protein product	127	70
341	U43360	Peromyscus maniculatus	reverse transcriptase	115	75
342	AF118086	Homo sapiens	PRO1992	141	73
343	X92485	Plasmodium vivax	pva1	96	59
344	AF106677	Drosophila melanogaster	dissatisfaction	90	48
345	U12693	Homo sapiens	cytochrome oxidase subunit II	239	91
346	L27428	Homo sapiens	reverse transcriptase	95	56
347	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	133	69
348	G02552	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	81	51
349	X51616	Volvox carteri	SULFATED SURFACE GLYCOPROTEIN 185	110	41

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
350	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	158	55
351	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	183	60
352	AI390114	Leishmania major	extremely cysteine/valine rich protein	151	51
353	R95913	Homo sapiens	Neural thread protein.	95	56
354	AF061340	Artibeus jamaicensis	cytochrome c oxidase subunit III	346	70
355	AF090895	Homo sapiens	PRO0117	126	60
356	AF016099	Mus musculus	endonuclease/reverse transcriptase	121	48
357	AF118086	Homo sapiens	PRO1992	159	73
358	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	85	89
359	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	98	50
360	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	110	57
361	M13100	Rattus norvegicus	unknown protein	122	34
362	Y36203	Homo sapiens	Human secreted protein #75.	108	63
363	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	83	75
364	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	212	65
365	AF130051	Homo sapiens	PRO0898	136	71
366	AF068294	Homo sapiens	HDICMB45P	188	65
367	M10546	Homo sapiens	cytochrome oxidase I	225	70
368	S80119	Rattus sp.	reverse transcriptase homolog	188	45
369	U70935	Peromyscus maniculatus	reverse transcriptase	75	48
370	AF118082	Homo sapiens	PRO1902	98	79
371	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	106	40
372	AF014903	Pan troglodytes	NADH dehydrogenase subunit 2	169	41
373	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	93	48
374	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	66
375	G03107	Homo sapiens	Human secreted protein, SEQ ID NO: 7188.	90	80
376	U93568	Homo sapiens	putative p150	140	56
377	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	140	50
378	AF090942	Homo sapiens	PRO0657	154	66
379	U93568	Homo sapiens	putative p150	149	36
380	U93570	Homo sapiens	p40	184	57
381	L27428	Homo sapiens	reverse transcriptase	128	60
382	AF194537	Homo sapiens	NAG13	114	35
383	AF116712	Homo sapiens	PRO2738	109	56
384	D38112	Homo sapiens	cytochrome c oxidase subunit 3	405	81
385	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	63
386	M22334	Homo sapiens	unknown protein	124	39
387	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	97	52
388	D38112	Homo sapiens	NADH dehydrogenase subunit 5	327	94
389	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	157	70
390	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	129	62
391	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	259	66

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
392	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	137	63
393	U43360	Peromyscus maniculatus	reverse transcriptase	129	54
394	AK023582	Homo sapiens	unnamed protein product	148	46
395	M22332	Homo sapiens	unknown protein	128	41
396	AF118086	Homo sapiens	PRO1992	160	71
397	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	101	52
398	D38112	Homo sapiens	cytochrome c oxidase subunit 3	199	66
399	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	234	78
400	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein thala.	107	40
401	AF000996	Homo sapiens	ubiquitous TPR motif, Y isoform	116	61
402	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	145	37
403	AF118082	Homo sapiens	PRO1902	97	55
404	AF020635	Homo sapiens	PP1200	126	55
405	V00662	Homo sapiens	cytochrome oxidase I	352	68
406	AF229067	Homo sapiens	PADI-H protein	129	71
407	AL390114	Leishmania major	extremely cysteine/valine rich protein	197	38
408	L26251	Trypanosoma brucei	CR5	95	46
409	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	310	62
410	X92485	Plasmodium vivax	pva1	96	68
411	M64793	Rattus norvegicus	salivary proline-rich protein	128	40
412	Y19192	Talpa europaea	cytochrome oxidase subunit I	431	83
413	M10546	Homo sapiens	cytochrome oxidase I	299	86
414	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	220	81
415	AF205385	Pan troglodytes	NADH dehydrogenase subunit 5	296	89
416	X58438	Mus musculus	proline rich protein	112	50
417	U70932	Peromyscus leucopus	reverse transcriptase	89	51
418	V00662	Homo sapiens	cytochrome oxidase III	200	84
419	AF017789	Homo sapiens	putative transcription factor CA150	120	41
420	M10546	Homo sapiens	cytochrome oxidase I	183	69
421	AL359782	Trypanosoma brucei	possible (hhv-6) u1 102, variant a dna, complete virion genome.	166	44
422	AF130051	Homo sapiens	PRO0898	158	59
423	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	86	52
424	D38116	Pan paniscus	cytochrome c oxidase subunit 3	342	82
425	U93570	Homo sapiens	putative p150	133	41
426	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	67
427	D13951	Nicotiana glauca	extensin precursor	140	42
428	L27428	Homo sapiens	reverse transcriptase	104	34
429	R95913	Homo sapiens	Neural thread protein.	118	49
430	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	206	97
431	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	88	55
432	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	98	54
433	J05042	Oryctolagus	alpha-1 (VIII) collagen precursor	91	48

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		cuniculus			
434	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	105	56
435	U93572	Homo sapiens	putative p150	118	38
436	U93569	Homo sapiens	putative p150	100	30
437	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	126	81
438	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	71
439	U52077	Homo sapiens	mariner transposase	187	52
440	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	80	45
441	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	71
442	AE003727	Drosophila melanogaster	CG 16718 gene product	301	48
443	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	221	74
444	U35730	Mus musculus	jerky	159	26
445	X53581	Rattus norvegicus	ORF3	192	46
446	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	142	52
447	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	156	38
448	AF194537	Homo sapiens	NAG13	315	70
449	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	93	66
450	X92099	Brugia pahangi	collagen	126	44
451	AF090930	Homo sapiens	PRO0478	88	60
452	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	93	40
453	AF081114	Mus musculus domesticus	ORF2	108	32
454	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	173	65
455	S80119	Rattus sp.	reverse transcriptase homolog	197	54
456	G02535	Homo sapiens	Human secreted protein, SEQ ID NO: 6616.	89	68
457	R95913	Homo sapiens	Neural thread protein.	114	48
458	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	160	39
459	X92485	Plasmodium vivax	pva1	99	52
460	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	100	52
461	S80119	Rattus sp.	reverse transcriptase homolog	138	48
462	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	211	67
463	X97707	Pongo pygmaeus abelii	stopcodon created by posttranscriptional polyadenylation	229	76
464	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	119	67
465	L27428	Homo sapiens	reverse transcriptase	154	40
466	AK000496	Homo sapiens	unnamed protein product	140	69
467	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	114	61
468	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	146	69
469	D38112	Homo sapiens	cytochrome c oxidase subunit 3	286	79
470	D38112	Homo sapiens	NADH dehydrogenase subunit 4	448	86
471	M10546	Homo sapiens	cytochrome oxidase I	296	79

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
472	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	102	48
473	AL080253	Arabidopsis thaliana	putative snRNP protein	103	42
474	X99452	Lycopersicon esculentum	extensin-like protein Dif54	108	25
475	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	68	34
476	AB012223	Canis familiaris	ORF2	78	66
477	AF130089	Homo sapiens	PRO2550	113	71
478	G03652	Homo sapiens	Human secreted protein, SEQ ID NO: 7733.	390	97
479	AF210651	Homo sapiens	NAG18	146	80
480	AB029309	Homo sapiens	Npw38-binding protein NpwBP	103	40
481	AF194537	Homo sapiens	NAG13	118	31
482	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	115	45
483	L27428	Homo sapiens	reverse transcriptase	184	47
484	U93570	Homo sapiens	putative p150	101	50
485	AF194537	Homo sapiens	NAG13	213	52
486	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	82
487	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	204	86
488	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	140	53
489	U93574	Homo sapiens	putative p150	86	54
490	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	83	56
491	AJ271872	Nicotiana sylvestris	extensin	220	47
492	U11288	Drosophila melanogaster	diaphanous protein	113	33
493	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	184	70
494	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	68
495	AF119900	Homo sapiens	PRO2822	148	65
496	AB026542	Homo sapiens	WASP-family protein	96	38
497	D86853	Catharanthus roseus	extensin	104	34
498	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	109	47
499	G00492	Homo sapiens	Human secreted protein, SEQ ID NO: 4573.	109	67
500	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	112	62
501	AF119901	Homo sapiens	PRO2831	116	82
502	AF238235	Entamoeba histolytica	diaphanous protein	120	41
503	M22332	Homo sapiens	unknown protein	123	49
504	AF119851	Homo sapiens	PRO1722	204	52
505	X61296	Rattus norvegicus	open reading frame 2	107	45
506	AF118082	Homo sapiens	PRO1902	145	52
507	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	103	68
508	X55685	Lycopersicon esculentum	extensin (class I)	175	39
509	X92485	Plasmodium	pva1	117	52

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
510	AF090942	Homo sapiens	PRO0657	95	77
511	U93569	Homo sapiens	putative p150	120	54
512	U93574	Homo sapiens	putative p150	140	49
513	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	196	63
514	L27428	Homo sapiens	reverse transcriptase	132	37
515	U93565	Homo sapiens	putative p150	101	45
516	U93574	Homo sapiens	putative p150	178	35
517	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	81	27
518	AF053538	Alvinella pompejana	fibrillar collagen chain FAp1 alpha	112	36
519	X52235	Homo sapiens	ORFII	148	35
520	AF130051	Homo sapiens	PRO0898	98	61
521	L02106	Drosophila melanogaster	ribonucleoprotein	143	40
522	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	202	70
523	U93570	Homo sapiens	putative p150	159	43
524	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	210	100
525	L27428	Homo sapiens	reverse transcriptase	128	38
526	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	96	65
527	X53581	Rattus norvegicus	ORF4	130	42
528	U93570	Homo sapiens	putative p150	195	35
529	AF130089	Homo sapiens	PRO2550	132	43
530	AK024455	Homo sapiens	FLJ00047 protein	126	54
531	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	123	61
532	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	210	44
533	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	109	42
534	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	120	62
535	M64793	Rattus norvegicus	salivary proline-rich protein	124	37
536	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	122	50
537	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	118	43
538	A23786	Beta vulgaris	chitinase 1	91	33
539	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	39
540	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	102	67
541	S80119	Rattus sp.	reverse transcriptase homolog	191	50
542	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	155	77
543	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	125	91
544	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	146	62
545	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	74	45
546	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCAC381.	94	75
547	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	510	86
548	AF000616	Oryza sativa	similar to RING-H2 finger protein	146	68

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SEQ ID NO.	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			RHA1a (AF078683)		
549	Y08061	Homo sapiens	Human c-myc protein fragment.	128	82
550	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	153	77
551	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	121	56
552	X92485	Plasmodium vivax	pva1	103	50
553	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	129	46
554	L27428	Homo sapiens	reverse transcriptase	149	44
555	AF194537	Homo sapiens	NAG13	157	45
556	Y13247	Homo sapiens	FB19 protein	106	42
557	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	100	54
558	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	176	68
559	S80119	Rattus sp.	reverse transcriptase homolog	113	43
560	AY008270	Homo sapiens	cholesterol ester transfer protein	107	95
561	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	140	63
562	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	347	68
563	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	93	40
564	D38114	Gorilla gorilla	cytochrome c oxidase subunit 3 (COIII)	329	74
565	Y36156	Homo sapiens	Human secreted protein #28.	153	56
566	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	131	48
567	D38112	Homo sapiens	cytochrome c oxidase subunit 3	406	94
568	AF130079	Homo sapiens	PRO2852	101	55
569	AF081114	Mus musculus domesticus	ORF2	123	40
570	L22030	Glycine max	hydroxyproline-rich glycoprotein	65	45
571	D86853	Catharanthus roseus	extensin	168	39
572	AF104415	Mus musculus	gene trap locus-13	179	66
573	AF130089	Homo sapiens	PRO2550	114	56
574	X67863	Mus musculus	T2	115	42
575	S80119	Rattus sp.	reverse transcriptase homolog	101	28
576	S80119	Rattus sp.	reverse transcriptase homolog	150	57
577	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	142	74
578	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	106	57
579	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	46
580	L24521	Homo sapiens	transformation-related protein	110	38
581	D38112	Homo sapiens	cytochrome c oxidase subunit 3	537	84
582	AF090895	Homo sapiens	PRO0117	127	80
583	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	145	70
584	X55681	Lycopersicon esculentum	extensin (class I)	112	38
585	D38112	Homo sapiens	cytochrome c oxidase subunit 3	473	60
586	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	144	68
587	U47855	Araneus diadematus	fibroin-3	124	30
588	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	150	75
589	U93567	Homo sapiens	putative p150	225	47

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
590	X71602	Nicotiana tabacum	extensin	147	33
591	X57527	Homo sapiens	alpha 1(VIII) collagen	103	42
592	G03112	Homo sapiens	Human secreted protein, SEQ ID NO: 7193.	75	47
593	R28916	Homo sapiens	Type III procollagen (prior art).	116	48
594	R95913	Homo sapiens	Neural thread protein.	116	37
595	U11880	Petromyzon marinus	cytochrome oxidase subunit I	127	52
596	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	84	62
597	L27428	Homo sapiens	reverse transcriptase	158	40
598	M55251	Canis familiaris	glycoprotein 80	559	86
599	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
600	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	143	33
601	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	154	54
602	X73481	Drosophila hydei	mst101(2)	107	42
603	M81321	Macaca fascicularis	proline-rich protein	114	39
604	X05561	Homo sapiens	alpha-1 chain precursor (AA -27 to 917) (2953 is 2nd base in codon)	109	42
605	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	82	62
606	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	83	64
607	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhala.	107	44
608	L27428	Homo sapiens	reverse transcriptase	147	43
609	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438	113	61
610	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	151	82
611	U93568	Homo sapiens	putative p150	144	32
612	AB022223	Arabidopsis thaliana	extensin protein-like	186	58
613	Z70684	Caenorhabditis elegans	F28D1.8	108	49
614	M11901	Rattus norvegicus	proline-rich salivary protein	133	36
615	X92485	Plasmodium vivax	pva1	120	42
616	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	175	89
617	U83280	Leishmania donovani	39 kDa antigen	111	51
618	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	137	67
619	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	120	53
620	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	92	45
621	AF130089	Homo sapiens	PRO2550	123	34
622	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	133	59
623	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	127	45
624	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	205	66



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
625	X07882	Homo sapiens	Po protein	119	39
626	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	70	100
627	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	141	51
628	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	141	54
629	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	115	46
630	X63368	Homo sapiens	HSJ1b	151	52
631	AF130089	Homo sapiens	PRO2550	155	47
632	X92485	Plasmodium vivax	pva1	102	61
633	K03205	Homo sapiens	salivary proline-rich protein precursor	102	39
634	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	171	74
635	X92485	Plasmodium vivax	pva1	95	73
636	S80119	Rattus sp.	reverse transcriptase homolog	114	58
637	U15647	Mus musculus	reverse transcriptase	170	42
638	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	130	76
639	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	83	36
640	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	96	34
641	X61296	Rattus norvegicus	open reading frame 2	166	35
642	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	127	35
643	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP-CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	115	35
644	AF081111	Mus musculus domesticus	ORF2	168	33
645	AK027208	Homo sapiens	unnamed protein product	90	51
646	AF016099	Mus musculus	endonuclease/reverse transcriptase	101	59
647	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	149	76
648	AF273441	Pongo pygmaeus	NADH dehydrogenase subunit 3	121	58
649	L27428	Homo sapiens	reverse transcriptase	173	58
650	AF119851	Homo sapiens	PRO1722	176	53
651	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	168	68
652	AF130089	Homo sapiens	PRO2550	130	36
653	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	126	41
654	AK000385	Homo sapiens	unnamed protein product	195	63
655	AB041881	Rattus norvegicus	cytoplasmic dynein heavy chain	158	100
656	X61047	Hydra sp.	mini-collagen	60	38
657	M22332	Homo sapiens	unknown protein	100	50
658	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	143	62
659	AF194537	Homo sapiens	NAG13	95	48
660	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	120	50
661	U83303	Homo sapiens	line-1 reverse transcriptase	86	32
662	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	169	53
663	W48351	Homo sapiens	Human breast cancer related protein	120	72

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2.		
664	U15647	Mus musculus	reverse transcriptase	148	50
665	R95913	Homo sapiens	Neural thread protein.	161	59
666	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	134	80
667	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	117	44
668	AB018705	Mus musculus	ORF2	115	32
669	D38112	Homo sapiens	NADH dehydrogenase subunit 4	280	75
670	X53581	Rattus norvegicus	ORF4	71	39
671	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	201	66
672	R95913	Homo sapiens	Neural thread protein.	144	78
673	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	164	46
674	AF118082	Homo sapiens	PRO1902	137	49
675	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	91	43
676	D00570	Mus musculus	open reading frame (251 AA)	112	72
677	AF194537	Homo sapiens	NAG13	238	56
678	M13100	Rattus norvegicus	unknown protein	146	51
679	U15647	Mus musculus	reverse transcriptase	123	54
680	R95913	Homo sapiens	Neural thread protein.	145	55
681	R59842	Homo sapiens	ApoE4L1 protease.	107	63
682	AF130089	Homo sapiens	PRO2550	94	51
683	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	129	69
684	AF093748	Homo sapiens	KH type splicing regulatory protein; KSRP	93	50
685	U93569	Homo sapiens	putative p150	133	58
686	G03095	Homo sapiens	Human secreted protein, SEQ ID NO: 7176.	117	64
687	Y36243	Homo sapiens	Human secreted protein encoded by gene 20.	69	73
688	AF116712	Homo sapiens	PRO2738	133	56
689	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	134	53
690	U93563	Homo sapiens	putative p150	132	49
691	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	349	70
692	AF090895	Homo sapiens	PRO0117	115	63
693	AF130089	Homo sapiens	PRO2550	132	80
694	S80119	Rattus sp.	reverse transcriptase homolog	101	43
695	U15647	Mus musculus	reverse transcriptase	120	64
696	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	132	59
697	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	128	72
698	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	182	47
699	D38112	Homo sapiens	cytochrome c oxidase subunit 1	459	83
700	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	148	73
701	AF003535	Homo sapiens	ORF2-like protein	125	49
702	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	89	41
703	L27428	Homo sapiens	reverse transcriptase	255	50
704	AF130089	Homo sapiens	PRO2550	87	55
705	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 113	113	52

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7133.		
706	Y79140	Homo sapiens	Human haemopoietic stem cell regulatory protein SCM3.	211	88
707	U15647	Mus musculus	reverse transcriptase	94	47
708	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	153	66
709	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	107	50
710	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	163	64
711	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	65
712	U93565	Homo sapiens	putative p150	108	33
713	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	108	37
714	M24732	Homo sapiens	lamin-like protein	92	35
715	D38112	Homo sapiens	cytochrome c oxidase subunit 3	306	79
716	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	462	85
717	AF004715	Homo sapiens	jerky gene product homolog	100	42
718	X92485	Plasmodium vivax	pva1	84	48
719	AF130089	Homo sapiens	PRO2550	132	74
720	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	125	43
721	AK024455	Homo sapiens	FLJ00047 protein	108	68
722	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	146	46
723	X83413	Human herpesvirus 6	U88	269	41
724	X92485	Plasmodium vivax	pva1	117	43
725	X92485	Plasmodium vivax	pva1	97	41
726	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	102	73
727	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	118	43
728	A23786	Beta vulgaris	chitinase I	91	33
729	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	107	49
730	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	131	59
731	W49717	Homo sapiens	Protein polymer adhesive substrate PPAS1-C.	148	29
732	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	95	45
733	X96731	Ostertagia circumcincta	cuticular collagen	104	37
734	AF130089	Homo sapiens	PRO2550	118	40
735	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	166	100
736	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	494	86
737	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	188	69
738	D38112	Homo sapiens	cytochrome c oxidase subunit 3	593	91
739	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	102	62

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
740	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	111	54
741	A23786	Beta vulgaris	chitinase I	106	36
742	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	71	72
743	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	184	61
744	AE003629	Drosophila melanogaster	CG17108 gene product	76	36
745	U93563	Homo sapiens	putative p150	145	50
746	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	68	66
747	AF217973	Homo sapiens	unknown	113	79
748	AC006161	Arabidopsis thaliana	putative CENP-B/ARS-binding protein-like protein	112	31
749	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	106	47
750	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	115	54
751	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	99	72
752	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	85	48
753	X92485	Plasmodium vivax	pval	89	73
754	U93563	Homo sapiens	putative p150	186	68
755	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	50
756	AF194537	Homo sapiens	NAG13	138	40
757	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	112	79
758	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	119	61
759	AF130079	Homo sapiens	PRO2852	138	40
760	X92485	Plasmodium vivax	pval	88	77
761	U93050	Mus musculus	poly(A) binding protein II	95	35
762	V01555	Human herpesvirus 4	BYRF1, encodes EBNA-2 (Dambaugh et al, 1984; Dillner et al, 1984)	80	41
763	V00662	Homo sapiens	ATPase 6	337	83
764	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	117	41
765	V00662	Homo sapiens	URF I (NADH dehydrogenase subunit)	423	81
766	R59513	Homo sapiens	Neural thread protein.	114	66
767	V00662	Homo sapiens	cytochrome oxidase I	223	83
768	D38112	Homo sapiens	NADH dehydrogenase subunit 4	268	83
769	V00662	Homo sapiens	cytochrome oxidase I	357	81
770	D38112	Homo sapiens	NADH dehydrogenase subunit 4	296	71
771	AF026211	Caenorhabditis elegans	Similar to cuticular collagen	95	39
772	AK024455	Homo sapiens	FLJ00047 protein	108	53
773	X92485	Plasmodium vivax	pval	95	39
774	AF130051	Homo sapiens	PRO0898	123	38
775	AB012223	Canis familiaris	ORF2	174	51
776	AB028664	Paratichthys olivaceus	cytochrome oxidase subunit-3	268	57
777	V00662	Homo sapiens	cytochrome oxidase I	436	85
778	X52235	Homo sapiens	ORFII	125	47
779	U93569	Homo sapiens	putative p150	235	49

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
780	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	262	76
781	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	239	70
782	AF090942	Homo sapiens	PRO0657	146	69
783	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	85	66
784	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	209	62
785	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	184	60
786	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	158	60
787	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	293	86
788	AF130089	Homo sapiens	PRO2550	153	64
789	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	131	57
790	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	100	51
791	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	116	80
792	Y36203	Homo sapiens	Human secreted protein #75.	104	77
793	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	117	58
794	AF090930	Homo sapiens	PRO0478	130	68
795	AK024455	Homo sapiens	FLJ00047 protein	114	61
796	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	141	70
797	AF130089	Homo sapiens	PRO2550	273	85
798	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	134	66
799	AF130051	Homo sapiens	PRO0898	162	80
800	G03560	Homo sapiens	Human secreted protein, SEQ ID NO: 7641.	179	70
801	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	75	51
802	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	103	34
803	D38484	Hyalobates syndactylus	Cytochrome C oxidase subunit 1 (COXI)	263	70
804	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	112	41
805	X92485	Plasmodium vivax	pval	103	38
806	AF194537	Homo sapiens	NAG13	285	51
807	AF121360	Drosophila melanogaster	DNZDHHC/NEW1 zinc finger protein 11	179	47
808	X92485	Plasmodium vivax	pval	131	46
809	D13951	Nicotiana tabacum	extensin precursor	88	41
810	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	174	73
811	U93565	Homo sapiens	putative p150	118	38
812	AF118082	Homo sapiens	PRO1902	88	54
813	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	132	42
814	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	114	50
815	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	113	43
816	K02576	Homo sapiens	salivary proline-rich protein 1	148	40

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
817	AF217449	Schistosoma mekongi	NADH dehydrogenase subunit 6	102	37
818	AB012223	Canis familiaris	ORF2	101	54
819	X71602	Nicotiana tabacum	extensin	162	45
820	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	154	36
821	R95913	Homo sapiens	Neural thread protein.	153	61
822	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	125	61
823	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	364	57
824	U43360	Peromyscus maniculatus	reverse transcriptase	121	48
825	AF194537	Homo sapiens	NAG13	224	58
826	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	437	72
827	AF051782	Homo sapiens	diaphanous 1	108	38
828	AF194537	Homo sapiens	NAG13	92	45
829	D38112	Homo sapiens	cytochrome c oxidase subunit 3	492	75
830	M64791	Rattus norvegicus	salivary proline-rich protein	110	46
831	X35685	Lycopersicon esculentum	extensin (class I)	108	31
832	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	117	34
833	U93564	Homo sapiens	putative p150	84	40
834	U93563	Homo sapiens	putative p150	262	54
835	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	214	80
836	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhla.	107	48
837	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	158	76
838	AF194537	Homo sapiens	NAG13	153	60
839	U52077	Homo sapiens	mariner transposase	344	67
840	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	104	46
841	W90847	Homo sapiens	Human lymphocyte targeted peptide #15.	130	92
842	M64791	Rattus norvegicus	salivary proline-rich protein	114	36
843	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	196	43
844	X92485	Plasmodium vivax	pva1	102	73
845	X61048	Hydra sp.	mini-collagen	106	41
846	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	48
847	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	54
848	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	128	68
849	AF194537	Homo sapiens	NAG13	141	46
850	U43360	Peromyscus maniculatus	reverse transcriptase	121	45
851	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	153	58
852	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	220	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
853	X92485	Plasmodium vivax	pva1	127	45
854	AF134305	Homo sapiens	Scar3	99	38
855	D38112	Homo sapiens	NADH dehydrogenase subunit 2	343	68
856	S80119	Rattus sp.	reverse transcriptase homolog	159	56
857	AF130089	Homo sapiens	PRO2550	112	40
858	AK024372	Homo sapiens	unnamed protein product	129	50
859	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	103	76
860	D38112	Homo sapiens	cytochrome c oxidase subunit 3	279	80
861	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	96	44
862	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	83	40
863	AF210651	Homo sapiens	NAG18	122	63
864	AF016099	Mus musculus	endonuclease/reverse transcriptase	109	51
865	X55685	Lycopersicon esculentum	extensin (class I)	115	34
866	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	107	80
867	X92485	Plasmodium vivax	pva1	105	41
868	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	127	62
869	X92485	Plasmodium vivax	pva1	105	38
870	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	90	56
871	Y27571	Homo sapiens	Human secreted protein encoded by gene No. 5.	128	72
872	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	123	36
873	AF130089	Homo sapiens	PRO2550	160	82
874	AF118082	Homo sapiens	PRO1902	143	65
875	U93564	Homo sapiens	putative p150	180	44
876	M10546	Homo sapiens	cytochrome oxidase I	248	75
877	U83303	Homo sapiens	line-1 reverse transcriptase	127	52
878	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	106	35
879	U11288	Drosophila melanogaster	diaphanous protein	93	46
880	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhala.	71	47
881	B08942	Homo sapiens	Human secreted protein sequence encoded by gene 18 SEQ ID NO:99.	95	40
882	AF130089	Homo sapiens	PRO2550	137	44
883	AF090942	Homo sapiens	PRO0657	142	73
884	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	97	60
885	X61296	Rattus norvegicus	open reading frame 2	106	43
886	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	91	57
887	X14963	Homo sapiens	collagen-like protein (447 AA)	130	51
888	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	117	55
889	L25616	Homo sapiens	CG1 protein	150	62
890	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	171	66
891	Y86472	Homo sapiens	Human gene 52-encoded protein	107	40

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			fragment, SEQ ID NO:387.		
892	X52318	Bos taurus	histone H2A.Z (AA 1-127)	356	79
893	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	102	46
894	D38112	Homo sapiens	cytochrome c oxidase subunit 1	173	75
895	X92485	Plasmodium vivax	pval	109	47
896	L76159	Homo sapiens	FRG1 gene product	100	35
897	D50926	Homo sapiens	The KIAA0136 gene product is novel.	280	89
898	X04011	Homo sapiens	precursor polypeptide	114	95
899	M90656	Homo sapiens	gamma-glutamylcysteine synthetase	101	90
900	R95913	Homo sapiens	Neural thread protein.	95	75
901	L27428	Homo sapiens	reverse transcriptase	81	47
902	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	104	53
903	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	105	76
904	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	126	37
905	AF130089	Homo sapiens	PRO2550	88	82
906	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	230	50
907	L27428	Homo sapiens	reverse transcriptase	114	64
908	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	142	71
909	U93570	Homo sapiens	putative p150	130	41
910	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	91	63
911	L27428	Homo sapiens	reverse transcriptase	168	46
912	X92485	Plasmodium vivax	pval	91	60
913	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	103	64
914	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	96	64
915	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	121	51
916	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	87	77
917	M12099	Mus musculus	proline-rich protein	129	44
918	M15530	Homo sapiens	B-cell growth factor	88	51
919	AF130079	Homo sapiens	PRO2852	158	88
920	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	103	77
921	X53581	Rattus norvegicus	ORF4	124	32
922	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	110	50
923	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	99	36
924	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	80	47
925	AC006127	Homo sapiens	BRG-1-HUMAN; nuclear protein GRB1; homeotic gene regulator; SNF2-BETA; MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR; POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4	442	92
926	L17318	Rattus norvegicus	proline-rich proteoglycan	126	39
927	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	321	76



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
928	AC006161	Arabidopsis thaliana	putative CENP-B/ARS-binding protein-like protein	97	35
929	X02873	Daucus carota	put. precursor	112	38
930	U93563	Homo sapiens	putative p150	125	70
931	AB012223	Canis familiaris	ORF2	202	50
932	AF053538	Alvinella pompejana	fibrillar collagen chain FAp1 alpha	114	37
933	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	107	57
934	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	283	54
935	U41017	Caenorhabditis elegans	repetitive region; weakly similar to E. gracilis major membrane skeletal protein (PIR:A43417)	107	33
936	U47855	Araneus diadematus	fibroin-3	109	33
937	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	95	43
938	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	108	50
939	M13101	Rattus norvegicus	unknown protein	121	40
940	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	117	46
941	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	88	62
942	L27428	Homo sapiens	reverse transcriptase	86	45
943	U93564	Homo sapiens	putative p150	279	40
944	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	110	48
945	L27428	Homo sapiens	reverse transcriptase	238	66
946	AF194537	Homo sapiens	NAG13	146	47
947	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	81	55
948	AC006161	Arabidopsis thaliana	putative CENP-B/ARS-binding protein-like protein	113	37
949	AF194537	Homo sapiens	NAG13	106	66
950	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSA WA27.	74	75
951	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	78	66
952	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	85	72
953	U44838	Glycine max	extensin	145	39
954	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	131	39
955	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	128	53
956	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	103	74
957	AF130089	Homo sapiens	PRO2550	120	37
958	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	115	71
959	AF090942	Homo sapiens	PRO0657	83	63
960	L27428	Homo sapiens	reverse transcriptase	121	30
961	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	157	68
962	AF090942	Homo sapiens	PRO0657	138	61
963	U83280	Leishmania donovani	39 kDa antigen	101	53
964	U93566	Homo sapiens	p40	102	31

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
965	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	104	63
966	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	136	40
967	AF090930	Homo sapiens	PRO0478	158	80
968	AB012223	Canis familiaris	ORF2	94	36
969	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	127	54
970	X53581	Rattus norvegicus	ORF4	163	43
971	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	109	56
972	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	82	47
973	Y69166	Homo sapiens	A mature human N-acetylglycosaminyl transferase protein.	95	80
974	G03095	Homo sapiens	Human secreted protein, SEQ ID NO: 7176.	74	51
975	U93574	Homo sapiens	putative p150	140	43
976	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	79	65
977	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	116	55
978	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	148	63
979	AF130114	Homo sapiens	PRO2459	121	61
980	K03202	Homo sapiens	salivary proline-rich protein precursor	99	40
981	AF116909	Homo sapiens	unknown	115	42
982	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	106	75
983	Y14674	Plasmodium falciparum	glutamate-cysteine ligase	106	66
984	AF229067	Homo sapiens	PADI-H protein	152	60
985	AF119900	Homo sapiens	PRO2822	142	48
986	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	70
987	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	106	60
988	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	81	51
990	U35730	Mus musculus	jerky	133	29
991	AF113685	Homo sapiens	PRO0974	136	63
992	U52077	Homo sapiens	mariner transposase	497	77
993	Z97211	Schizosaccharomyces pombe	kinesin-like protein	197	47
994	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	124	68
995	U93563	Homo sapiens	putative p150	157	50
996	AB015802	Acetobacter xylinus	similar to cellulose complementing protein of A. xylinum ATCC23869	140	54
997	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	144	60
998	D38116	Pan paniscus	cytochrome c oxidase subunit I	352	75
999	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	524	78
1000	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	377	70
1001	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	109	50
1002	AL390114	Leishmania major	extremely cysteine/valine rich protein	249	61
1003	M14702	Murine leukemia	pol polyprotein	206	48

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		virus			
1004	Z21507	Homo sapiens	human elongation factor-1-delta	511	85
1005	L27428	Homo sapiens	reverse transcriptase	176	63
1006	D38112	Homo sapiens	NADH dehydrogenase subunit 5	332	77
1007	AF090895	Homo sapiens	PRO0117	162	66
1008	G03102	Homo sapiens	Human secreted protein, SEQ ID NO: 7183.	140	65
1009	U44838	Glycine max	extensin	166	33
1010	AF251290	Plasmodium falciparum	glutamic acid-rich protein	114	52
1011	L27428	Homo sapiens	reverse transcriptase	114	52
1012	AF130089	Homo sapiens	PRO2550	114	77
1013	G04092	Homo sapiens	Human secreted protein, SEQ ID NO: 8173.	81	44
1014	AF090895	Homo sapiens	PRO0117	97	65
1015	AF130089	Homo sapiens	PRO2550	168	83
1016	AF079367	Mesocricetus auratus	cytochrome c oxidase subunit III	276	52
1017	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	94	44
1018	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	114	46
1019	AF090944	Homo sapiens	PRO0663	137	50
1020	Y21166	Homo sapiens	Human bcl2 proto-oncogene mutant protein fragment 14.	84	36
1021	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	140	37
1022	AL049608	Arabidopsis thaliana	extensin-like protein	105	34
1023	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	152	52
1024	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	66
1025	MI2140	Homo sapiens	envelope protein	143	62
1026	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	200	58
1027	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	266	67
1028	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	97	31
1029	G02950	Homo sapiens	Human secreted protein, SEQ ID NO: 7031.	102	56
1030	G02482	Homo sapiens	Human secreted protein, SEQ ID NO: 6563.	76	63
1031	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	74	56
1032	X90568	Homo sapiens	Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABETT@EMBL-Heidelberg DE	389	100
1033	G02654	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.	96	40
1034	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	316	60
1035	AF194537	Homo sapiens	NAG13	208	52
1036	L27428	Homo sapiens	reverse transcriptase	166	51
1037	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	107	44
1038	AF116638	Homo sapiens	PRO1546	56	61
1039	U93570	Homo sapiens	putative p150	138	40
1040	AF130089	Homo sapiens	PRO2550	150	91
1041	AK024455	Homo sapiens	FLJ00047 protein	151	68

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1042	Y36156	Homo sapiens	Human secreted protein #28.	97	41
1043	U93568	Homo sapiens	putative p150	124	34
1044	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	208	71
1045	U93563	Homo sapiens	putative p150	246	54
1046	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	131	64
1047	U93563	Homo sapiens	putative p150	127	30
1048	AF130114	Homo sapiens	PRO2459	117	67
1049	U12919	Mus musculus	adenylyl cyclase type VII	170	68
1050	AC008054	Leishmania major	L8453.1	129	30
1051	X99467	Medicago truncatula	ENOD20	110	38
1052	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	150	76
1053	AF116712	Homo sapiens	PRO2738	109	44
1054	M96256	Homo sapiens	rapamycin binding protein	168	56
1055	U15647	Mus musculus	reverse transcriptase	86	37
1056	AL024498	Homo sapiens	dJ417M14.2 (novel serine/threonine-protein kinase (ortholog of mouse and rat MAK (male germ cell-associated kinase)))	190	72
1057	AF090942	Homo sapiens	PRO0657	103	63
1058	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	156	68
1059	AF081114	Mus musculus domesticus	ORF2	134	47
1060	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	180	83
1061	U70935	Peromyscus maniculatus	reverse transcriptase	126	45
1062	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	84	55
1063	U15647	Mus musculus	reverse transcriptase	95	38
1064	U93567	Homo sapiens	putative p150	128	58
1065	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	130	66
1066	X92483	Plasmodium vivax	pval	119	62
1067	U93567	Homo sapiens	p40	161	48
1068	D38112	Homo sapiens	cytochrome c oxidase subunit 3	540	84
1069	U93570	Homo sapiens	putative p150	107	59
1070	AF321051	Chalinoctonus tuberculatus	cytochrome c oxidase subunit III	333	71
1071	U93567	Homo sapiens	p40	99	28
1072	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	105	66
1073	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	59
1074	U93572	Homo sapiens	putative p150	140	53
1075	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	66	43
1076	AL049608	Arabidopsis thaliana	extensin-like protein	105	37
1077	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	94	66
1078	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	81	57
1079	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	83	35

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			8172.		
1080	AF162149	Mycoplasma bovis	variable surface lipoprotein	103	41
1081	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	148	75
1082	U43360	Peromyscus maniculatus	reverse transcriptase	121	42
1083	U93564	Homo sapiens	p40	97	42
1084	AF229067	Homo sapiens	PADJ-H protein	145	61
1085	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	221	60
1086	U88573	Homo sapiens	NBR2	165	67
1087	Y36156	Homo sapiens	Human secreted protein #28.	93	72
1088	AF194537	Homo sapiens	NAG13	142	62
1089	B08976	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:133.	93	62
1090	AF194537	Homo sapiens	NAG13	155	40
1091	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	103	35
1092	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	195	40
1093	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	91	46
1094	X53581	Rattus norvegicus	ORF4	106	62
1095	AL160493	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	129	51
1096	Y86473	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:388.	72	33
1097	U40342	Mus musculus	ninein	152	44
1098	M24732	Homo sapiens	lamin-like protein	92	37
1099	X92485	Plasmodium vivax	pva1	111	67
1100	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	156	86
1101	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	90
1102	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	158	71
1103	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	97	36
1104	U93572	Homo sapiens	putative p150	168	56
1105	U93570	Homo sapiens	putative p150	96	40
1106	L27428	Homo sapiens	reverse transcriptase	188	43
1107	X53581	Rattus norvegicus	ORF4	141	43
1108	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	344	77
1109	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	126	68
1110	U93569	Homo sapiens	putative p150	156	38
1111	AF118086	Homo sapiens	PRO1992	135	54
1112	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	71	63
1113	AF016099	Mus musculus	endonuclease/reverse transcriptase	124	62
1114	L27428	Homo sapiens	reverse transcriptase	200	40
1115	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	101	50
1116	L27428	Homo sapiens	reverse transcriptase	122	70
1117	G00637	Homo sapiens	Human secreted protein, SEQ ID NO:	148	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4718.		
1118	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	116	65
1119	D38484	Hylobates syndactylus	Cytochrome C oxidase subunit 1 (COXI)	315	89
1120	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	115	76
1121	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	136	68
1122	AF013990	Homo sapiens	ubiquitin C-terminal hydrolase	163	50
1123	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	94	55
1124	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	154	65
1125	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	106	53
1126	AF130089	Homo sapiens	PRO2550	76	72
1127	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	92	59
1128	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	80	59
1129	AF119855	Homo sapiens	PRO1847	146	70
1130	AF194537	Homo sapiens	NAG13	182	66
1131	L27428	Homo sapiens	reverse transcriptase	173	38
1132	U93570	Homo sapiens	putative p150	119	34
1133	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	157	68
1134	AJ004810	Zea mays	cytochrome P450 monooxygenase	79	87
1135	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	138	70
1136	G01502	Homo sapiens	Human secreted protein, SEQ ID NO: 5583.	81	73
1137	AB018705	Mus musculus	ORF2	138	36
1138	L20321	Homo sapiens	protein serine/threonine kinase	150	63
1139	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	60
1140	AF194537	Homo sapiens	NAG13	115	33
1141	U93564	Homo sapiens	putative p150	135	51
1142	D86853	Catharanthus roseus	extensin	142	37
1143	D00570	Mus musculus	open reading frame (251 AA)	213	50
1144	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	62	38
1145	Z70684	Caenorhabditis elegans	F28D1.8	105	32
1146	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	79	54
1147	Y36156	Homo sapiens	Human secreted protein #28.	151	62
1148	A23786	Beta vulgaris	chitinase I	98	37
1149	AF129756	Homo sapiens	BAT2	177	52
1150	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	147	73
1151	L27428	Homo sapiens	reverse transcriptase	77	31
1152	U34044	Homo sapiens	selenium donor protein	238	48
1153	AK024455	Homo sapiens	FLJ00047 protein	78	78
1154	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	197	67
1155	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	120	64
1156	U25281	Rattus norvegicus	SH3 domain binding protein	98	34
1157	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	138	54

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1158	AF194537	Homo sapiens	NAG13	106	48
1159	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	357	69
1160	U93572	Homo sapiens	p40	89	47
1161	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	184	68
1162	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	123	57
1163	AF116712	Homo sapiens	PRO2738	129	69
1164	V00662	Homo sapiens	cytochrome oxidase I	465	69
1165	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	118	57
1166	L26163	Mus musculus	histone H1c	104	37
1167	X70343	Nicotiana glauca	extensin	95	33
1168	AF130051	Homo sapiens	PRO0898	117	43
1169	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	104	48
1170	L27428	Homo sapiens	reverse transcriptase	149	33
1171	G00497	Homo sapiens	Human secreted protein, SEQ ID NO: 4578.	108	62
1172	AF030277	Tragelaphus spekei	cytochrome oxidase subunit III	266	54
1173	L22030	Glycine max	hydroxyproline-rich glycoprotein	87	38
1174	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	168	45
1175	U43627	Arabidopsis thaliana	extensin	111	42
1176	U43627	Arabidopsis thaliana	extensin	98	29
1177	U93565	Homo sapiens	putative p150	89	58
1178	J01047	Caenorhabditis elegans	collagen	108	39
1179	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	170	68
1180	AF016099	Mus musculus	endonuclease/reverse transcriptase	113	36
1181	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	134	65
1182	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	107	62
1183	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	124	45
1184	D38112	Homo sapiens	NADH dehydrogenase subunit 2	418	86
1185	U87607	Rattus norvegicus	putative RNA binding protein 1	106	41
1186	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	381	75
1187	D38112	Homo sapiens	cytochrome c oxidase subunit I	434	79
1188	U83303	Homo sapiens	line-1 reverse transcriptase	75	35
1189	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	159	68
1190	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	146	68
1191	AF118086	Homo sapiens	PRO1992	146	81
1192	W12842	Homo sapiens	Truncated pro-alpha1(III) chain.	106	35
1193	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	67	34
1194	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	116	74
1195	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	132	82

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1196	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	75	48
1197	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	254	73
1198	U93570	Homo sapiens	p40	103	30
1199	AL390114	Leishmania major	extremely cysteine/valine rich protein	145	39
1200	AK024455	Homo sapiens	FLJ00047 protein	115	56
1201	AF090942	Homo sapiens	PRO0657	88	64
1202	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	124	70
1203	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	113	46
1204	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	81	41
1205	U35730	Mus musculus	jerky	107	27
1206	U15647	Mus musculus	reverse transcriptase	191	45
1207	U15647	Mus musculus	reverse transcriptase	124	50
1208	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	140	58
1209	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	91	54
1210	AF119900	Homo sapiens	PRO2822	160	81
1211	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	68
1212	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	45
1213	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	125	61
1214	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	102	61
1215	G03560	Homo sapiens	Human secreted protein, SEQ ID NO: 7641.	101	46
1216	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-IRGP	270	58
1217	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	105	46
1218	AC002483	Homo sapiens	putative product from mRNA sequence CG003 from BRCA2 region; match to U50534 (NID:g1685103)	378	97
1219	AF090895	Homo sapiens	PRO0117	130	58
1220	AF113685	Homo sapiens	PRO0974	117	60
1221	X61295	Rattus norvegicus	L1 retroposon, a portion of its ORF2 sequence	126	50
1222	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	148	70
1223	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	99	56
1224	U93574	Homo sapiens	putative p150	93	44
1225	AF130051	Homo sapiens	PRO0898	133	69
1226	U93563	Homo sapiens	putative p150	125	47
1227	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	220	47
1228	U93564	Homo sapiens	putative p150	116	47
1229	W21733	Homo sapiens	NIP-1 encoded by clone 59.	138	63
1230	U15647	Mus musculus	reverse transcriptase	105	42
1231	U93563	Homo sapiens	putative p150	299	54
1232	R93913	Homo sapiens	Neural thread protein.	138	51
1233	AF130079	Homo sapiens	PRO2852	203	70
1234	X53581	Rattus norvegicus	ORF3	106	60



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1235	AF118086	Homo sapiens	PRO1992	144	81
1236	X92485	Plasmodium vivax	pval	125	71
1237	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	75
1238	U93572	Homo sapiens	putative p150	133	40
1239	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	69	56
1240	AF130089	Homo sapiens	PRO2550	136	41
1241	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	109	53
1242	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	75
1243	G02752	Homo sapiens	Human secreted protein, SEQ ID NO: 6833.	87	45
1244	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	128	58
1245	U93570	Homo sapiens	putative p150	161	50
1246	Z70684	Caenorhabditis elegans	F28D1.8	121	45
1247	AF257305	Homo sapiens	ASH1	576	89
1248	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	98	68
1249	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	107	43
1250	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	91
1251	U63542	Homo sapiens	FAP protein	116	61
1252	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	109	53
1253	AF068294	Homo sapiens	HDCMB45P	251	63
1254	AF090895	Homo sapiens	PRO0117	111	60
1255	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	201	75
1256	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	51
1257	AB033032	Homo sapiens	KIAA1206 protein	115	80
1258	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	122	60
1259	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	137	68
1260	AB032906	Hylobates pileatus	dopamine receptor D4	96	35
1261	AF022985	Caenorhabditis elegans	Similar to collagen; coded for by C. elegans cDNA yk55B.3; coded for by C. elegans cDNA yk66d5.3; coded for by C. elegans cDNA yk71e4.3; coded for by C. elegans cDNA yk55B.5; coded for by C. elegans cDNA yk66d5.5; coded for by C. elegans cDNA yk71e4.5	106	38
1262	U93566	Homo sapiens	p40	182	39
1263	L20096	Manduca sexta	ribosomal protein s7	227	59
1264	AF119901	Homo sapiens	PRO2831	103	71
1265	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	219	97
1266	D90279	Homo sapiens	collagen alpha 1(V) chain precursor	120	42
1267	L27428	Homo sapiens	reverse transcriptase	111	41
1268	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	126	68
1269	AF016099	Mus musculus	endonuclease/reverse transcriptase	102	34

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1270	AF130089	Homo sapiens	PRO2550	96	69
1271	U12707	Homo sapiens	Wiskott-Aldrich syndrome protein	121	45
1272	AF165310	Homo sapiens	ATP cassette binding transporter 1	243	100
1273	R95913	Homo sapiens	Neural thread protein.	110	70
1274	X92485	Plasmodium vivax	pva1	106	65
1275	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	104	56
1276	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	53	36
1277	X03725	Mus musculus	ORF 2 (466 aa)	103	41
1278	U93570	Homo sapiens	putative p150	98	43
1279	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	159	83
1280	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	167	71
1281	AJ271871	Nicotiana sylvestris	putative extensin	105	36
1282	K03205	Homo sapiens	salivary proline-rich protein precursor	119	32
1283	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	124	66
1284	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	135	50
1285	A31039	Nicotiana glauca	PRP3	112	36
1286	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	116	72
1287	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	289	67
1288	S80119	Rattus sp.	reverse transcriptase homolog	112	33
1289	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	203	76
1290	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	151	53
1291	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	128	82
1292	AF130089	Homo sapiens	PRO2550	127	62
1293	AF003535	Homo sapiens	ORF2-like protein	101	48
1294	Y19610	Homo sapiens	SEQ ID NO 328 from WO9922243.	100	42
1295	J27428	Homo sapiens	reverse transcriptase	126	36
1296	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	140	71
1297	L24433	Oncorhynchus mykiss	complement component C3	359	31
1298	AC004381	Homo sapiens	SA gene	443	55
1299	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	180	64
1300	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	135	66
1301	D84391	Mus musculus	reverse transcriptase	106	48
1302	D13951	Nicotiana tabacum	extensin precursor	134	42
1303	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	73
1304	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	93	38
1305	Y13620	Homo sapiens	BCL9	102	39
1306	U93567	Homo sapiens	putative p150	245	63
1307	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	130	70
1308	AI355774	Streptomyces coelicolor A3(2)	putative integral membrane protein	136	40
1309	W54966	Homo sapiens	Synthetic human type III collagen	124	41

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SYN-C3,		
1310	M20670	Plasmodium vivax	circumsporozoite protein	107	34
1311	AF151366	Arabidopsis thaliana	arginine/serine-rich protein	114	36
1312	G03099	Homo sapiens	Human secreted protein, SEQ ID NO: 7180.	76	43
1313	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	109	85
1314	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	111	37
1315	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	123	62
1316	R55913	Homo sapiens	Neural thread protein.	98	58
1317	AF113685	Homo sapiens	PRO0974	170	47
1318	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	122	61
1319	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	99	68
1320	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	270	56
1321	U93569	Homo sapiens	putative p150	124	37
1322	AF090931	Homo sapiens	PRO0483	111	85
1323	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	85	44
1324	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	131	43
1325	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	144	54
1326	AF194537	Homo sapiens	NAG13	125	49
1327	L27428	Homo sapiens	reverse transcriptase	111	45
1328	U93568	Homo sapiens	putative p150	112	30
1329	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	110	51
1330	L27428	Homo sapiens	reverse transcriptase	142	53
1331	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	98	88
1332	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	55
1333	X71602	Nicotiana tabacum	extensin	113	35
1334	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	129	41
1335	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	112	50
1336	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	102	68
1337	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	95	51
1338	U43360	Peromyscus maniculatus	reverse transcriptase	114	60
1339	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	142	55
1340	X55685	Lycopersicon esculentum	extensin (class I)	123	31
1341	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	118	70
1342	X71629	Mus musculus	msg1	106	57
1343	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	105	79

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1344	G03435	Homo sapiens	Human secreted protein, SEQ ID NO: 7516.	116	85
1345	AF161356	Homo sapiens	HSPC093	88	88
1346	J01435	Rattus norvegicus	ATPase	348	66
1347	U93563	Homo sapiens	putative p150	142	36
1348	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	87	66
1349	AF090942	Homo sapiens	PRO0657	152	54
1350	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	143	63
1351	U93572	Homo sapiens	putative p150	113	84
1352	X92485	Plasmodium vivax	pval	130	70
1353	X61047	Hydra sp.	mini-collagen	105	36
1354	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	128	46
1355	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	91	39
1356	AF194537	Homo sapiens	NAG13	148	63
1357	AF130079	Homo sapiens	PRO2852	139	73
1358	X53581	Rattus norvegicus	ORF4	208	43
1359	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	50
1360	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	328	69
1361	W80406	Homo sapiens	A secreted protein encoded by clone din40_3.	126	65
1362	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	97	47
1363	X53581	Rattus norvegicus	ORF4	110	35
1364	U93569	Homo sapiens	putative p150	123	41
1365	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	114	63
1366	X61294	Rattus norvegicus	L1 retroposon, a portion of its ORF2 sequence	153	43
1367	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	69	80
1368	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	80	46
1369	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	113	26
1370	X92485	Plasmodium vivax	pval	106	46
1371	U90946	Dictyostelium discoideum	myosin heavy chain kinase B	114	62
1372	L27428	Homo sapiens	reverse transcriptase	98	61
1373	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	124	80
1374	U49974	Homo sapiens	mariner transposase	137	57
1375	AC004891	Homo sapiens	contactin-like; similar to U87224 (PID:1857710)	234	58
1376	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	132	60
1377	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	317	51
1378	AF118082	Homo sapiens	PRO1902	102	42
1379	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	186	45
1380	U93567	Homo sapiens	putative p150	116	38
1381	U49973	Homo sapiens	ORF1; MER37; putative transposase	218	47

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			similar to pogo element		
1382	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	87	66
1383	AF090895	Homo sapiens	PRO0117	68	82
1384	U93570	Homo sapiens	putative p150	178	39
1385	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	132	43
1386	AF130089	Homo sapiens	PRO2550	142	35
1387	L27428	Homo sapiens	reverse transcriptase	163	49
1388	X61296	Rattus norvegicus	open reading frame 2	123	44
1389	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	138	67
1390	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	147	57
1391	U93570	Homo sapiens	putative p150	110	28
1392	R95913	Homo sapiens	Neural thread protein.	104	35
1393	L27428	Homo sapiens	reverse transcriptase	101	39
1394	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	147	47
1395	AF216972	Homo sapiens	p8 protein	118	49
1396	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	160	58
1397	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	312	62
1398	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	97	62
1399	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	54
1400	X92485	Plasmodium vivax	pva1	124	39
1401	U93563	Homo sapiens	putative p150	131	36
1402	X67863	Mus musculus	T2	160	48
1403	K02576	Homo sapiens	salivary proline-rich protein 1	94	39
1404	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	84	73
1405	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	71	71
1406	M18094	Phaseolus vulgaris	hydroxycyproline-rich glycoprotein	138	31
1407	AF134304	Homo sapiens	Scar2	118	40
1408	Y08061	Homo sapiens	Human c-myb protein fragment.	121	82
1409	U93574	Homo sapiens	putative p150	179	43
1410	U93563	Homo sapiens	putative p150	98	43
1411	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	124	46
1412	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	149	56
1413	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	148	48
1414	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	155	82
1415	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	92	52
1416	AF119855	Homo sapiens	PRO1847	82	70
1417	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	130	34
1418	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	99	39
1419	AF130079	Homo sapiens	PRO2852	114	69
1420	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	133	52

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1421	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	115	44
1422	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	111	77
1423	R95913	Homo sapiens	Neural thread protein.	128	80
1424	L26953	Homo sapiens	chromosomal protein	104	34
1425	U83280	Leishmania donovani	39 kDa antigen	105	51
1426	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	98	75
1427	U83303	Homo sapiens	line-1 reverse transcriptase	149	40
1428	AF090895	Homo sapiens	PRO0117	111	75
1429	AF119855	Homo sapiens	PRO1847	88	56
1430	AF229067	Homo sapiens	PADI-H protein	157	51
1431	D38112	Homo sapiens	cytochrome c oxidase subunit 3	509	79
1432	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	333	62
1433	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	149	57
1434	AF161356	Homo sapiens	HSPC093	180	46
1435	U93570	Homo sapiens	putative p150	116	48
1436	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	171	73
1437	U83280	Leishmania donovani	39 kDa antigen	106	80
1438	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	103	73
1439	U15647	Mus musculus	reverse transcriptase	233	44
1440	L27428	Homo sapiens	reverse transcriptase	78	40
1441	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	115	68
1442	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	77	63
1443	M22332	Homo sapiens	unknown protein	153	62
1444	M11901	Rattus norvegicus	proline-rich salivary protein	102	40
1445	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	101	66
1446	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	125	74
1447	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	90	66
1448	X76208	Drosophila melanogaster	protein 33-specific exons	123	48
1449	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	178	79
1450	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	109	45
1451	S80119	Rattus sp.	reverse transcriptase homolog	115	54
1452	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	70	63
1453	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	105	40
1454	AK024455	Homo sapiens	FLJ00047 protein	109	53
1455	AC007258	Arabidopsis thaliana	Hypothetical protein	105	37
1456	AF194537	Homo sapiens	NAG13	208	52
1457	U63542	Homo sapiens	FAP protein	111	84
1458	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	111	65
1459	AF090931	Homo sapiens	PRO0483	84	43

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1460	R95913	Homo sapiens	Neural thread protein.	106	69
1461	R95913	Homo sapiens	Neural thread protein.	109	40
1462	U93564	Homo sapiens	putative p150	237	42
1463	AB029309	Homo sapiens	Npw38-binding protein NpwBP	97	37
1464	U44838	Glycine max	extensin	97	33
1465	AL050341	Homo sapiens	dJ39G22.1 (rearranged L-myc fusion sequence (ZIN-15 related zinc finger protein))	121	45
1466	L27428	Homo sapiens	reverse transcriptase	94	34
1467	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	58
1468	Y17221	Homo sapiens	Human secreted protein (clone fk317-3).	98	48
1469	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	123	55
1470	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	147	67
1471	AF109907	Homo sapiens	S164	133	35
1472	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	142	36
1473	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	152	90
1474	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	157	45
1475	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	398	58
1476	U49974	Homo sapiens	mariner transposase	201	59
1477	U49974	Homo sapiens	mariner transposase	206	60
1478	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	117	72
1479	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	146	82
1480	U93567	Homo sapiens	putative p150	202	42
1481	K02576	Homo sapiens	salivary proline-rich protein 1	101	46
1482	U87607	Rattus norvegicus	putative RNA binding protein 1	100	37
1483	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	124	75
1484	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	108	62
1485	U15647	Mus musculus	reverse transcriptase	115	73
1486	AF194537	Homo sapiens	NAG13	132	42
1487	M11902	Mus musculus	proline-rich salivary protein	118	40
1488	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	102	64
1489	AF009668	multiple sclerosis associated retrovirus	polyprotein	110	48
1490	AK023542	Homo sapiens	unnamed protein product	114	37
1491	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	133	50
1492	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	184	47
1493	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	222	53
1494	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	94	50
1495	AF109907	Homo sapiens	S164	259	45
1496	R95913	Homo sapiens	Neural thread protein.	110	51
1497	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	299	80

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1498	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	158	65
1499	L26953	Homo sapiens	chromosomal protein	104	67
1500	AF090895	Homo sapiens	PRO0117	145	68
1501	U93572	Homo sapiens	p40	115	42
1502	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	133	50
1503	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	143	56
1504	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	119	69
1505	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	105	52
1506	AF109907	Homo sapiens	S164	184	43
1507	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	288	67
1508	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	131	69
1509	AK000241	Homo sapiens	unnamed protein product	167	72
1510	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	153	60
1511	S62928	Homo sapiens	PRB1M protein precursor	157	39
1512	AB012223	Canis familiaris	ORF2	116	40
1513	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	109	59
1514	AF220264	Homo sapiens	MOST-1	108	80
1515	X53581	Rattus norvegicus	ORF4	96	44
1516	V00662	Homo sapiens	cytochrome oxidase III	433	74
1517	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	263	70
1518	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	266	70
1519	M24732	Homo sapiens	lamin-like protein	107	44
1520	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	131	51
1521	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	81	68
1522	AF194537	Homo sapiens	NAG13	116	42
1523	X92485	Plasmodium vivax	pval	85	42
1524	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	125	50
1525	AB041228	Homo sapiens	G protein-coupled receptor TGR-1	220	100
1526	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	138	70
1527	U52077	Homo sapiens	mariner transposase	237	56
1528	L27428	Homo sapiens	reverse transcriptase	189	40
1529	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	355	78
1530	L13610	Mus musculus	IFN-response element binding factor 2	90	37
1531	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	90	64
1532	U11288	Drosophila melanogaster	diaphanous protein	138	38
1533	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	429	63
1534	L27428	Homo sapiens	reverse transcriptase	249	55
1535	U93570	Homo sapiens	putative p150	114	31
1536	AF130089	Homo sapiens	PRO2550	111	47



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1537	X55687	Lycopersicon esculentum	extensin (class II)	63	28
1538	U15647	Mus musculus	reverse transcriptase	110	42
1539	AK024455	Homo sapiens	FLJ00047 protein	139	80
1540	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	128	48
1541	AC024788	Caenorhabditis elegans	Hypothetical protein Y46E12A.d	80	46
1542	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	132	73
1543	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	90	32
1544	G02971	Homo sapiens	Human secreted protein, SEQ ID NO: 7052.	71	63
1545	R59513	Homo sapiens	Neural thread protein.	118	55
1546	D38116	Pan paniscus	cytochrome c oxidase subunit 1	218	78
1547	D38112	Homo sapiens	cytochrome c oxidase subunit 1	370	71
1548	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	119	65
1549	AJ004810	Zea mays	cytochrome P450 monooxygenase	140	70
1550	AF113685	Homo sapiens	PRO0974	115	47
1551	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	172	75
1552	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	366	94
1553	W40113	Homo sapiens	Human alpha-2(IV) collagen protein.	117	59
1554	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	138	76
1555	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	113	40
1556	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	502	89
1557	AF130089	Homo sapiens	PRO2550	98	55
1558	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	109	43
1559	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	183	52
1560	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	180	52
1561	AF202893	Mus musculus	Klf21b	254	85
1562	M63421	Drosophila melanogaster	csp32	104	39
1563	G03652	Homo sapiens	Human secreted protein, SEQ ID NO: 7733.	129	69
1564	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	98	59
1565	AJ132106	Bos taurus	SCO-spondin	114	40
1566	AL390114	Leishmania major	extremely cysteine/valine rich protein	119	66
1567	AF161356	Homo sapiens	HSPC093	100	38
1568	AF119851	Homo sapiens	PRO1722	94	72
1569	L27428	Homo sapiens	reverse transcriptase	107	48
1570	X99451	Lycopersicon esculentum	extensin-like protein Difi10	104	32
1571	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	126	59
1572	X73481	Drosophila hydei	mst101(2)	105	41
1573	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	133	50
1574	G04063	Homo sapiens	Human secreted protein, SEQ ID NO:	154	51

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			8144.		
1575	D38112	Homo sapiens	NADH dehydrogenase subunit 4	323	83
1576	AF062008	Caenorhabditis elegans	unknown	111	54
1577	X92485	Plasmodium vivax	pval	81	57
1578	U93570	Homo sapiens	p40	102	33
1579	AF090944	Homo sapiens	PRO0663	132	59
1580	AL137798	Homo sapiens	dJ1182A14.5.1 (novel gene (isoform 1))	182	53
1581	X92485	Plasmodium vivax	pval	120	44
1582	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	160	47
1583	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	135	54
1584	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	119	52
1585	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	82	55
1586	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	152	60
1587	D28482	Homo sapiens	SCR2	390	83
1588	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	122	59
1589	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	50
1590	AF118078	Homo sapiens	PRO1848	118	59
1591	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	56	78
1592	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	118	80
1593	U93571	Homo sapiens	p40	170	77
1594	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	230	51
1595	L27428	Homo sapiens	reverse transcriptase	138	45
1596	X97707	Pongo pygmaeus abelii	stopcodon created by posttranscriptional polyadenylation	139	61
1597	X98710	Homo sapiens	COL1A1 and PDGFB fusion transcript	107	31
1598	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	97	58
1599	AF210651	Homo sapiens	NAG18	86	89
1600	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	148	48
1601	J03770	Mus musculus	homeobox protein	99	35
1602	AF119901	Homo sapiens	PRO2831	119	56
1603	AL031673	Homo sapiens	dJ694B14.1 (PUTATIVE novel KRAB box protein with 18 C2H2 type Zinc finger domains)	233	44
1604	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	66
1605	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	89	44
1606	D88461	Rattus rattus	N-WASP	123	43
1607	AF090942	Homo sapiens	PRO0657	107	61
1608	U35730	Mus musculus	jerky	105	34
1609	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	108	45
1610	B06334	Homo sapiens	Human subtilisin-kexin isoenzyme 1.	474	84
1611	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	101	90
1612	AK024455	Homo sapiens	FLJ00047 protein	83	55
1613	D86853	Catharanthus	extensin	123	39

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		roseus			
1614	AF119851	Homo sapiens	PRO1722	135	59
1615	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	142	57
1616	AF194537	Homo sapiens	NAG13	154	63
1617	AF119851	Homo sapiens	PRO1722	91	62
1618	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	48
1619	AK024455	Homo sapiens	FLJ00047 protein	147	60
1620	AE217973	Homo sapiens	unknown	116	67
1621	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	102	41
1622	K02576	Homo sapiens	salivary proline-rich protein 1	108	40
1623	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	135	44
1624	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	322	62
1625	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	356	72
1626	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	113	65
1627	X92485	Plasmodium vivax	pva1	90	45
1628	AF090895	Homo sapiens	PRO0117	156	61
1629	AF116661	Homo sapiens	PRO1438	87	54
1630	M13100	Rattus norvegicus	unknown protein	109	76
1631	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	147	60
1632	AF119851	Homo sapiens	PRO1722	107	70
1633	M64792	Rattus norvegicus	salivary proline-rich protein	109	46
1634	L27428	Homo sapiens	reverse transcriptase	109	38
1635	AF118082	Homo sapiens	PRO1902	80	40
1636	R95913	Homo sapiens	Neural thread protein.	118	88
1637	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	79	60
1638	U93570	Homo sapiens	putative p150	128	54
1639	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	127	69
1640	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	171	68
1641	AF194537	Homo sapiens	NAG13	140	66
1642	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	101	50
1643	M64793	Rattus norvegicus	salivary proline-rich protein	117	33
1644	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	50
1645	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	96	70
1646	L27428	Homo sapiens	reverse transcriptase	86	84
1647	X92485	Plasmodium vivax	pva1	137	40
1648	U15647	Mus musculus	reverse transcriptase	93	68
1649	K02576	Homo sapiens	salivary proline-rich protein 1	131	41
1650	AF116712	Homo sapiens	PRO2738	107	57
1651	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	139	72
1652	X05472	Rattus	ORF 3	84	51

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		<i>norvegicus</i>			
1653	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	122	71
1654	U93566	Homo sapiens	p40	117	52
1655	AF217536	Homo sapiens	truncated mevalonate kinase	141	70
1656	AF090895	Homo sapiens	PRO0117	125	60
1657	X92485	Plasmodium vivax	pval	114	45
1658	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	192	61
1659	Y86473	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:388.	73	30
1660	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	331	74
1661	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	127	69
1662	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	312	67
1663	S80119	Rattus sp.	reverse transcriptase homolog	99	59
1664	U43360	Peromyscus maniculatus	reverse transcriptase	106	45
1665	M76729	Homo sapiens	pro-alpha-1 type V collagen	172	47
1666	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	97	54
1667	AF169388	Mus musculus	alpha 4 collagen IV	84	38
1668	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	84	66
1669	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	428	80
1670	M29622	Mus musculus	open reading frame 2	74	46
1671	W90838	Homo sapiens	Human lymphocyte targeted peptide #6.	98	100
1672	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	55	58
1673	AF090931	Homo sapiens	PRO0483	72	39
1674	AF051782	Homo sapiens	diaphanous 1	116	49
1675	U57361	Rattus norvegicus	collagen XII alpha 1	108	48
1676	AF182844	Homo sapiens	VPS28 protein	395	95
1677	L27428	Homo sapiens	reverse transcriptase	189	47
1678	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	142	53
1679	U93565	Homo sapiens	putative p150	214	40
1680	AK002129	Homo sapiens	unnamed protein product	128	57
1681	X03145	Homo sapiens	pot. ORF V	93	48
1682	X63005	Mus musculus	proline-rich protein	108	38
1683	AF118082	Homo sapiens	PRO1902	117	42
1684	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	157	58
1685	R95913	Homo sapiens	Neural thread protein.	92	66
1686	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	111	61
1687	X61296	Rattus norvegicus	open reading frame 2	104	38
1688	AB012223	Canis familiaris	ORF2	98	39
1689	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	278	72
1690	U52077	Homo sapiens	mariner transposase	175	56
1691	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	83	46

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1692	AF061128	<i>Plasmodium falciparum</i>	merozoite surface protein 1	85	44
1693	X77722	<i>Homo sapiens</i>	interferon alpha/beta receptor	89	60
1694	M13100	<i>Rattus norvegicus</i>	unknown protein	94	40
1695	AF202635	<i>Homo sapiens</i>	PP1200	114	60
1696	AK001116	<i>Homo sapiens</i>	unnamed protein product	127	53
1697	G00403	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 4484.	162	53
1698	AF118078	<i>Homo sapiens</i>	PRO1848	93	42
1699	X92485	<i>Plasmodium vivax</i>	pval	147	49
1700	M63819	<i>Plasmodium falciparum</i>	malaria antigen	101	64
1701	AF090930	<i>Homo sapiens</i>	PRO0478	146	76
1702	AB009993	<i>Mus musculus</i>	collagen a1(V)	94	40
1703	AL390114	<i>Leishmania major</i>	extremely cysteine/valine rich protein	169	66
1704	AF130089	<i>Homo sapiens</i>	PRO2550	145	38
1705	X83413	<i>Human herpesvirus 6</i>	U88	113	58
1706	S60088	<i>Homo sapiens</i>	putative adhesion molecule=ADMLX	151	86
1707	G01246	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 5327.	176	52
1708	AF130079	<i>Homo sapiens</i>	PRO2852	174	41
1709	Y28682	<i>Homo sapiens</i>	Human pp392_3 secreted protein.	557	99
1710	M14423	<i>Mus musculus</i>	pro-alpha-1 type I collagen	112	34
1711	D13623	<i>Rattus sp.</i>	p34 protein	128	45
1712	G04063	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 8144.	84	41
1713	X97675	<i>Homo sapiens</i>	plakophilin 2b	121	60
1714	G03453	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7534.	102	51
1715	U49973	<i>Homo sapiens</i>	ORF1; MER37; putative transposase similar to pogo element	171	48
1716	G00357	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 4438.	99	63
1717	S80119	<i>Rattus sp.</i>	reverse transcriptase homolog	140	57
1718	L27428	<i>Homo sapiens</i>	reverse transcriptase	103	46
1719	G03790	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7871.	154	78
1720	AF130089	<i>Homo sapiens</i>	PRO2550	106	35
1721	G03652	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7733.	147	49
1722	G03703	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7784.	111	72
1723	AF016099	<i>Mus musculus</i>	endonuclease/reverse transcriptase	132	60
1724	X92485	<i>Plasmodium vivax</i>	pval	96	62
1725	U49973	<i>Homo sapiens</i>	ORF1; MER37; putative transposase similar to pogo element	249	52
1726	M81321	<i>Macaca fascicularis</i>	proline-rich protein	132	45
1727	G02507	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 6588.	119	69
1728	U93564	<i>Homo sapiens</i>	p40	129	58
1729	U93574	<i>Homo sapiens</i>	putative p150	113	76
1730	AF130089	<i>Homo sapiens</i>	PRO2550	136	61
1731	I05608	<i>Cercopithecine</i>	glycoprotein gI	100	46

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		herpesvirus 2			
1732	U15647	Mus musculus	reverse transcriptase	138	36
1733	U93574	Homo sapiens	putative p150	187	43
1734	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	155	64
1735	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	102	64
1736	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	118	64
1737	G00490	Homo sapiens	Human secreted protein, SEQ ID NO: 4571.	110	58
1738	AF090942	Homo sapiens	PRO0657	163	55
1739	U11288	Drosophila melanogaster	diaphanous protein	149	46
1740	L27428	Homo sapiens	reverse transcriptase	108	33
1741	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	76	54
1742	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	165	59
1743	AC003682	Homo sapiens	R28830_1	179	63
1744	X65165	Volvox carteri	extensin	173	49
1745	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	114	62
1746	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	89	41
1747	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	115	42
1748	U93565	Homo sapiens	putative p150	125	37
1749	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	121	45
1750	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	139	53
1751	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	87	80
1752	L27428	Homo sapiens	reverse transcriptase	133	42
1753	U93570	Homo sapiens	putative p150	126	37
1754	U22376	Homo sapiens	alternatively spliced product using exon 13A	134	50
1755	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	175	76
1756	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	60
1757	U54788	Mus musculus	Wiskott-Aldrich Syndrome Protein	158	44
1758	Y86579	Homo sapiens	Human gene 92-encoded protein fragment, SEQ ID NO:496.	109	88
1759	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	123	73
1760	Y86579	Homo sapiens	Human gene 92-encoded protein fragment, SEQ ID NO:496.	113	92
1761	Y86579	Homo sapiens	Human gene 92-encoded protein fragment, SEQ ID NO:496.	110	81
1762	U08020	Mus musculus	collagen pro-alpha-1 type I chain	105	34
1763	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	90	45
1764	U93569	Homo sapiens	putative p150	148	36
1765	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	116	45
1766	X02873	Daucus carota	put. precursor	112	47
1767	X92485	Plasmodium vivax	pval	100	45
1768	R95913	Homo sapiens	Neural thread protein.	96	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1769	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	114	51
1770	X97675	Homo sapiens	plakophilin 2b	115	70
1771	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	151	58
1772	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	131	85
1773	AF130089	Homo sapiens	PRO2550	158	69
1774	U23552	Ailuropoda melanoleuca	cytochrome b	206	78
1775	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	98	53
1776	AF116715	Homo sapiens	PRO2829	134	67
1777	AC008054	Leishmania major	L8453.1	114	28
1778	AF037364	Homo sapiens	paraneoplastic neuronal antigen MA1	397	73
1779	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	132	60
1780	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	168	64
1781	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	80	36
1782	AF174482	Homo sapiens	polycomb 3	133	46
1783	U93563	Homo sapiens	putative p150	196	70
1784	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	59
1785	AF194537	Homo sapiens	NAG13	114	38
1786	U21123	Drosophila melanogaster	ena polypeptide	120	44
1787	AF200187	cercopithecine herpesvirus 15	EBNA2-like protein	108	30
1788	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	97	56
1789	M64792	Rattus norvegicus	salivary proline-rich protein	128	40
1790	X92485	Plasmodium vivax	pva1	98	51
1791	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	114	34
1792	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	197	81
1793	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	145	71
1794	AF104923	Homo sapiens	putative transcription factor	142	59
1795	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	133	60
1796	AC003113	Arabidopsis thaliana	F24O1.6	57	62
1797	M22332	Homo sapiens	unknown protein	118	29
1798	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	100	71
1799	AL390114	Leishmania major	extremely cysteine/valine rich protein	154	37
1800	U93570	Homo sapiens	p40	103	56
1801	X99452	Lycopersicon esculentum	extensin-like protein Di54	101	28
1802	L27428	Homo sapiens	reverse transcriptase	102	34
1803	L27428	Homo sapiens	reverse transcriptase	141	43
1804	M18933	Mus musculus	alpha-1 type-III collagen precursor	118	30
1805	X92485	Plasmodium vivax	pva1	106	67
1806	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	118	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1807	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	105	33
1808	X97675	Homo sapiens	plakophilin 2b	154	61
1809	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	130	53
1810	X92485	Plasmodium vivax	pval	133	54
1811	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	121	66
1812	Y17833	Human endogenous retrovirus K	env protein	119	81
1813	AF119851	Homo sapiens	PRO1722	130	58
1814	X53581	Rattus norvegicus	ORF4	158	50
1815	G03473	Homo sapiens	Human secreted protein, SEQ ID NO: 7554.	111	74
1816	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	153	68
1817	M19155	Plasmodium falciparum	S-antigen precursor	164	50
1818	AF118082	Homo sapiens	PRO1902	90	75
1819	W40353	Homo sapiens	Human unspecified protein from US5702907.	110	52
1820	U93563	Homo sapiens	putative p150	114	35
1821	U41538	Caenorhabditis elegans	proline rich	95	52
1822	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	154	45
1823	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	131	53
1824	AF130089	Homo sapiens	PRO2550	128	40
1825	AF090944	Homo sapiens	PRO0663	103	45
1826	AC003113	Arabidopsis thaliana	F24O1.18	107	40
1827	AF194537	Homo sapiens	NAG13	85	28
1828	AF009668	multiple sclerosis associated retrovirus	polyprotein	185	41
1829	AF016099	Mus musculus	endonuclease/reverse transcriptase	155	42
1830	X69465	Sus scrofa	ryanodine receptor 1	516	86
1831	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	108	40
1832	U88966	Homo sapiens	rapamycin associated protein FRAP2	434	89
1833	M19155	Plasmodium falciparum	S-antigen precursor	105	32
1834	AF085809	Mus musculus	synapsin 1b	98	33
1835	AK023003	Homo sapiens	unnamed protein product	393	81
1836	Y41740	Homo sapiens	Human PRO701 protein sequence.	429	78
1837	M36913	Zea mays	cell wall protein (put.); putative	72	35
1838	X63005	Mus musculus	proline-rich protein	98	40
1839	X83413	Human herpesvirus 6	U88	149	45
1840	AF134304	Homo sapiens	Scar2	87	37
1841	AC024772	Caenorhabditis elegans	contains similarity to Mus musculus alpha-NAC, muscle-specific form (GB:U48363)	131	25
1842	AB002366	Homo sapiens	KIAA0368	153	75
1843	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	140	47



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1844	AL035526	Arabidopsis thaliana	extensin-like protein	93	33
1845	D26156	Homo sapiens	hSNF2b	91	34
1846	M14228	Gallus gallus	c-beta-3 beta-tubulin	598	83
1847	AK022217	Homo sapiens	unnamed protein product	97	56
1848	AJ250042	Homo sapiens	Rab5 GDP/GTP exchange factor homologue	174	83
1849	W23949	Homo sapiens	Human phosphoinositide 3OH-kinase p101 subunit.	143	28
1850	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	101	63
1851	AB017114	Homo sapiens	AD 3	113	100
1852	D00570	Mus musculus	open reading frame (251 AA)	174	55
1853	A67510	Mus musculus	MUS MUSCULUS GENOMIC DNA CONTAINING N ALLELE OF FV1 GENE.	133	42
1854	U49974	Homo sapiens	mariner transposase	214	82
1855	U93569	Homo sapiens	p40	95	31
1856	D89729	Homo sapiens	CRM1 protein	475	90
1857	AF090895	Homo sapiens	PRO0117	89	36
1858	AF015926	Homo sapiens	e2rin-radixin-moesin binding phosphoprotein-50	117	73
1859	D13721	Gallus gallus	NF-kB p65 subunit	223	56
1860	K03204	Homo sapiens	salivary proline-rich protein precursor	111	32
1861	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	195	52
1862	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	331	69
1863	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	80	35
1864	L27428	Homo sapiens	reverse transcriptase	84	51
1865	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	106	46
1866	U53585	Mycobacterium avium	fibronectin attachment protein	86	36
1867	AF255446	Cryptocodinium cohnii	Dip1-associated protein C	134	45
1868	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	81	63
1869	AP000001	Pyrococcus horikoshii	235aa long hypothetical protein	108	40
1870	M13100	Rattus norvegicus	unknown protein	121	53
1871	X67863	Mus musculus	T2	101	35
1872	S80119	Rattus sp.	reverse transcriptase homolog	151	43
1873	W73633	Homo sapiens	Human secreted protein clone.	140	44
1874	U57053	Homo sapiens	myosin-ID	203	82
1875	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	54
1876	M21097	Homo sapiens	CD19 differentiation antigen	432	79
1877	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	150	52
1878	U25281	Rattus norvegicus	SH3 domain binding protein	108	36
1879	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	117	48
1880	X73113	Homo sapiens	fast MyBP-C	399	77
1881	AX028128	Homo sapiens	unnamed protein product	162	43
1882	G03789	Homo sapiens	Human secreted protein, SEQ ID NO:	138	62

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7870.		
1883	Y00664	Homo sapiens	open reading frame 1 (AA 1 - 86)	74	34
1884	U86587	Mus musculus	phosphatidylinositol 3-kinase catalytic subunit p110 delta	204	77
1885	X67337	Homo sapiens	Human pre-mRNA cleavage factor I 68 kDa subunit	148	37
1886	Y13829	Homo sapiens	MBNL protein	117	63
1887	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	119	80
1888	R95913	Homo sapiens	Neural thread protein.	91	64
1889	L39059	Homo sapiens	transcription factor SL1	92	34
1890	M69297	Homo sapiens	ORF 3	169	48
1891	R95913	Homo sapiens	Neural thread protein.	91	62
1892	Z28201	Saccharomyces cerevisiae	ORF YKL202w	95	51
1893	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	90	51
1894	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	183	73
1895	Y10055	Homo sapiens	phosphoinositide 3-kinase	564	84
1896	AF093775	Mus musculus	alpha-actinin 3	375	85
1897	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	82	66
1898	M21904	Homo sapiens	4F2 heavy chain antigen	386	80
1899	AB028997	Homo sapiens	KIAA1074 protein	145	38
1900	U97553	murid herpesvirus 4	unknown	98	41
1901	AB011142	Homo sapiens	KIAA0570 protein	209	95
1902	AF194537	Homo sapiens	NAG13	161	55
1903	U93564	Homo sapiens	putative p150	142	33
1904	M29399	Homo sapiens	erythrocyte membrane protein band 4.2	413	90
1905	Y27400	Homo sapiens	Human P450 reductase functional fragment sequence.	294	67
1906	Y28503	Homo sapiens	HGFH3 Human Growth Factor Homologue 3.	167	100
1907	AF128625	Homo sapiens	CDC42-binding protein kinase beta	509	89
1908	AB029147	Cucumis sativus	expressed in cucumber hypocotyls	98	41
1909	X13783	Homo sapiens	alpha-1 type 2 collagen (714 AA)	87	43
1910	AF240630	Mus musculus	IQ motif containing GTPase activating protein 1	330	48
1911	AF129075	Homo sapiens	T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)	511	90
1912	AF011450	Mus musculus	type XV collagen	87	28
1913	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	124	75
1914	AF171230	Vigna unguiculata	phosphatidic acid phosphatase beta	112	53
1915	AF016099	Mus musculus	endonuclease/reverse transcriptase	100	47
1916	M94131	Homo sapiens	mucin	97	37
1917	X13885	Nicotiana tabacum	extensin (AA 1-620)	120	34
1918	AF186605	Homo sapiens	MLL2 protein	115	29
1919	M12130	Mus musculus	RNA polymerase II	498	83
1920	AL049794	Homo sapiens	dJ777L9.1 (novel protein similar to mouse kinesin-like proteins KIF1A and KIF1B)	514	90
1921	D83703	Homo sapiens	peroxisome assembly factor-2	233	64
1922	Y11922	Homo sapiens	Human 5' EST secreted protein SEQ ID No: 522.	162	77

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1923	AC002481	Homo sapiens	similar to nitrogen permease regulator, similar to P39923 (PID:g730170), match to AA233630 (NID:g1856833) and AA399402 (NID:g2053147)	223	79
1924	D82060	Homo sapiens	membrane protein with histidine rich charge clusters	115	40
1925	U49974	Homo sapiens	mariner transposase	195	61
1926	S80119	Rattus sp.	reverse transcriptase homolog	104	40
1927	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	79	68
1928	S79639	Homo sapiens	EXT1=putative tumour suppressor/hereditary multiple exostoses candidate gene	430	88
1929	X58063	Brugia pahangi	major protein component of the microfilarial sheath	104	43
1930	AF119855	Homo sapiens	PRO1847	132	64
1931	AJ005577	Homo sapiens	6-phosphofructo-2-kinase	326	90
1932	AF020261	Santalum album	proline rich protein	93	33
1933	AJ272204	Homo sapiens	hypothetical protein	321	52
1934	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	116	39
1935	A61971	unidentified	MCSF	328	79
1936	U93564	Homo sapiens	putative p150	217	54
1937	U97553	murid herpesvirus 4	unknown	113	38
1938	AF194537	Homo sapiens	NAG13	90	37
1939	AF226044	Homo sapiens	HSNFRK	403	85
1940	X83413	Human herpesvirus 6	U88	303	50
1941	AJ007628	Rattus norvegicus	ELK channel 1	112	38
1942	AF104328	Arabidopsis thaliana	cell wall-plasma membrane linker protein homolog	135	35
1943	AF130089	Homo sapiens	PRO2550	93	63
1944	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	102	34
1945	M19419	Mus musculus	proline-rich salivary protein	121	40
1946	U57316	Homo sapiens	histone acetyltransferase	132	73
1947	AL163302	Homo sapiens	human type XVIII collagen	79	34
1948	AB020746	Arabidopsis thaliana	protein kinase-like protein	117	36
1949	AJ011738	Homo sapiens	In1b	209	85
1950	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	155	48
1951	AF119569	Homo sapiens	patched 2	166	89
1952	AB002107	Homo sapiens	hPer	118	39
1953	X98834	Homo sapiens	zinc finger protein Hs12	430	70
1954	Y19641	Homo sapiens	SEQ ID NO 359 from WO9922243.	96	64
1955	U93569	Homo sapiens	putative p150	157	44
1956	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	85	53
1957	AB013729	Mus musculus	semaphorin Y	106	38
1958	AC005360	Homo sapiens	FAA	338	68
1959	AJ223075	Homo sapiens	TRIP protein	598	95
1960	AC004022	Homo sapiens	serum paraoxonase/arylesterase 3	147	62
1961	AF076776	Drosophila melanogaster	helicase DOMINO A	157	45
1962	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON	587	77
1963	AF229642	Mus musculus	DXImx46e protein	127	91

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SEQ ID NO:	Accession No.	Species	Description	Smith-Idenit y Score	% Identit y
1964	U72520	Mus musculus	mena protein	89	31
1965	W40309	Homo sapiens	Human ITAK protein.	179	32
1966	AJ388557	Canis familiaris	zinc finger protein	826	56
1967	Y92515	Homo sapiens	Human OXRE-12.	224	53
1968	Y17832	Human endogenous retrovirus K	pol protein	187	49
1969	Y41245	Homo sapiens	Human Y218 protein.	220	78
1970	AB052738	Sus scrofa	Smad3	366	85
1971	AB007644	Arabidopsis thaliana	contains similarity to phytoecyanin/early nodulin-like protein--gene id:K19P17.3	106	32
1972	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	122	57
1973	AL357472	Homo sapiens	VPS33B	112	31
1974	AF151902	Homo sapiens	CGI-144 protein	112	95
1975	AL137260	Homo sapiens	hypothetical protein	148	92
1976	U89505	Homo sapiens	Hlark	408	89
1977	U67328	Mus musculus	NIP1-like protein	168	73
1978	AK026435	Homo sapiens	unnamed protein product	601	94
1979	Y14318	Homo sapiens	peroxisomal ABC-transporter	507	96
1980	U63630	Homo sapiens	MCM4	570	90
1981	AF118090	Homo sapiens	PRO2044	154	84
1982	AF016370	Homo sapiens	U4/U6 small nuclear ribonucleoprotein hPrp3	422	63
1983	AB011154	Homo sapiens	KIAA0582 protein	420	80
1984	AB011422	Homo sapiens	Trad	201	67
1985	AL390156	Homo sapiens	hypothetical protein	230	97
1986	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	163	44
1987	M12523	Homo sapiens	allobumin Venezia	411	91
1988	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	145	63
1989	Y36156	Homo sapiens	Human secreted protein #28.	107	80
1990	AF161356	Homo sapiens	HSPC093	156	57
1991	G03443	Homo sapiens	Human secreted protein, SEQ ID NO: 7524.	132	72
1992	AF119851	Homo sapiens	PRO1722	126	52
1993	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	228	60
1994	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	40
1995	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	118	58
1996	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	137	57
1997	X75068	Bos taurus	plasmalemmal porin	85	85
1998	Y64869	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1030.	92	80
1999	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	275	79
2000	AF118078	Homo sapiens	PRO1848	111	57
2001	S80119	Rattus sp.	reverse transcriptase homolog	120	61
2002	AB011110	Homo sapiens	KIAA0538 protein	146	73
2003	M15530	Homo sapiens	B-cell growth factor	94	64
2004	AF225918	Mus musculus	intestinal cell kinase	216	77
2005	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	125	85
2006	D84391	Mus musculus	reverse transcriptase	135	38
2007	AF090930	Homo sapiens	PRO0478	101	86

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2008	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	156	66
2009	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	165	49
2010	AF113685	Homo sapiens	PRO0974	124	63
2011	AF130079	Homo sapiens	PRO2852	141	78
2012	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	94	51
2013	AF090944	Homo sapiens	PRO0663	67	53
2014	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	151	58
2015	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	223	75
2016	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	137	78
2017	L26953	Homo sapiens	chromosomal protein	120	74
2018	G03646	Homo sapiens	Human secreted protein, SEQ ID NO: 7727.	68	57
2019	G03646	Homo sapiens	Human secreted protein, SEQ ID NO: 7727.	64	42
2020	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	334	63
2021	L26953	Homo sapiens	chromosomal protein	112	64
2022	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	139	69
2023	U93569	Homo sapiens	putative p150	187	89
2024	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	80	72
2025	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	71
2026	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	77	66
2027	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	372	73
2028	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	80
2029	AF194537	Homo sapiens	NAG13	158	57
2030	L26251	Trypanosoma brucei	CR5	110	41
2031	AF197913	Helicoverpa armigera nuclear polyhedrosis virus	basic DNA-binding protein BDBP	149	55
2032	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	115	80
2033	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	157	82
2034	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	133	75
2035	G03646	Homo sapiens	Human secreted protein, SEQ ID NO: 7727.	104	67
2036	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	137	71
2037	AF130089	Homo sapiens	PRO2550	146	55
2038	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	81	73
2039	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	66
2040	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	68

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2041	B01372	Homo sapiens	Neuron-associated protein.	95	79
2042	V01555	Human herpesvirus 4	BYRF1, encodes EBNA-2 (Dambaugh et al, 1984; Dillner et al, 1984)	108	77
2043	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	125	65
2044	AF118086	Homo sapiens	PRO1992	103	64
2045	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	64
2046	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	108	51
2047	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	133	68
2048	AL590114	Leishmania major	probable (hiv-6) u1 I02, variant a DNA, complete virion genome	155	64
2049	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	125	53
2050	AL390114	Leishmania major	extremely cysteine/valine rich protein	112	56
2051	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	70	62
2052	X61045	Hydra sp.	mini-collagen	99	46
2053	X83413	Human herpesvirus 6	U88	148	73
2054	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	75	63
2055	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	104	75
2056	X16524	Dictyostelium discoideum	coding region (AA 1 - 437)	104	51
2057	R95913	Homo sapiens	Neural thread protein.	83	77
2058	AF118080	Homo sapiens	PRO1880	126	61
2059	AJ276003	Homo sapiens	GARI protein	136	59
2060	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	120	70
2061	X01918	Drosophila melanogaster	salivary gland glue protein	179	40
2062	U00029	Saccharomyces cerevisiae	Yhr217cp	110	46
2063	AF130051	Homo sapiens	PRO0898	143	80
2064	AF006061	Homo sapiens	placental growth hormone isoform hGH-V3	121	85
2065	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	129	66
2066	U82303	Homo sapiens	unknown	92	68
2067	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	368	79
2068	L27428	Homo sapiens	reverse transcriptase	186	58
2069	AF130051	Homo sapiens	PRO0898	164	73
2070	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	271	73
2071	AF130051	Homo sapiens	PRO0898	110	56
2072	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	67
2073	AF157706	Human herpesvirus 6B	B4	104	49
2074	AL049608	Arabidopsis thaliana	extensin-like protein	120	41
2075	AP002460	Arabidopsis thaliana	gene_id:F1D9.26-unknown protein	150	27
2076	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	130	85

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2077	M11897	Mus musculus	proline-rich salivary protein	125	42
2078	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	66	75
2079	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	185	47
2080	AJ006470	Homo sapiens	cartilage-associated protein (CASP)	139	84
2081	AK024509	Homo sapiens	unnamed protein product	132	83
2082	U93564	Homo sapiens	putative p150	137	67
2083	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	99	71
2084	B01372	Homo sapiens	Neuron-associated protein.	148	81
2085	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	114	76
2086	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	255	63
2087	AF194537	Homo sapiens	NAG13	122	78
2088	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	108	74
2089	AF130079	Homo sapiens	PRO2852	149	77
2090	U93574	Homo sapiens	p40	260	96
2091	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	99	76
2092	AF194537	Homo sapiens	NAG13	125	51
2093	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	319	72
2094	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	56
2095	U93572	Homo sapiens	putative p150	195	57
2096	X83413	Human herpesvirus 6	U88	132	57
2097	AF010400	Homo sapiens	transaldolase-related protein	463	89
2098	U93563	Homo sapiens	putative p150	128	35
2099	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	160	43
2100	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	133	43
2101	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	97	71
2102	K02401	Homo sapiens	chorionic somatomammotropin	628	90
2103	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	80
2104	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	309	63
2105	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	192	37
2106	Y59772	Homo sapiens	Human normal ovarian tissue derived protein 49.	261	89
2107	AF202051	Homo sapiens	NM23-H8	680	100
2108	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	127	54
2109	L22029	Glycine max	hydroxyproline-rich glycoprotein	121	36
2110	D26135	Homo sapiens	diacylglycerol kinase gamma	172	100
2111	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	56
2112	X65488	Homo sapiens	hnRNP U protein	117	70
2113	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein thalA.	116	35
2114	AF130051	Homo sapiens	PRO0898	93	62
2115	AJ242540	Volvox carterii f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	260	53
2116	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	70

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2117	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	304	71
2118	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	70	66
2119	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	118	84
2120	S79410	Mus musculus	nuclear localization signal binding protein	94	94
2121	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	304	73
2122	M11901	Rattus norvegicus	proline-rich salivary protein	83	32
2123	AK025047	Homo sapiens	unnamed protein product	116	48
2124	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	95	72
2125	AF138883	Bos taurus	type II collagen cyanogen bromide fragment CB10	103	40
2126	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	186	100
2127	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	117	52
2128	AF194537	Homo sapiens	NAG13	126	66
2129	AB015802	Acetobacter xylinus	similar to cellulose complementing protein of A. xylinum ATCC23869	109	80
2130	AF187147	Mus musculus	drebrin A	110	38
2131	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	148	42
2132	L36341	Aspergillus nidulans	regulatory protein	130	49
2133	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	119	58
2134	AF116689	Homo sapiens	PRO2168	113	81
2135	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	191	38
2136	M81321	Macaca fascicularis	proline-rich protein	125	43
2137	A18812	Brassica napus	extensin	106	34
2138	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	104	41
2139	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	191	92
2140	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	196	90
2141	Y57285	Homo sapiens	Human GPCR protein (HGPRP) sequence (clone ID 2214673).	507	78
2142	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	201	47
2143	AF090944	Homo sapiens	PRO0663	164	53
2144	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	390	76
2145	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	198	70
2146	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	119	82
2147	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	194	45
2148	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	91	60
2149	AF090942	Homo sapiens	PRO0657	129	66
2150	AF130089	Homo sapiens	PRO2550	372	82
2151	AC009991	Arabidopsis	unknown protein	81	59



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		thaliana			
2152	AF090942	Homo sapiens	PRO0657	93	53
2153	R13319	Homo sapiens	Partial Human Natural Killer receptor.	215	89
2154	AC008075	Arabidopsis thaliana	F24J5.4	139	36
2155	AL390114	Leishmania major	extremely cysteine/valine rich protein	148	50
2156	S79410	Mus musculus	nuclear localization signal binding protein	112	58
2157	AK024455	Homo sapiens	FLJ00047 protein	152	66
2158	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	85	80
2159	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	165	75
2160	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	145	45
2161	AF119900	Homo sapiens	PRO2822	138	71
2162	AJ223953	Homo sapiens	hPTTG	106	62
2163	AK023542	Homo sapiens	unnamed protein product	76	52
2164	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	118	84
2165	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	137	65
2166	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	348	88
2167	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	108	84
2168	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	114	48
2169	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	125	67
2170	AF130089	Homo sapiens	PRO2550	142	65
2171	Y19609	Homo sapiens	SEQ ID NO 327 from WO9922243.	103	65
2172	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	39
2173	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	91	50
2174	D38435	Homo sapiens	homologue of yeast PMS1	314	96
2175	AF119851	Homo sapiens	PRO1722	230	69
2176	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	100	63
2177	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	137	44
2178	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP-CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	139	42
2179	AL049608	Arabidopsis thaliana	extensin-like protein	286	57
2180	L17318	Rattus norvegicus	proline-rich proteoglycan	148	40
2181	AK024455	Homo sapiens	FLJ00047 protein	97	63
2182	R95913	Homo sapiens	Neural thread protein.	100	69
2183	AF266479	Homo sapiens	rectachrome 1	148	81
2184	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	64	70
2185	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	107	40
2186	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	110	84

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2187	AF137273	Gallus gallus	alpha 1 (V) collagen	103	43
2188	K03205	Homo sapiens	salivary proline-rich protein precursor	115	36
2189	D90064	Homo sapiens	NCA-W272	271	100
2190	AF130089	Homo sapiens	PRO2550	137	68
2191	X65165	Volvox carteri	extensin	113	62
2192	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	154	59
2193	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	148	59
2194	U52077	Homo sapiens	mariner transposase	257	53
2195	B12310	Homo sapiens	Human secreted protein encoded by gene 10 clone HDPGP94.	98	79
2196	D38112	Homo sapiens	NADH dehydrogenase subunit 5	180	77
2197	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	121	65
2198	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	126	64
2199	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	101	67
2200	AJ007042	Homo sapiens	TRX5 protein	264	75
2201	AF130051	Homo sapiens	PRO0898	71	61
2202	AK024455	Homo sapiens	FLJ00047 protein	153	62
2203	U83303	Homo sapiens	line-1 reverse transcriptase	95	52
2204	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	128	82
2205	AF090895	Homo sapiens	PRO0117	163	69
2206	G03806	Homo sapiens	Human secreted protein, SEQ ID NO: 7887.	154	69
2207	R95913	Homo sapiens	Neural thread protein.	103	86
2208	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	144	78
2209	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	100	65
2210	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	111	45
2211	AF090931	Homo sapiens	PRO0483	63	90
2212	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	100	74
2213	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	98	41
2214	M76671	Lycopersicon esculentum	extensin (class II)	137	35
2215	X03717	Homo sapiens	pot. unidentified reading frame	98	54
2216	R95913	Homo sapiens	Neural thread protein.	109	48
2217	AF118086	Homo sapiens	PRO1992	138	79
2218	AF081484	Homo sapiens	alpha-tubulin isoform 1	343	95
2219	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	157	84
2220	AF141347	Homo sapiens	alpha-tubulin	571	94
2221	AF071172	Homo sapiens	HERC2	187	84
2222	M17783	Homo sapiens	glia-derived nexin precursor	529	83
2223	AF081484	Homo sapiens	alpha-tubulin isoform 1	588	85
2224	AK026072	Homo sapiens	unnamed protein product	199	57
2225	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	161	61
2226	Z70684	Caenorhabditis elegans	F28D1.8	126	41
2227	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	124	63

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2228	AF119855	Homo sapiens	PRO1847	108	74
2229	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	122	55
2230	AF090944	Homo sapiens	PRO0663	146	61
2231	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	152	74
2232	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	80	59
2233	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	129	58
2234	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	143	60
2235	AK024455	Homo sapiens	FLJ00047 protein	133	71
2236	Y87105	Homo sapiens	Human secreted protein sequence SEQ ID NO:142.	99	59
2237	U87607	Rattus norvegicus	putative RNA binding protein 1	111	38
2238	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	119	63
2239	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	75	65
2240	L27428	Homo sapiens	reverse transcriptase	136	40
2241	R96800	Homo sapiens	Human histocyte-secreted factor HSF.	122	82
2242	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	105	95
2243	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	79	48
2244	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	145	75
2245	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	346	87
2246	U82303	Homo sapiens	unknown	153	79
2247	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	105	45
2248	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	105	47
2249	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	63
2250	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	124	62
2251	X81206	Drosophila hydei	histone H3.3	101	71
2252	AF155581	Danio rerio	proteasome subunit beta 7	92	52
2253	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	172	60
2254	AF084225	Homo sapiens	cytochrome P450 2E1	114	46
2255	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	136	64
2256	AL132841	Caenorhabditis elegans	Y15E3A.3	147	90
2257	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	297	59
2258	U93563	Homo sapiens	putative p150	218	66
2259	L22650	Homo sapiens	early lymphoid activation protein	82	55
2260	AF194537	Homo sapiens	NAG13	117	56
2261	U43360	Peromyscus maniculatus	reverse transcriptase	130	82
2262	G00366	Homo sapiens	Human secreted protein, SEQ ID NO: 4447.	86	66
2263	AL021918	Homo sapiens	b3418.1 (Kruppel related Zinc Finger protein 184)	372	61
2264	AL390114	Leishmania major	extremely cysteine/valine rich protein	122	71

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2265	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	123	79
2266	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	204	95
2267	L29029	Chlamydomonas reinhardtii	amino acid feature: Rod protein domain, aa 266 .. 468; amino acid feature: globular protein domain, aa 32 .. 265	141	58
2268	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	499	84
2269	A11693	Homo sapiens	start codon not included	594	87
2270	AB014554	Homo sapiens	KIAA0654 protein	141	63
2271	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	112	60
2272	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	118	54
2273	Y20852	Homo sapiens	Human neurofilament-H mutant protein fragment 11.	125	35
2274	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	92	66
2275	AL359782	Trypanosoma brucei	possible (hly-6) u1102, variant a dna, complete virion genome.	198	64
2276	U15647	Mus musculus	reverse transcriptase	100	72
2277	AJ004810	Zea mays	cytochrome P450 monooxygenase	129	43
2278	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	111	67
2279	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	112	68
2280	L27428	Homo sapiens	reverse transcriptase	150	60
2281	K03202	Homo sapiens	salivary proline-rich protein precursor	142	40
2282	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	121	54
2283	D00570	Mus musculus	open reading frame (251 AA)	169	56
2284	Y02887	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	86	54
2285	AL359782	Trypanosoma brucei	possible (hly-6) u1102, variant a dna, complete virion genome.	144	50
2286	AF119901	Homo sapiens	PRO2831	116	82
2287	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	126	73
2288	AF130089	Homo sapiens	PRO2550	102	75
2289	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	113	70
2290	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	127	64
2291	L26953	Homo sapiens	chromosomal protein	137	53
2292	AF161356	Homo sapiens	HSPC093	100	57
2293	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	138	68
2294	X03145	Homo sapiens	pot. ORF I	120	43
2295	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	83	52
2296	AK024455	Homo sapiens	FLJ00047 protein	98	66
2297	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	123	73
2298	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	349	73
2299	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	109	61

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2300	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	100	81
2301	AF251290	Plasmodium falciparum	glutamic acid-rich protein	112	40
2302	AF155232	Pisum sativum	extensin	89	36
2303	AF130089	Homo sapiens	PRO2550	83	50
2304	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	84	51
2305	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	86	30
2306	AF002031	Arabidopsis thaliana	gene_id:K3D20.3~	168	44
2307	AF157321	Homo sapiens	30 kDa protein	309	64
2308	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	170	57
2309	M76546	Helianthus annuus	hydroxyproline-rich protein	198	42
2310	Y27607	Homo sapiens	Human secreted protein encoded by gene No. 41.	207	100
2311	AF130089	Homo sapiens	PRO2550	106	66
2312	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	117	60
2313	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phage clone lambda HC2533.	114	80
2314	A032910	Hylobates muelleri	dopamine receptor D4	108	40
2315	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	59
2316	AK024455	Homo sapiens	FLJ00047 protein	134	58
2317	AF238235	Entamoeba histolytica	diaphanous protein	103	51
2318	U15647	Mus musculus	reverse transcriptase	101	37
2319	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	117	51
2320	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	163	78
2321	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	97	48
2322	D00570	Mus musculus	open reading frame (196 AA)	122	39
2323	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	122	75
2324	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	118	79
2325	U44838	Glycine max	extensin	126	36
2326	Y87103	Homo sapiens	Human secreted protein sequence SEQ ID NO:142.	99	59
2327	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	408	79
2328	AF194537	Homo sapiens	NAG13	181	66
2329	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	405	75
2330	X53581	Rattus norvegicus	ORF4	116	45
2331	L26953	Homo sapiens	chromosomal protein	108	67
2332	L27428	Homo sapiens	reverse transcriptase	117	76
2333	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	84	50
2334	AF191687	Homo sapiens	alanine-glyoxylate aminotransferase homolog	100	37
2335	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	84	68

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2336	AL390114	Leishmania major	extremely cysteine/valine rich protein	106	53
2337	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	65
2338	R95913	Homo sapiens	Neural thread protein.	164	67
2339	AF090942	Homo sapiens	PRO0657	122	81
2340	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	107	90
2341	AF090942	Homo sapiens	PRO0657	124	60
2342	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	126	83
2343	AB013454	Rattus norvegicus	NaPi-2 beta	143	77
2344	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	127	73
2345	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	146	45
2346	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	120	40
2347	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	55
2348	Y36203	Homo sapiens	Human secreted protein #75.	138	78
2349	L26953	Homo sapiens	chromosomal protein	131	57
2350	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	120	65
2351	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	144	58
2352	AF130051	Homo sapiens	PRO0898	155	70
2353	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	134	76
2354	L27428	Homo sapiens	reverse transcriptase	141	71
2355	L26953	Homo sapiens	chromosomal protein	128	66
2356	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	148	75
2357	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	115	62
2358	B12310	Homo sapiens	Human secreted protein encoded by gene 10 clone HDPGP94.	115	50
2359	M76546	Helianthus annuus	hydroxyproline-rich protein	103	43
2360	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	82	80
2361	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	95	72
2362	M64793	Rattus norvegicus	salivary proline-rich protein	117	41
2363	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	98	80
2364	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	152	45
2365	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	85	55
2366	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	101	77
2367	AF093097	Homo sapiens	putative RNA-binding protein Q99	248	97
2368	U52077	Homo sapiens	inaret transposase	227	74
2369	X07882	Homo sapiens	Po protein	102	38
2370	U44838	Glycine max	extensin	102	32
2371	AB012223	Canis familiaris	ORF2	158	60
2372	AF025467	Caenorhabditis	contains similarity to drosophila DNA-	104	42

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		<i>elegans</i>	binding protein K10 (NID:g8148)		
2373	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	107	40
2374	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	106	67
2375	AF118086	Homo sapiens	PRO1992	169	65
2376	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	95	55
2377	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	121	59
2378	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICE1) protein sequence.	141	70
2379	R95913	Homo sapiens	Neural thread protein.	120	50
2380	U93572	Homo sapiens	putative p150	124	53
2381	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	195	66
2382	U52077	Homo sapiens	mariner transposase	282	67
2383	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	113	43
2384	A1242540	<i>Volvox carterii nagariensis</i>	hydroxyproline-rich glycoprotein DZ-HRGP	112	37
2385	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	88	75
2386	AF130089	Homo sapiens	PRO2550	160	62
2387	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	166	61
2388	AF130089	Homo sapiens	PRO2550	103	71
2389	AB027890	<i>Schizosaccharomyces pombe</i>	Hypothetical protein	116	100
2390	U93570	Homo sapiens	putative p150	151	54
2391	Y19767	Homo sapiens	SEQ ID NO:485 from WO9922243.	110	71
2392	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	109	67
2393	AE001381	<i>Plasmodium falciparum</i>	hypothetical protein	94	34
2394	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	62
2395	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	57	56
2396	U42471	<i>Mus musculus</i>	Wiscott-Aldrich Syndrome protein homolog	107	43
2397	AF210651	Homo sapiens	NAG18	162	54
2398	M11901	<i>Rattus norvegicus</i>	proline-rich salivary protein	116	34
2399	S80864	Homo sapiens	cytochrome c-like polypeptide	115	68
2400	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	141	54
2401	M13100	<i>Rattus norvegicus</i>	unknown protein	148	46
2402	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	133	70
2403	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	366	94
2404	AF113685	Homo sapiens	PRO0974	112	56
2405	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	98	67
2406	R41001	Homo sapiens	Human myotonic dystrophy gene protein.	207	68
2407	AL390114	<i>Leishmania</i>	probable (hhv-6) u1102, variant a	127	63

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		major	DNA, complete virion genome		
2408	G03101	Homo sapiens	Human secreted protein, SEQ ID NO: 7182.	378	95
2409	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	250	86
2410	U72520	Mus musculus	mena protein	115	40
2411	AF000616	Oryza sativa	similar to RING-H2 finger protein RH1A1a (AF078683)	132	44
2412	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	109	85
2413	AF119901	Homo sapiens	PRO2831	113	66
2414	R95913	Homo sapiens	Neural thread protein.	93	57
2415	B01372	Homo sapiens	Neuron-associated protein.	104	83
2416	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	130	50
2417	J02459	bacteriophage lambda	K (tail component;199)	720	92
2418	J04694	Mus musculus	alpha-1 type IV collagen	103	43
2419	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	145	61
2420	W26496	Homo sapiens	CD2 associated intracellular protein CAIP LS02-21.	115	80
2421	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	145	38
2422	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	158	73
2423	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	70
2424	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	122	61
2425	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	95	59
2426	U93565	Homo sapiens	putative p150	147	75
2427	AL390114	Leishmania major	extremely cysteine/valine rich protein	246	53
2428	R96800	Homo sapiens	Human histocyte-secreted factor HSF.	138	61
2429	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	112	75
2430	D13892	Homo sapiens	carboxyl methyltransferase	181	68
2431	X97675	Homo sapiens	plakophilin 2b	131	65
2432	G02896	Homo sapiens	Human secreted protein, SEQ ID NO: 6977.	108	70
2433	X03145	Homo sapiens	pot. ORF III	180	82
2434	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	77	86
2435	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	421	67
2436	M64793	Rattus norvegicus	salivary proline-rich protein	111	38
2437	AF210651	Homo sapiens	NAG18	128	72
2438	AF016099	Mus musculus	endonuclease/reverse transcriptase	232	46
2439	AL160493	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	122	53
2440	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	136	80
2441	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	139	54
2442	AF090895	Homo sapiens	PRO0117	115	61
2443	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	125	70



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2444	G00594	Homo sapiens	Human secreted protein, SEQ ID NO: 4675.	71	80
2445	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	81	37
2446	AF090895	Homo sapiens	PRO0117	86	64
2447	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	103	86
2448	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	61
2449	L21936	Homo sapiens	succinate dehydrogenase flavoprotein subunit	168	91
2450	AF090942	Homo sapiens	PRO0657	134	71
2451	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	126	87
2452	K03179	Homo sapiens	pro-alpha-1 type-I collagen	120	44
2453	AF118082	Homo sapiens	PRO1902	143	46
2454	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	114	68
2455	AF130089	Homo sapiens	PRO2550	125	89
2456	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	134	71
2457	Y36243	Homo sapiens	Human secreted protein encoded by gene 20.	93	75
2458	Y09945	Rattus norvegicus	putative integral membrane transport protein	166	46
2459	AF130052	Homo sapiens	PRO0956	75	48
2460	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	162	76
2461	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	123	69
2462	AL390114	Leishmania major	probable (hvh-6) u1102, variant a DNA, complete virion genome	157	48
2463	X83413	Human herpesvirus 6	U88	236	50
2464	G00517	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	181	53
2465	X83413	Human herpesvirus 6	U88	218	50
2466	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	147	57
2467	X83413	Human herpesvirus 6	U88	196	53
2468	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	165	61
2469	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	101	46
2470	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	221	56
2471	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	136	63
2472	AL359782	Trypanosoma brucei	possible (hvh-6) u1102, variant a dna, complete virion genome.	122	94
2473	AF161361	Homo sapiens	HSPC098	120	60
2474	M76546	Helianthus annuus	hydroxyproline-rich protein	142	40
2475	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	150	58
2476	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	78	48
2477	AL160371	Leishmania	probable (hvh-6) u1102, variant a	86	46

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		major	DNA, complete virion genome		
2478	G01478	Homo sapiens	Human secreted protein, SEQ ID NO: 5559.	96	66
2479	AL033545	Arabidopsis thaliana	extensin-like protein	114	40
2480	AL359782	Trypanosoma brucei	possible (hiv-6) u1102, variant a dna, complete virion genome.	142	59
2481	AL390114	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	146	62
2482	AL132902	Caenorhabditis elegans	Y71A12B.4	160	37
2483	AF154502	Homo sapiens	quiescent cell proline dipeptidase	439	88
2484	AF010326	Drosophila melanogaster	short form of CHIP	56	42
2485	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	119	50
2486	W31186	Homo sapiens	Human p160 polypeptide 160.2.	115	60
2487	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	103	74
2488	L26953	Homo sapiens	chromosomal protein	129	68
2489	Y21418	Homo sapiens	Human high mobility group protein HMGI-C mutant fragment 2.	96	46
2490	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	366	94
2491	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	158	76
2492	U12707	Homo sapiens	Wiskott-Aldrich syndrome protein	144	47
2493	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	117	81
2494	X92485	Plasmodium vivax	pval	116	64
2495	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	92	64
2497	AF161483	Homo sapiens	HSPC134	211	78
2498	X05006	Homo sapiens	S-protein	298	92
2499	AB032911	Hylobates agilis	dopamine receptor D4	89	42
2500	M98502	Mus musculus	pMLZ-4	325	90
2501	Y94920	Homo sapiens	Human secreted protein clone pm412_12 protein sequence SEQ ID NO:46.	569	85
2502	AB049054	Homo sapiens	brain link protein-1	224	90
2503	AF064604	Homo sapiens	KE03 protein	224	37
2504	Z69727	Schizosaccharomyces pombe	putative dna-directed rna polymerase iii 130 kd polypeptide (ec 2.7.7.6)	384	61
2505	M11901	Rattus norvegicus	proline-rich salivary protein	147	43
2506	AJ010604	Mus musculus	L-Sox5 protein	366	87
2507	X83413	Human	U88	203	46
2508	AJ277425	Globodera pallida	putative cuticular collagen	125	40
2509	AB017919	Homo sapiens	peptidylarginine deiminase type V	148	81
2510	AF001947	Homo sapiens	U4/U6-associated RNA splicing factor	583	97
2511	AJ238520	Homo sapiens	putative transcription factor-like nuclear regulator	722	100
2512	AL390736	Homo sapiens	bA209J19.1.1 (GW112 protein)	557	84
2513	D84223	Homo sapiens	leucyl tRNA synthetase	1113	100
2514	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	174	56

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2515	U60803	Homo sapiens	clathrin heavy chain 2	111	92
2516	AJ388557	Canis familiaris	zinc finger protein	826	56
2517	AB027251	Homo sapiens	zinc finger protein (ZFD25)	631	85
2518	AK023160	Homo sapiens	unnamed protein product	168	54
2519	D87326	Mus musculus	GSG2	575	73
2520	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	100	42
2521	X67688	Homo sapiens	transketolase	120	66
2522	AF074086	Homo sapiens	protease	390	86
2523	AF220509	Homo sapiens	transcription associated factor TAFII31L	801	99
2524	AL078463	Homo sapiens	dJ365119.1 (KIAA0456)	374	92
2525	AF038995	Mus musculus	putative RNA helicase RCK	160	93
2526	M60618	Homo sapiens	nuclear autoantigen	116	75
2527	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	101	57
2528	X68790	Homo sapiens	Bactericidal /Permeability Increasing Protein	136	90
2529	A01592	Homo sapiens	haemoglobin A beta chain	508	94
2530	U89277	Homo sapiens	polyhomeotic 1 homolog	404	79
2531	X90845	Rattus norvegicus	alpha1 spectrin	507	87
2532	AL137081	Arabidopsis thaliana	phenylalanine-tRNA synthetase-like protein	178	33
2533	Y18046	Homo sapiens	FGFR1 oncogene partner (FOP)	363	100
2534	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	113	42
2535	X61047	Hydra sp.	mini-collagen	102	38
2536	AB006330	Mus musculus	SOX5	559	94
2537	AC006283	Arabidopsis thaliana	En/Spm-like transposon protein	149	33
2538	AF196779	Homo sapiens	JM11 protein	139	57
2539	AK000741	Homo sapiens	unnamed protein product	233	47
2540	Y18046	Homo sapiens	FGFR1 oncogene partner (FOP)	315	84
2541	U54996	Homo sapiens	HZW10	371	81
2542	G02631	Homo sapiens	Human secreted protein, SEQ ID NO: 6712.	99	45
2543	M95610	Homo sapiens	alpha-2 IX collagen	93	34
2544	AF071173	Mus musculus	Herc2	349	82
2545	AB000516	Homo sapiens	DSIF p160	600	93
2546	AL355178	Homo sapiens	dJ947L8.1.6 (novel CUB and Sushi (SCR repeat) domain protein)	39.5	90
2547	U93574	Homo sapiens	putative p150	235	76
2548	X80035	Oryctolagus cuniculus	cysteine rich hair keratin associated protein	99	31
2549	U58088	Homo sapiens	Hs-CUL-2	592	86
2550	L26953	Homo sapiens	chromosomal protein	131	63
2551	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	99	61
2552	U39412	Homo sapiens	alpha SNAP	159	54
2553	AF248651	Homo sapiens	RNA-binding protein BRUNOL4	569	93
2554	AJ006519	Rattus norvegicus	ASIC-beta	164	73
2555	U93570	Homo sapiens	putative p150	169	52
2556	AF104328	Arabidopsis thaliana	cell wall-plasma membrane linker protein homolog	105	29
2557	AB028975	Homo sapiens	KIAA1052 protein	610	83
2558	AJ245621	Homo sapiens	CTL2 protein	286	47

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2559	AF090944	Homo sapiens	PRO0663	174	78
2560	Y17832	Human: endogenous retrovirus K	pol protein	411	63
2561	AF109907	Homo sapiens	S164	279	44
2562	A09561	synthetic construct	human serum albumin	680	91
2563	U48359	Gallus gallus	kinesin light chain	575	81
2564	R63235	Homo sapiens	CNS neural thread protein HB4.	435	88
2565	D38112	Homo sapiens	NADH dehydrogenase subunit 4	623	89
2566	AF154916	Chlamydomonas reinhardtii	variable flagellar number protein	117	36
2567	AF181657	Drosophila melanogaster	BcDNA.LD34475	261	42
2568	M12530	Homo sapiens	transferrin precursor	693	87
2569	U96915	Homo sapiens	sin3 associated polypeptide p18	651	93
2570	R74205	Homo sapiens	Human death associated protein DAP-2.	285	27
2571	AL078593	Homo sapiens	dJ210B1.1 (KIAA0680)	107	37
2572	AF295405	Phaseolus coccineus	seed-microphyllar-endothelium-specific protein	88	39
2573	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	110	49
2574	AB024601	Pseudomonas aeruginosa	uridylyl transferase	120	37
2575	AB050893	Anadara nodifera	cytochrome c oxidase subunit I	111	79
2576	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	130	72
2577	M17697	Homo sapiens	glutamate dehydrogenase	369	61
2578	AF045640	Caenorhabditis elegans	C11D2.4 gene product	264	43
2579	U71382	Homo sapiens	OB binding protein-1	273	86
2580	AF116661	Homo sapiens	PRO1438	114	61
2581	AK000496	Homo sapiens	unnamed protein product	153	55
2582	A67510	Mus musculus	MUS MUSCULUS GENOMIC DNA CONTAINING N ALLELE OF FV1 GENE.	190	38
2583	Y44851	Homo sapiens	Human CD39-L66 protein.	205	97
2584	AB029151	Homo sapiens	D29	253	73
2585	AF039023	Homo sapiens	Ran-GTP binding protein; RanBP6	765	94
2586	AF054180	Homo sapiens	hematopoietic cell derived zinc finger protein	116	34
2587	AF283645	Homo sapiens	folate transporter/carrier	580	82
2588	AF090930	Homo sapiens	PRO0478	132	67
2589	AC002339	Arabidopsis thaliana	putative ABC transporter	238	34
2590	M34668	Homo sapiens	protein tyrosine phosphatase (EC 3.1.3.48)	627	86
2591	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	141	63
2592	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	142	63
2593	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	146	54
2594	AF047437	Homo sapiens	sperm acrosomal protein	526	74
2595	U28789	Mus musculus	PACT	528	71
2596	AB002366	Homo sapiens	KIAA0368	615	83
2597	AL049610	Homo sapiens	dJ1055C14.2 (KIAA0026 (transcription factor-like protein	704	93

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			MRGX)		
2598	G01279	Homo sapiens	Human secreted protein, SEQ ID NO: 5360.	385	79
2599	AF090895	Homo sapiens	PRO0117	142	61
2600	D29763	Mus musculus	seizure-related gene product 6 precursor	119	76
2601	U20158	Homo sapiens	SLP-76	108	53
2602	D38112	Homo sapiens	NADH dehydrogenase subunit 2	242	78
2603	D38112	Homo sapiens	NADH dehydrogenase subunit 2	233	73
2604	L24804	Homo sapiens	p23	259	62
2605	Y12102	Homo sapiens	Human 5' EST secreted protein SEQ ID NO: 415.	132	92
2606	U79284	Homo sapiens	SEC14L	614	81
2607	AF202635	Homo sapiens	PP1200	105	47
2608	AF277374	Homo sapiens	enhancer of polycomb	254	85
2609	X03484	Homo sapiens	raf protein (aa 1-648)	600	82
2610	U15637	Homo sapiens	CD40 binding protein	465	82
2611	U40265	Trypanosoma cruzi	ATPase subunit 6	98	31
2612	AF090942	Homo sapiens	PRO0657	125	48
2613	V00662	Homo sapiens	cytochrome oxidase I	605	82
2614	U46920	Homo sapiens	metaxin	748	94
2615	Y19757	Homo sapiens	SEQ ID NO 475 from WO9922243.	113	87
2616	AK025047	Homo sapiens	unnamed protein product	173	58
2617	D13866	Homo sapiens	alpha-catenin	569	96
2618	U20536	Homo sapiens	cysteine protease Mch2 isoform alpha	588	87
2619	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	608	86
2620	AF190168	Homo sapiens	serum albumin precursor	522	78
2621	A06977	Homo sapiens	albumin	607	93
2622	R14584	Homo sapiens	TGF beta 1 binding protein encoded by clone BPA 13.	339	81
2623	X56698	Xenopus laevis	42Sp48	117	47
2624	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	131	57
2625	X07881	Homo sapiens	proline-rich protein G1	116	32
2626	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	89	58
2627	A00279	synthetic construct	Human serum albumin	564	95
2628	AK021613	Homo sapiens	unnamed protein product	214	70
2629	M23613	Homo sapiens	nucleophosmin	486	82
2630	AF243424	Homo sapiens	SG2NA beta isoform	256	98
2631	G00506	Homo sapiens	Human secreted protein, SEQ ID NO: 4587.	81	60
2632	A06977	Homo sapiens	albumin	457	74
2633	A06977	Homo sapiens	albumin	563	93
2634	M81088	Rattus norvegicus	EF-1-alpha	165	68
2635	AL359587	Homo sapiens	hypothetical protein	496	82
2636	A03758	Homo sapiens	serum albumin	576	91
2637	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	127	39
2638	U93563	Homo sapiens	putative p150	186	38
2639	U68729	Meloidogyne incognita	cuticle preprocollagen	113	34
2640	AB033056	Homo sapiens	KIAA1230 protein	269	94
2641	AF116712	Homo sapiens	PRO2738	115	61
2642	W48353	Homo sapiens	Human breast cancer related protein	124	72

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCFLT2.		
2643	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	98	54
2644	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	127	64
2645	AK025116	Homo sapiens	unnamed protein product	104	64
2646	X92485	Plasmodium vivax	pva1	100	47
2647	AF130089	Homo sapiens	PRO2550	122	51
2648	AF194537	Homo sapiens	NAG13	279	83
2649	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	90	66
2650	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	148	63
2651	AF116661	Homo sapiens	PRO1438	112	46
2652	U63542	Homo sapiens	FAP protein	128	79
2653	AI.359782	Trypanosoma brucei	possible (hiv-6) u1102, variant a dna, complete virion genome.	133	46
2654	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICE1) protein sequence.	139	72
2655	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	72
2656	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	145	51
2657	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	166	64
2658	B25722	Homo sapiens	Human secreted protein sequence encoded by gene 9 SEQ ID NO:111.	91	88
2659	X92485	Plasmodium vivax	pva1	141	60
2660	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	68	68
2661	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	96	59
2662	AF090931	Homo sapiens	PRO0483	114	74
2663	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	129	57
2664	AF090930	Homo sapiens	PRO0478	170	78
2665	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	460	77
2666	D38112	Homo sapiens	cytochrome c oxidase subunit I	368	67
2667	AF090931	Homo sapiens	PRO0483	90	88
2668	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	121	66
2669	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	169	73
2670	AF194537	Homo sapiens	NAG13	170	42
2671	X86003	Rattus norvegicus	neuron-derived orphan receptor	104	50
2672	U63542	Homo sapiens	FAP protein	139	75
2673	AF090930	Homo sapiens	PRO0478	130	69
2674	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	161	75
2675	AK024455	Homo sapiens	FLJ00047 protein	105	53
2676	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	142	67
2677	AK000496	Homo sapiens	unnamed protein product	110	67
2678	AF116715	Homo sapiens	PRO2829	151	78
2679	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	160	72
2680	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	110	81

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6613.		
2681	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	131	75
2682	U76604	Homo sapiens	180 kDa bullous pemphigoid antigen 2/type XVII collagen	96	37
2683	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	85	55
2684	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488	127	80
2685	AF090895	Homo sapiens	PRO0117	81	51
2686	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	119	52
2687	M64793	Rattus norvegicus	salivary proline-rich protein	122	41
2688	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	145	71
2689	AF130089	Homo sapiens	PRO2550	149	78
2690	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	102	47
2691	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	116	74
2692	G03064	Homo sapiens	Human secreted protein, SEQ ID NO: 7145.	130	60
2693	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	106	26
2694	AE001158	Borrelia burgdorferi	conserved hypothetical integral membrane protein	81	37
2695	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	162	76
2696	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	100
2697	AF194537	Homo sapiens	NAG13	126	90
2698	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	69
2699	U93563	Homo sapiens	putative p150	138	37
2700	AF090928	Homo sapiens	PRO0470	177	57
2701	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	75
2702	X92485	Plasmodium vivax	pva1	116	50
2703	AK024455	Homo sapiens	FLJ00047 protein	103	57
2704	D38114	Gorilla gorilla	NADH dehydrogenase subunit 2 (ND2)	137	81
2705	AF090895	Homo sapiens	PRO0117	105	51
2706	AF090944	Homo sapiens	PRO0663	121	45
2707	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	104	57
2708	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	157	85
2709	D38112	Homo sapiens	NADH dehydrogenase subunit 1	283	84
2710	AF130079	Homo sapiens	PRO2852	125	48
2711	M22334	Homo sapiens	unknown protein	131	50
2712	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	123	58
2713	S80119	Rattus sp.	reverse transcriptase homolog	230	57
2714	AF090931	Homo sapiens	PRO0483	98	85
2715	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	104	79
2716	L00016	Homo sapiens	urfs	295	93
2717	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HIDAD22.	135	82
2718	M81321	Macaca fascicularis	proline-rich protein	117	38

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2719	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	124	57
2720	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	147	56
2721	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	132	67
2722	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	129	56
2723	D38112	Homo sapiens	cytochrome c oxidase subunit I	392	68
2724	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	182	79
2725	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	92
2726	W97293	Homo sapiens	An annexin binding protein (NABP-1).	193	40
2727	U12690	Homo sapiens	cytochrome oxidase subunit II	547	85
2728	V00662	Homo sapiens	cytochrome oxidase I	500	92
2729	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	110	56
2730	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	124	75
2731	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	113	57
2732	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	149	51
2733	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	101	44
2734	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	288	81
2735	Z74036	Caenorhabditis elegans	contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=58.9, E-value=3.5e-14, N=3	117	37
2736	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	154	62
2737	AK024455	Homo sapiens	FLJ00047 protein	136	60
2738	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	110	63
2739	AP002460	Arabidopsis thaliana	gene_id:FD9.26-unknown protein	363	90
2740	D38113	Fan troglodytes	cytochrome c oxidase subunit I	358	69
2741	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	143	64
2742	L27428	Homo sapiens	reverse transcriptase	119	45
2743	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	76	63
2744	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	155	79
2745	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	114	51
2746	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	75
2747	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	162	79
2748	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	107	49
2749	AK024455	Homo sapiens	FLJ00047 protein	165	69
2750	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	167	72
2751	M22332	Homo sapiens	unknown protein	208	46



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2752	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	125	56
2753	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	150	65
2754	AF220264	Homo sapiens	MOST-1	130	52
2755	AK024455	Homo sapiens	FLJ00047 protein	128	58
2756	AF130051	Homo sapiens	PRO0898	162	73
2757	D38112	Homo sapiens	NADH dehydrogenase subunit 3	259	86
2758	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	124	58
2759	AJ243666	Homo sapiens	NICE-5 protein	118	84
2760	D38112	Homo sapiens	NADH dehydrogenase subunit 4	533	90
2761	G02482	Homo sapiens	Human secreted protein, SEQ ID NO: 6563.	110	39
2762	U12690	Homo sapiens	cytochrome oxidase subunit II	257	88
2763	Y73345	Homo sapiens	HTRM clone 438283 protein sequence.	624	67
2764	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	156	45
2765	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	132	58
2766	X92485	Plasmodium vivax	pval	149	53
2767	AF113685	Homo sapiens	PRO0974	131	63
2768	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	109	56
2769	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	154	71
2770	X97707	Pongo pygmaeus abelli	stopcodon created by posttranscriptional polyadenylation	185	87
2771	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	110	59
2772	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	145	60
2773	AF090944	Homo sapiens	PRO0663	118	62
2774	L26953	Homo sapiens	chromosomal protein	112	58
2775	AF090930	Homo sapiens	PRO0478	127	59
2776	AK024455	Homo sapiens	FLJ00047 protein	154	56
2777	R59843	Homo sapiens	ApoE4Lx2 protease.	103	42
2778	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	101	55
2779	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	131	64
2780	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	89	56
2782	D38113	Pan troglodytes	NADH dehydrogenase subunit 4	194	97
2783	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	124	68
2784	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	49
2785	U43360	Peromyscus maniculatus	reverse transcriptase	175	50
2786	W58700	Homo sapiens	Human ST-1 partial sequence.	219	100
2787	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	137	90
2788	D38112	Homo sapiens	cytochrome c oxidase subunit 3	519	76
2789	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	104	44
2790	AF130089	Homo sapiens	PRO2550	121	39
2791	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	135	63
2792	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 124	124	50

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7133.		
2793	M10546	Homo sapiens	cytochrome oxidase I	153	80
2794	D38112	Homo sapiens	cytochrome c oxidase subunit 1	461	84
2795	AF090931	Homo sapiens	PRO0483	114	76
2796	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	107	53
2797	D38112	Homo sapiens	NADH dehydrogenase subunit 2	114	78
2798	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	115	71
2799	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	113	79
2800	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNF029.	117	48
2801	X92485	Plasmodium vivax	pva1	97	80
2802	D38112	Homo sapiens	cytochrome c oxidase subunit 3	471	80
2803	AF130051	Homo sapiens	PRO0898	118	78
2804	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	78	73
2805	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	143	69
2806	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	102	62
2807	K02401	Homo sapiens	chorionic somatomammotropin	543	88
2808	Y18522	Corvus frugilegus	cytochrome oxidase subunit I	382	60
2809	G01194	Homo sapiens	Human secreted protein, SEQ ID NO: 5275.	555	93
2810	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	399	77
2811	AF007826	Homo sapiens	bax epsilon	94	39
2812	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	220	67
2813	U12690	Homo sapiens	cytochrome oxidase subunit II	495	81
2814	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	112	48
2815	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	102	75
2816	D38112	Homo sapiens	cytochrome c oxidase subunit 3	437	83
2817	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	143	66
2818	X55733	Homo sapiens	initiation factor 4B	458	80
2819	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	132	65
2820	D38112	Homo sapiens	cytochrome c oxidase subunit 3	347	68
2821	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	94	62
2822	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	118	54
2823	AF130079	Homo sapiens	PRO2852	143	54
2824	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	140	52
2825	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	161	67
2826	AF119851	Homo sapiens	PRO1722	104	70
2827	D49489	Homo sapiens	human P5	523	91
2828	M10546	Homo sapiens	cytochrome oxidase I	206	81
2829	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	138	42
2830	AF090931	Homo sapiens	PRO0483	97	80
2831	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	144	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7871.		
2832	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	112	35
2833	X92485	Plasmodium vivax	pva1	103	43
2834	R32010	Homo sapiens	Rp15-TIA-1.	152	54
2835	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	153	59
2836	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	148	59
2837	AF090931	Homo sapiens	PRO0483	149	81
2838	AF130089	Homo sapiens	PRO2550	123	49
2839	AF090942	Homo sapiens	PRO0657	135	54
2840	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	124	54
2841	AF090895	Homo sapiens	PRO0117	146	55
2842	AF132200	Homo sapiens	PRO1751	98	74
2843	U12690	Homo sapiens	cytochrome oxidase subunit II	194	75
2844	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	61	59
2845	AL390114	Leishmania major	extremely cysteine/valine rich protein	171	37
2846	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	155	69
2847	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	141	58
2848	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	108	65
2849	U12690	Homo sapiens	cytochrome oxidase subunit II	441	77
2850	D38112	Homo sapiens	cytochrome c oxidase subunit 1	490	88
2851	K02401	Homo sapiens	chorionic somatomammotropin	488	90
2852	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	110	49
2853	U83280	Leishmania donovani	39 kDa antigen	131	47
2854	AF090944	Homo sapiens	PRO0663	173	72
2855	V00662	Homo sapiens	ATPase 6	392	71
2856	R13556	Homo sapiens	Protein encoded downstream of hhc. M oncprotein.	147	50
2857	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICE1) protein sequence.	113	76
2858	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	178	84
2859	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	192	92
2860	Z81068	Caenorhabditis elegans	contains similarity to Pfam domain: PF00102 (Protein-tyrosine phosphatase), Score=232.1, E-value=2.6e-66, N=1-cDNA EST yk299h6.3 comes from this gene-cDNA EST yk420b4.3 comes from this gene-cDNA EST yk439g6.3 comes from this gene-cDNA EST yk299h6.5 comes from this gene-cDNA EST yk420b4.5 comes from this gene-cDNA EST yk439g6.5 comes from this gene	104	36
2861	D38112	Homo sapiens	NADH dehydrogenase subunit 2	444	85
2862	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	168	61
2863	U93564	Homo sapiens	putative p150	132	34

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2864	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	152	50
2865	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	124	76
2866	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	145	46
2867	AF090930	Homo sapiens	PRO0478	161	61
2868	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	117	48
2869	U15647	Mus musculus	reverse transcriptase	197	40
2870	U09500	Homo sapiens	cytochrome b	394	68
2871	U09500	Homo sapiens	cytochrome b	614	92
2872	D38112	Homo sapiens	NADH dehydrogenase subunit 4	516	87
2873	D38112	Homo sapiens	NADH dehydrogenase subunit 4	458	84
2874	D38112	Homo sapiens	NADH dehydrogenase subunit 4	516	92
2875	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	87	55
2876	D38112	Homo sapiens	NADH dehydrogenase subunit 5	624	96
2877	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	160	58
2878	U32174	Dictyostelium discoideum	non-receptor tyrosine kinase	120	33
2879	D38112	Homo sapiens	ATPase subunit 6	141	54
2880	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	140	84
2881	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	93	79
2882	V00662	Homo sapiens	ATPase 6	130	87
2883	AL390114	Leishmania major	probable proteophosphoglycan	117	50
2884	AF119851	Homo sapiens	PRO1722	79	55
2885	X92485	Plasmodium vivax	pval	106	48
2886	V00662	Homo sapiens	ATPase 6	127	87
2887	D38112	Homo sapiens	NADH dehydrogenase subunit 4	191	83
2888	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	138	58
2889	X92485	Plasmodium vivax	pval	107	63
2890	M10546	Homo sapiens	cytochrome oxidase I	163	89
2891	AF090942	Homo sapiens	PRO0657	72	37
2892	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	136	56
2893	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	139	66
2894	AK024455	Homo sapiens	FLJ00047 protein	139	57
2895	AL359782	Trypanosoma brucei	possible (hly-6) u1102, variant a dna, complete virion genome.	111	44
2896	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	182	62
2897	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	143	73
2898	D38112	Homo sapiens	cytochrome c oxidase subunit 3	248	53
2899	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	366	68
2900	X07882	Homo sapiens	Po protein	146	41
2901	V00662	Homo sapiens	cytochrome B	517	91
2902	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 3	378	67
2903	AF090931	Homo sapiens	PRO0483	117	67
2904	AF003540	Homo sapiens	Krueppel family zinc finger protein	99	54



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2949	V00662	Homo sapiens	cytochrome oxidase I	449	86
2950	D38112	Homo sapiens	NADH dehydrogenase subunit 4	438	82
2951	D38112	Homo sapiens	NADH dehydrogenase subunit 4	363	76
2952	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	92
2953	X56015	Citridia oncopelti	NADH dehydrogenase subunit 5	102	32
2954	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	110	68
2955	Y76287	Homo sapiens	Fragment of human secreted protein encoded by gene 20.	345	78
2956	D38112	Homo sapiens	cytochrome c oxidase subunit 3	340	71
2957	D38112	Homo sapiens	cytochrome c oxidase subunit 1	456	83
2958	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	102	76
2959	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	96	84
2960	D38112	Homo sapiens	cytochrome c oxidase subunit 1	400	70
2961	X69978	Homo sapiens	XP-G factor	539	88
2962	AF203687	Homo sapiens	prolactin regulatory element-binding protein	433	77
2963	D38112	Homo sapiens	cytochrome c oxidase subunit 1	561	83
2964	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	187	92
2965	W80406	Homo sapiens	A secreted protein encoded by clone db40_3.	119	63
2966	U52077	Homo sapiens	mariner transposase	469	83
2967	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCA381.	130	53
2968	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	103	42
2969	X92485	Plasmodium vivax	pva1	144	42
2970	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	127	63
2971	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	129	63
2972	Y17221	Homo sapiens	Human secreted protein (clone fl317-3).	91	56
2973	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	101	72
2974	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	130	68
2975	AF130089	Homo sapiens	PRO2550	167	46
2976	V00662	Homo sapiens	cytochrome oxidase I	539	79
2977	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	121	44
2978	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	126	72
2979	U93568	Homo sapiens	putative p150	122	30
2980	M12099	Mus musculus	proline-rich protein	119	39
2981	Z38128	Mus musculus	histone H1	117	36
2982	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	172	51
2983	AC002291	Arabidopsis thaliana	extensin	110	35
2984	M10546	Homo sapiens	cytochrome oxidase I	295	92
2985	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	171	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2986	U18985	Homo sapiens	triadin	416	83
2987	AF155232	Pisum sativum	extensin	159	41
2988	X03145	Homo sapiens	pot. ORF V	133	44
2989	U12690	Homo sapiens	cytochrome oxidase subunit II	565	84
2990	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	127	53
2991	D38112	Homo sapiens	cytochrome c oxidase subunit I	538	83
2992	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	471	75
2993	D38113	Pan troglodytes	cytochrome c oxidase subunit I	511	72
2994	D38112	Homo sapiens	cytochrome c oxidase subunit I	301	79
2995	D38112	Homo sapiens	cytochrome c oxidase subunit I	526	78
2996	L97674	Mesocricetus auratus	cytochrome c oxidase chain I	634	82
2997	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	158	76
2998	X77816	Rattus norvegicus	PR-Vbeta1	103	50
2999	V00662	Homo sapiens	cytochrome oxidase I	535	78
3000	L38908	Nicotiana tabacum	extensin	146	38
3001	D38112	Homo sapiens	NADH dehydrogenase subunit 2	494	87
3002	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	66
3003	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	117	46
3004	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhala.	93	47
3005	U43627	Arabidopsis thaliana	extensin	118	37
3006	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	150	44
3007	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	114	73
3008	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	111	39
3009	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	84
3010	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	212	77
3011	X65718	Prunus dulcis	extensin	129	42
3012	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	71	76
3013	Z38128	Mus musculus	histone H1	104	32
3014	X56010	Sorghum bicolor	hydroxyproline-rich glycoprotein	102	34
3015	Y86248	Homo sapiens	Human secreted protein IICHPF68, SEQ ID NO:163.	128	80
3016	Y34068	Homo sapiens	Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).	99	34
3017	X55685	Lycopersicon esculentum	extensin (class I)	142	32
3018	AJ133050	Parulirus argus	cytochrome c oxidase subunit I	125	71
3019	G03597	Homo sapiens	Human secreted protein, SEQ ID NO: 7678.	175	68
3020	U93564	Homo sapiens	putative p150	97	57
3021	D38116	Pan paniscus	cytochrome c oxidase subunit I	555	82
3022	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	147	76
3023	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	632	82
3024	AF155232	Pisum sativum	extensin	181	42
3025	V00662	Homo sapiens	cytochrome oxidase I	567	85

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3026	G05787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	130	58
3027	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	141	67
3028	AF130089	Homo sapiens	PRO2550	149	55
3029	AF090944	Homo sapiens	PRO0663	168	76
3030	D38112	Homo sapiens	NADH dehydrogenase subunit 2	122	92
3031	D38112	Homo sapiens	NADH dehydrogenase subunit 4	507	91
3032	D38112	Homo sapiens	NADH dehydrogenase subunit 2	351	87
3033	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	99	75
3034	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	113	85
3035	U93567	Homo sapiens	putative p150	173	41
3036	X92485	Plasmodium vivax	pval	122	41
3037	AF202635	Homo sapiens	PP1200	128	67
3038	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	151	83
3039	D38112	Homo sapiens	cytochrome c oxidase subunit 1	415	74
3040	D86853	Catharanthus roseus	extensin	198	40
3041	M76546	Helianthus annuus	hydroxyproline-rich protein	110	47
3042	D38112	Homo sapiens	cytochrome c oxidase subunit 3	377	95
3043	S80119	Rattus sp.	reverse transcriptase homolog	106	50
3044	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	137	55
3045	Y36156	Homo sapiens	Human secreted protein #28.	91	58
3046	U93574	Homo sapiens	putative p150	177	49
3047	AF063866	Melanoplus sanguinipes entomopoxvirus	ORF MSV233 hypothetical protein	98	37
3048	D38112	Homo sapiens	cytochrome c oxidase subunit 3	568	87
3049	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	144	63
3050	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	80
3051	AK027208	Homo sapiens	unnamed protein product	145	72
3052	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	166	75
3053	AF118082	Homo sapiens	PRO1902	84	50
3054	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	118	41
3055	X92485	Plasmodium vivax	pval	132	52
3056	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	117	74
3057	AL390114	Leishmania major	extremely cysteine/valine rich protein	99	72
3058	D38112	Homo sapiens	cytochrome c oxidase subunit 3	627	89
3059	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	98	57
3060	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	100	38
3061	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	80
3062	D38112	Homo sapiens	cytochrome c oxidase subunit 3	529	80
3063	AF130051	Homo sapiens	PRO0898	159	71
3064	AF195418	Mus musculus	ODZ3	386	94
3065	Y01158	Homo sapiens	Secreted protein encoded by gene 18	109	51



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HCAC181.		
3066	D38112	Homo sapiens	NADH dehydrogenase subunit 2	338	80
3067	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	120	50
3068	U15647	Mus musculus	reverse transcriptase	134	41
3069	D38112	Homo sapiens	cytochrome c oxidase subunit 3	397	92
3070	AF130089	Homo sapiens	PRO2550	149	55
3071	U93565	Homo sapiens	putative p150	143	37
3072	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	112	45
3073	AF090930	Homo sapiens	PRO0478	135	78
3074	AF130089	Homo sapiens	PRO2550	156	58
3075	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	267	65
3076	U83280	Leishmania donovani	39 kDa antigen	98	51
3077	D38112	Homo sapiens	cytochrome c oxidase subunit 3	626	86
3078	AF116712	Homo sapiens	PRO2738	114	59
3079	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	112	46
3080	D38112	Homo sapiens	cytochrome c oxidase subunit 1	492	80
3081	D38112	Homo sapiens	NADH dehydrogenase subunit 4	523	86
3082	D38112	Homo sapiens	cytochrome c oxidase subunit 3	515	79
3083	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	150	41
3084	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	191	97
3085	U12690	Homo sapiens	cytochrome oxidase subunit II	537	78
3086	D38112	Homo sapiens	ATPase subunit 6	300	58
3087	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	104	37
3088	K02247	Rattus norvegicus	proline-rich protein	108	41
3089	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	130	48
3090	V00662	Homo sapiens	cytochrome oxidase I	597	84
3091	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	221	43
3092	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	392	59
3093	D38116	Pan paniscus	cytochrome c oxidase subunit 1	593	84
3094	D38112	Homo sapiens	cytochrome c oxidase subunit 1	471	76
3095	R63235	Homo sapiens	CNS neural thread protein HB4.	369	98
3096	L26953	Homo sapiens	chromosomal protein	115	57
3097	G00591	Homo sapiens	Human secreted protein, SEQ ID NO: 4672.	124	57
3098	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	91
3099	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	153	96
3100	AC006233	Arabidopsis thaliana	hypothetical protein	65	44
3101	AF289098	Cladrastis kentukea	ENOD2	107	35
3102	AF155232	Pisum sativum	extensin	142	43
3103	AF130089	Homo sapiens	PRO2550	122	81
3104	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	143	80
3105	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	104	59

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3106	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	76
3107	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	72
3108	D38112	Homo sapiens	NADH dehydrogenase subunit 4	334	85
3109	U43627	Arabidopsis thaliana	extensin	112	30
3110	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	100
3111	AF130089	Homo sapiens	PRO2550	137	37
3112	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	220	93
3113	A18812	Brassica napus	extensin	128	32
3114	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	63
3115	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	92	69
3116	X92485	Plasmodium vivax	pval	148	45
3117	D38112	Homo sapiens	cytochrome c oxidase subunit 1	574	80
3118	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	125	41
3119	U43627	Arabidopsis thaliana	extensin	129	32
3120	AF205385	Pan troglodytes	NADH dehydrogenase subunit 5	171	82
3121	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	90	59
3122	AF130051	Homo sapiens	PRO0898	134	82
3123	M81321	Macaca fascicularis	proline-rich protein	158	48
3124	U93563	Homo sapiens	putative p150	126	32
3125	D38114	Gorilla gorilla	NADH dehydrogenase subunit 1 (ND1)	337	92
3126	AF130089	Homo sapiens	PRO2550	155	77
3127	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	76
3128	AF090901	Homo sapiens	PRO0195	109	53
3129	AF003736	Murine leukemia virus	reverse transcriptase	164	40
3130	U25281	Rattus norvegicus	SH3 domain binding protein	88	39
3131	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	116	71
3132	D86853	Catharanthus roseus	extensin	110	33
3133	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	506	76
3134	V00662	Homo sapiens	cytochrome oxidase I	583	88
3135	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	68
3136	AJ242540	Voivox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	282	60
3137	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	119	54
3138	AF118082	Homo sapiens	PRO1902	118	51
3139	D38112	Homo sapiens	NADH dehydrogenase subunit 4	270	87
3140	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	103	48

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3141	D38112	Homo sapiens	NADH dehydrogenase subunit 5	353	74
3142	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	126	77
3143	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	115	72
3144	AF090930	Homo sapiens	PRO0478	138	73
3145	AF155232	Pisum sativum	extensin	110	34
3146	M69008	Homo sapiens	alpha-1 type XIII collagen	107	37
3147	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	103	63
3148	D38112	Homo sapiens	cytochrome c oxidase subunit 1	505	84
3149	M77194	Rat leukemia virus	polymerase	167	35
3150	AP002543	Arabidopsis thaliana	gb AAD23015.1-gene_id:F15M7.16-similar to unknown protein	105	31
3151	AK024455	Homo sapiens	FLJ00047 protein	109	59
3152	K02576	Homo sapiens	salivary proline-rich protein 1	89	39
3153	J04794	Homo sapiens	aldehyde reductase (EC 1.1.1.2)	137	58
3154	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	115	70
3155	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	160	53
3156	X92485	Plasmodium vivax	pval	104	50
3157	AF194537	Homo sapiens	NAG13	207	60
3158	AF063693	Mus musculus	type XIII collagen	104	37
3159	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	91
3160	AF020191	Mus musculus	proline-rich protein 13	107	51
3161	AF194537	Homo sapiens	NAG13	170	76
3162	G02535	Homo sapiens	Human secreted protein, SEQ ID NO: 6616.	103	41
3163	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	161	58
3164	K03205	Homo sapiens	salivary proline-rich protein precursor	139	46
3165	U93570	Homo sapiens	putative p150	151	68
3166	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	144	71
3167	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	147	66
3168	L27428	Homo sapiens	reverse transcriptase	94	51
3169	X97675	Homo sapiens	plakophilin 2b	103	76
3170	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	115	54
3171	AK024455	Homo sapiens	FLJ00047 protein	98	61
3172	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	146	38
3173	D38116	Pan paniscus	NADH dehydrogenase subunit 4	467	81
3174	X92485	Plasmodium vivax	pval	88	69
3175	L26953	Homo sapiens	chromosomal protein	124	78
3176	AF042169	Homo sapiens	putative ATP-dependent mitochondrial RNA helicase	223	95
3177	AF130079	Homo sapiens	PRO2852	96	44
3178	AF273217	Mus musculus	cell proliferation related protein CAP	97	36
3179	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	90	69
3180	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	146	78
3181	AF118082	Homo sapiens	PRO1902	150	58
3182	U60315	Molluscum contagiosum	MC107L	101	44

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		virus subtype 1			
3183	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	148	61
3184	U93565	Homo sapiens	putative p150	265	58
3185	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163	117	79
3186	U87607	Rattus norvegicus	putative RNA binding protein 1	167	39
3187	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	160	63
3188	S80119	Rattus sp.	reverse transcriptase homolog	152	49
3189	X05300	Rattus norvegicus	ribophorin I	122	46
3190	B01572	Homo sapiens	Neuron-associated protein.	106	80
3191	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	130	83
3192	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	135	80
3193	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	98	34
3194	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	140	87
3195	AF022985	Caenorhabditis elegans	Similar to collagen	97	40
3196	D38112	Homo sapiens	cytochrome c oxidase subunit 1	452	81
3197	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	110	58
3198	X99452	Lycopersicon esculentum	extensin-like protein Df54	100	36
3199	D86853	Catharanthus roseus	extensin	119	36
3200	AF025424	Rattus norvegicus	RNA polymerase I 127 kDa subunit	215	74
3201	U93563	Homo sapiens	putative p150	359	77
3202	K05202	Homo sapiens	salivary proline-rich protein precursor	112	37
3203	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	153	84
3204	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	128	39
3205	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	154	76
3206	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	127	64
3207	X97675	Homo sapiens	plakophilin 2b	142	51
3208	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	91	58
3209	AB026512	Ecnomiosia sp. Ecn1	cytochrome c oxidase subunit I	254	62
3210	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	163	59
3211	D38112	Homo sapiens	ATPase subunit 6	447	78
3212	V00662	Homo sapiens	ATPase 6	482	83
3213	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	151	66
3214	D38112	Homo sapiens	ATPase subunit 6	400	72
3215	D38112	Homo sapiens	cytochrome c oxidase subunit 3	569	88
3216	D38112	Homo sapiens	NADH dehydrogenase subunit 5	472	82
3217	AF090930	Homo sapiens	PRO0478	96	64
3218	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	137	46

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7253.		
3219	AF006061	Homo sapiens	placental growth hormone isoform hGH-V3	290	68
3220	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	115	63
3221	D38112	Homo sapiens	cytochrome c oxidase subunit 1	441	71
3222	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	111	59
3223	D38112	Homo sapiens	cytochrome c oxidase subunit 3	497	81
3224	L26953	Homo sapiens	chromosomal protein	95	59
3225	U83280	Leishmania donovani	39 kDa antigen	117	90
3226	AF239615	Manihot esculenta	CRANTZ hydroxyproline-rich glycoprotein	124	43
3227	D38112	Homo sapiens	NADH dehydrogenase subunit 4	442	74
3228	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	172	67
3229	X92591	Mus musculus	transcription factor	109	43
3230	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	81	54
3231	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 1	476	72
3232	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	100	54
3233	U96416	Dennys distinctus timjonesi	cytochrome b	95	40
3234	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	86
3235	M76546	Helianthus annuus	hydroxyproline-rich protein	101	40
3236	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	149	75
3237	D38112	Homo sapiens	NADH dehydrogenase subunit 5	532	76
3238	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	576	89
3239	U93567	Homo sapiens	p40	155	32
3240	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	79
3241	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	145	65
3242	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	76	62
3243	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	138	69
3244	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	115	39
3245	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	138	54
3246	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	153	69
3247	U58736	Caenorhabditis elegans	Similar to cuticular collagen	107	37
3248	U87607	Rattus norvegicus	putative RNA binding protein 1	148	45
3249	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	113	85
3250	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	166	61
3251	U15183	Mycobacterium leprae	proline-rich antigen	109	40
3252	AF130089	Homo sapiens	PRO2550	151	73

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3253	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	131	58
3254	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	80
3255	AI.359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	108	57
3256	J01415	Homo sapiens	cytochrome oxidase subunit 3	156	88
3257	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	206	93
3258	Y36205	Homo sapiens	Human secreted protein #75.	111	77
3259	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	98	57
3260	D38112	Homo sapiens	cytochrome c oxidase subunit 1	345	67
3261	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	97	56
3262	L38908	Nicotiana tabacum	extensin	155	40
3263	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	95	70
3264	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	198	87
3265	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	69
3266	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	158	59
3267	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	105	56
3268	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	72
3269	D38112	Homo sapiens	NADH dehydrogenase subunit 1	200	95
3270	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	138	73
3271	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	151	90
3272	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	193	95
3273	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	111	52
3274	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	87
3275	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	86
3276	S62928	Homo sapiens	PRB1M protein precursor	104	34
3277	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	154	55
3278	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	166	100
3279	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	212	91
3280	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	118	50
3281	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	130	46
3282	M10546	Homo sapiens	cytochrome oxidase I	303	95
3283	D38112	Homo sapiens	cytochrome c oxidase subunit 1	455	81
3284	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	502	83
3285	AF118086	Homo sapiens	PRO1992	99	88
3286	D38112	Homo sapiens	cytochrome c oxidase subunit 1	489	83

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3287	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	485	88
3288	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	124	73
3289	AI359782	Trypanosoma brucei	possible (hly-G) u1102, variant a dna, complete virion genome.	158	60
3290	X92485	Plasmodium vivax	pval	99	58
3291	AF116712	Homo sapiens	PRO2738	102	51
3292	AF119851	Homo sapiens	PRO1722	99	86
3293	AF090930	Homo sapiens	PRO0478	141	72
3294	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	151	66
3295	M64793	Rattus norvegicus	salivary proline-rich protein	107	41
3296	AK024455	Homo sapiens	FLJ00047 protein	97	53
3297	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	156	60
3298	AC007654	Arabidopsis thaliana	T19E23.7	97	49
3299	Y17221	Homo sapiens	Human secreted protein (clone fl317-3).	96	44
3300	AJ243905	Caenorhabditis elegans	SF1 protein	104	42
3301	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	96	41
3302	X89453	Rattus norvegicus	DRPLA	83	65
3303	U10099	Homo sapiens	POM-ZP3	227	52
3304	D38112	Homo sapiens	cytochrome c oxidase subunit 3	553	89
3305	L27428	Homo sapiens	reverse transcriptase	144	43
3306	D38112	Homo sapiens	cytochrome c oxidase subunit 3	388	71
3307	AF217374	Acanthaster planci	cytochrome oxidase subunit I	439	78
3308	D38112	Homo sapiens	cytochrome c oxidase subunit 1	439	82
3309	D38112	Homo sapiens	cytochrome c oxidase subunit 1	492	88
3310	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	81	65
3311	X53581	Rattus norvegicus	ORF4	140	48
3312	V00662	Homo sapiens	cytochrome B	487	88
3313	D38112	Homo sapiens	NADH dehydrogenase subunit 1	451	80
3314	V00662	Homo sapiens	cytochrome oxidase I	524	88
3315	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	518	87
3316	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	115	50
3317	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	356	69
3318	U12693	Homo sapiens	cytochrome c oxidase subunit II	477	78
3319	Z67990	Caenorhabditis elegans	contains similarity to Pfam domain: PF01484 (Nematode cuticle collagen N-terminal domain), Score=27.5, E-value=0.0001, N=1	75	40
3320	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	126	75
3321	AF090930	Homo sapiens	PRO0478	166	65
3322	X92485	Plasmodium vivax	pval	104	44
3323	D38112	Homo sapiens	cytochrome c oxidase subunit 3	513	80
3324	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	483	79

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3325	AF130089	Homo sapiens	PRO2550	121	88
3326	AC026234	Unknown	Contains weak similarity to an unknown protein T23E18.5	191	66
3327	V00662	Homo sapiens	cytochrome B	439	72
3328	U12690	Homo sapiens	cytochrome oxidase subunit II	316	75
3329	AF091711	Homo sapiens	splice variant AKAP350	106	52
3330	U93565	Homo sapiens	putative p150	125	45
3331	AF119851	Homo sapiens	PRO1722	88	72
3332	D38112	Homo sapiens	cytochrome c oxidase subunit 3	489	81
3333	V00662	Homo sapiens	cytochrome oxidase I	544	90
3334	D38112	Homo sapiens	cytochrome c oxidase subunit 1	475	80
3335	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	168	66
3336	AF146688	Takifugu rubripes	serine-threonine kinase 9	101	43
3337	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	101	50
3338	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	110	50
3339	V00662	Homo sapiens	cytochrome oxidase I	458	80
3340	K02401	Homo sapiens	chorionic somatomammotropin	209	97
3341	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	112	52
3342	X65165	Voivox carteri	extensin	146	41
3343	AL390114	Leishmania major	extremely cysteine/valine rich protein	119	51
3344	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	559	84
3345	U12690	Homo sapiens	cytochrome oxidase subunit II	508	89
3346	M11897	Mus musculus	proline-rich salivary protein	96	41
3347	U92435	Mus musculus	WW domain binding protein 7; WBP7	113	38
3348	U83280	Leishmania donovani	39 kDa antigen	105	40
3349	K03205	Homo sapiens	salivary proline-rich protein precursor	113	38
3350	D38112	Homo sapiens	cytochrome c oxidase subunit 1	542	79
3351	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	664	88
3352	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	117	85
3353	A18812	Brassica napus	extensin	103	31
3354	M10546	Homo sapiens	cytochrome oxidase I	125	78
3355	M81321	Macaca fascicularis	proline-rich protein	107	44
3356	M10546	Homo sapiens	cytochrome oxidase I	284	90
3357	D38112	Homo sapiens	cytochrome c oxidase subunit 1	513	80
3358	D38112	Homo sapiens	cytochrome c oxidase subunit 1	541	79
3359	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	543	87
3360	D38112	Homo sapiens	cytochrome c oxidase subunit 1	563	86
3361	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	179	57
3362	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	125	62
3363	AF016099	Mus musculus	endonuclease/reverse transcriptase	151	46
3364	D38112	Homo sapiens	cytochrome c oxidase subunit 3	569	82
3365	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	102	40
3366	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	143	76
3367	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	145	84



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3368	D38112	Homo sapiens	cytochrome c oxidase subunit 1	587	87
3369	D38112	Homo sapiens	cytochrome c oxidase subunit 1	549	82
3370	AL035526	Arabidopsis thaliana	extensin-like protein	130	39
3371	J04543	Homo sapiens	synexin	101	40
3372	Z29573	Didelphis virginiana	cytochrome c oxidase subunit 3	154	71
3373	U93568	Homo sapiens	putative p150	176	59
3374	L28748	Bos taurus	putative	146	67
3375	D38112	Homo sapiens	cytochrome c oxidase subunit 1	512	75
3376	D38112	Homo sapiens	cytochrome c oxidase subunit 1	509	78
3377	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	135	51
3378	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	557	82
3379	Y86248	Homo sapiens	Human secreted protein HCHIPF68, SEQ ID NO:163.	120	35
3380	X92485	Plasmodium vivax	pval	124	38
3381	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	110	78
3382	R96800	Homo sapiens	Human histocyte-secreted factor HSF.	108	67
3383	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	115	86
3384	X98296	Homo sapiens	ubiquitin hydrolase	238	83
3385	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	494	75
3386	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	155	66
3387	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	116	65
3388	W73624	Homo sapiens	Human secreted protein clone aw92.1.	327	62
3389	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	141	76
3390	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	73	61
3391	U35730	Mus musculus	jerky	152	30
3392	U54788	Mus musculus	Wiskott-Aldrich Syndrome Protein	100	41
3393	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	483	77
3394	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	539	81
3395	D38112	Homo sapiens	cytochrome c oxidase subunit 1	608	87
3396	X71602	Nicotiana tabacum	extensin	104	35
3397	L26953	Homo sapiens	chromosomal protein	100	60
3398	AF197832	Cyanocitta cristata	cytochrome oxidase I	488	76
3399	X53581	Rattus norvegicus	ORF4	140	42
3400	D38112	Homo sapiens	cytochrome c oxidase subunit 1	597	85
3401	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	656	89
3402	L26953	Homo sapiens	chromosomal protein	117	63
3403	AF052298	Drosophila silvestris	Y box protein	114	30
3404	U43360	Peromyscus maniculatus	reverse transcriptase	133	53
3405	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	151	65
3406	D38112	Homo sapiens	cytochrome c oxidase subunit 1	277	82
3407	U01849	Trypanosoma	ORF2	94	30

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		brucei			
3408	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	115	65
3409	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	86
3410	U93570	Homo sapiens	putative p150	233	52
3411	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	104	44
3412	AF090944	Homo sapiens	PRO0663	97	56
3413	X61048	Hydra sp.	mini-collagen	128	44
3414	AF118086	Homo sapiens	PRO1992	128	81
3415	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	145	61
3416	AF116695	Homo sapiens	PRO2221	169	69
3417	U31778	Human papillomavirus type 20	putative	107	50
3418	X92485	Plasmodium vivax	pva1	97	54
3419	U12690	Homo sapiens	cytochrome oxidase subunit II	195	94
3420	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	144	69
3421	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	139	71
3422	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	111	63
3423	X15917	Paramecium aurelia	ORF4 protein (AA 1-156)	93	41
3424	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	99	69
3425	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	115	60
3426	Y14486	Homo sapiens	cytosolic serine hydroxymethyltransferase	196	61
3427	U93569	Homo sapiens	putative p150	110	44
3428	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	120	67
3429	AB012223	Canis familiaris	ORF2	169	44
3430	X97675	Homo sapiens	plakophilin 2b	118	60
3431	AF220264	Homo sapiens	MOST-1	153	72
3432	X64173	Zea diploperennis	hydroxyproline-rich glycoprotein	104	41
3433	AF113685	Homo sapiens	PRO0974	104	72
3434	AB002306	Homo sapiens	KIAA0308	282	83
3435	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	113	83
3436	AB012223	Canis familiaris	ORF2	108	43
3437	AK024455	Homo sapiens	FLJ00047 protein	100	65
3438	U52077	Homo sapiens	mariner transposase	381	64
3439	D38112	Homo sapiens	cytochrome c oxidase subunit I	425	84
3440	AK024455	Homo sapiens	FLJ00047 protein	123	63
3441	G02624	Homo sapiens	Human secreted protein, SEQ ID NO: 6705.	90	78
3442	Y36156	Homo sapiens	Human secreted protein #28.	126	71
3443	AF191032	Myxine glutinosa	RING3	84	63
3444	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	141	57
3445	Y08061	Homo sapiens	Human c-myb protein fragment.	88	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3446	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	157	67
3447	U12690	Homo sapiens	cytochrome oxidase subunit II	281	86
3448	AF112481	Homo sapiens	RAD54B protein	392	87
3449	G00497	Homo sapiens	Human secreted protein, SEQ ID NO: 4578.	98	55
3450	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	133	90
3451	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	418	82
3452	AF130079	Homo sapiens	PRO2852	110	80
3453	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	143	73
3454	AB032254	Homo sapiens	bromodomain adjacent to zinc finger domain 2A	447	85
3455	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	134	62
3456	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	79	68
3457	D38112	Homo sapiens	cytochrome c oxidase subunit 3	545	84
3458	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	134	83
3459	D38112	Homo sapiens	NADH dehydrogenase subunit 2	277	80
3460	AK000867	Homo sapiens	unnamed protein product	474	98
3461	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	123	52
3462	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	89	30
3463	U93568	Homo sapiens	putative p150	100	46
3464	AL390114	Leishmania major	extremely cysteine/valine rich protein	156	43
3465	D38112	Homo sapiens	NADH dehydrogenase subunit 3	340	88
3466	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	119	100
3467	B01372	Homo sapiens	Neuron-associated protein.	142	75
3468	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	103	40
3469	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	139	80
3470	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSS1.	207	89
3471	AF116661	Homo sapiens	PRO1438	119	47
3472	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	129	59
3473	AF130089	Homo sapiens	PRO2550	108	86
3474	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	113	80
3475	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	590	79
3476	AF118086	Homo sapiens	PRO1992	126	69
3477	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	147	47
3478	J01415	Homo sapiens	MTND4	482	78
3479	X03404	Bos taurus	alpha subunit (aa 1-394)	583	89
3480	D38112	Homo sapiens	cytochrome c oxidase subunit 1	514	84
3481	G03628	Homo sapiens	Human secreted protein, SEQ ID NO: 7709.	242	80
3482	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	121	61
3483	X83427	Ornithorhynchus anatinus	cytochrome c oxidase subunit 1	508	78
3484	Y07754	Homo sapiens	Human secreted protein fragment	549	93

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded from gene 11.		
3485	X97567	Homo sapiens	por1	388	69
3486	X97567	Homo sapiens	por1	608	84
3487	K02401	Homo sapiens	chorionic somatomammotropin	641	93
3488	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	135	71
3489	S62941	Homo sapiens	Ps 2 <sup>nd</sup> -basic proline-rich protein(PRB1L precursor protein--basic proline-rich proteins (Ps, PmF, PmS, and Pe) precursor) {C-terminal}	116	36
3490	S74728	Homo sapiens	antiquitin=26g turgor protein homolog	549	84
3491	L13329	Homo sapiens	iduronate-2-sulfatase	564	85
3492	X79535	Homo sapiens	beta tubulin	620	88
3493	AF081484	Homo sapiens	alpha-tubulin isoform 1	578	87
3494	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	631	89
3495	AF081484	Homo sapiens	alpha-tubulin isoform 1	616	90
3496	M12140	Homo sapiens	envelope protein	430	53
3497	Q03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	123	70
3498	W48352	Homo sapiens	Human breast cancer related protein BCFL1.	104	51
3499	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	134	54
3500	Y36156	Homo sapiens	Human secreted protein #28.	143	75
3501	AF113685	Homo sapiens	PRO0974	77	81
3502	Q00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	157	62
3503	AF090944	Homo sapiens	PRO0663	164	81
3504	AF090931	Homo sapiens	PRO0483	103	70
3505	U93570	Homo sapiens	p40	258	47
3506	AB016601	Drosophila alpina	cytochrome c oxidase subunit I	108	82
3507	AB016601	Drosophila alpina	cytochrome c oxidase subunit I	108	82
3508	AF194537	Homo sapiens	NAG13	449	78
3509	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	153	60
3510	Z70684	Caenorhabditis elegans	F28D1.8	102	37
3511	AC008113	Arabidopsis thaliana	F12A21.10	90	48
3512	M64791	Rattus norvegicus	salivary proline-rich protein	104	33
3513	AF090944	Homo sapiens	PRO0663	115	52
3514	AF240630	Mus musculus	IQ motif containing GTPase activating protein 1	152	67
3515	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	123	48
3516	AF090942	Homo sapiens	PRO0657	128	47
3517	M10546	Homo sapiens	cytochrome oxidase I	286	56
3518	AF255661	Cryptocodium johnsonii	Dinap1-interacting protein 5; Dip5	108	36
3519	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	209	93
3520	M11901	Rattus norvegicus	proline-rich salivary protein	102	38
3521	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	131	64
3522	AL359782	Trypanosoma	possible (hlyv-6) u1102, variant a dna,	105	42

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		brucei	complete virion genome.		
3523	R95913	Homo sapiens	Neural thread protein.	118	72
3524	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	115	59
3525	L27428	Homo sapiens	reverse transcriptase	162	50
3526	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	118	58
3527	AF090930	Homo sapiens	PRO0478	146	66
3528	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	169	50
3529	AF194537	Homo sapiens	NAG13	119	88
3530	U93564	Homo sapiens	putative p150	234	84
3531	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	208	63
3532	U12690	Homo sapiens	cytochrome oxidase subunit II	275	92
3533	AF090931	Homo sapiens	PRO0483	126	66
3534	W05278	Homo sapiens	Tumour necrosis factor-related gene product CL6.5/40.	117	85
3535	G03076	Homo sapiens	Human secreted protein, SEQ ID NO: 7157.	173	77
3536	U21123	Drosophila melanogaster	ena polypeptide	117	45
3537	AF209061	Eubbranchipus sp.	cytochrome c oxidase I	127	80
3538	D38112	Homo sapiens	NADH dehydrogenase subunit 3	174	85
3539	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	118	45
3540	R13556	Homo sapiens	Protein encoded downstream of hnc_M oncoprotein.	88	50
3541	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	128	71
3542	U74612	Homo sapiens	hepatocyte nuclear factor-3/fork head homolog 11A	111	77
3543	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	149	69
3544	D38112	Homo sapiens	cytochrome c oxidase subunit I	470	80
3545	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	120	54
3546	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	106	42
3547	D38113	Pan troglodytes	cytochrome c oxidase subunit I	584	83
3548	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	635	95
3549	D38112	Homo sapiens	cytochrome c oxidase subunit 3	661	91
3550	D38112	Homo sapiens	cytochrome c oxidase subunit I	607	86
3551	AK024455	Homo sapiens	FLJ00047 protein	88	51
3552	W88957	Homo sapiens	Polypeptide fragment encoded by gene 128.	500	86
3553	D38113	Pan troglodytes	NADH dehydrogenase subunit 4	228	95
3554	AF130092	Homo sapiens	PRO2620	165	93
3555	AL121845	Homo sapiens	dJ583P15.5.1 (novel protein (isoform 1))	659	91
3556	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	170	72
3557	D38112	Homo sapiens	cytochrome c oxidase subunit 3	599	88
3558	D38112	Homo sapiens	cytochrome c oxidase subunit 3	578	84
3559	AK000385	Homo sapiens	unnamed protein product	138	47
3560	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	112	61
3561	X97675	Homo sapiens	plakophilin 2b	123	65
3562	G02514	Homo sapiens	Human secreted protein, SEQ ID NO:	94	62

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6595.		
3563	Y85248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	198	90
3564	X86029	Vigna unguiculata	extensin-like protein	141	36
3565	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	77	50
3566	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	94
3567	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	203	93
3568	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	72
3569	S62928	Homo sapiens	PRB1M protein precursor	102	44
3570	D86853	Catharanthus roseus	extensin	123	40
3571	U93574	Homo sapiens	putative p150	279	56
3572	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	94	82
3573	U45964	Herpesvirus papio	LMP1	127	35
3574	Y08319	Homo sapiens	kinesin-2	254	55
3575	X97675	Homo sapiens	plakophilin 2b	134	54
3576	AF003151	Caenorhabditis elegans	contains similarity to an RNA recognition motif	137	43
3577	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	126	66
3578	U80447	Caenorhabditis elegans	coded for by C. elegans cDNA yk187f6.5; coded for by C. elegans cDNA yk187f6.3; coded for by C. elegans cDNA yk146f1.5	117	50
3579	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP-CS24, HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	126	31
3580	AJ249395	Globodera pallida	NADH-ubiquinone oxidoreductase subunit 4	85	33
3581	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	139	55
3582	X97675	Homo sapiens	plakophilin 2b	125	73
3583	L26953	Homo sapiens	chromosomal protein	101	55
3584	S80343	Homo sapiens	arginyl-tRNA synthetase, ArgRS	110	67
3585	X97675	Homo sapiens	plakophilin 2b	116	84
3586	X92485	Plasmodium vivax	pval	124	50
3587	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	126	56
3588	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	136	56
3589	U63542	Homo sapiens	FAP protein	128	75
3590	D38112	Homo sapiens	cytochrome c oxidase subunit 3	642	88
3591	D38112	Homo sapiens	NADH dehydrogenase subunit 1	612	87
3592	K02401	Homo sapiens	chorionic somatomammotropin	576	86
3593	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	108	40
3594	V00662	Homo sapiens	cytochrome oxidase I	459	76
3595	AC008262	Arabidopsis thaliana	F4N2.10	136	31
3596	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	126	52

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3597	AF116645	Homo sapiens	PRO1708	623	91
3598	M23028	Human herpesvirus 4	nuclear antigen precursor	121	35
3599	W88816	Homo sapiens	Polypeptide fragment encoded by gene 58.	100	33
3600	X92485	Plasmodium vivax	pva1	156	36
3601	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	122	78
3602	AK000496	Homo sapiens	unnamed protein product	150	68
3603	AF083929	Mus musculus	ES18	98	40
3604	D38112	Homo sapiens	cytochrome c oxidase subunit 1	537	83
3605	U12690	Homo sapiens	cytochrome oxidase subunit II	548	85
3606	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	158	57
3607	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	429	75
3608	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	122	65
3609	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	88
3610	D38112	Homo sapiens	NADH dehydrogenase subunit 5	224	80
3611	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	481	70
3612	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	166	92
3613	D38112	Homo sapiens	cytochrome c oxidase subunit 1	582	83
3614	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	167	91
3615	U12690	Homo sapiens	cytochrome oxidase subunit II	582	77
3616	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	101	40
3617	D38112	Homo sapiens	cytochrome c oxidase subunit 1	591	85
3618	AB037275	Cynomolgus Epstein-Barr Virus TsB-B6	EBNA-1	119	42
3619	AF061944	Homo sapiens	kinase deficient protein KDP	581	91
3620	Y34068	Homo sapiens	Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).	100	33
3621	AL049608	Arabidopsis thaliana	extensin-like protein	105	27
3622	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	69
3623	S71569	Neocallimastix patriciarum, Peptide, 860 aa	Xylanase B, XYLB {EC 3.2.1.8}	108	43
3624	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	101	37
3625	D38112	Homo sapiens	NADH dehydrogenase subunit 5	390	83
3626	D38112	Homo sapiens	cytochrome c oxidase subunit 1	582	84
3627	D38112	Homo sapiens	cytochrome c oxidase subunit 3	637	90
3628	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	169	39
3629	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	142	77
3630	U93564	Homo sapiens	putative p150	330	90
3631	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	148	42

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3632	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	100	80
3633	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	139	65
3634	U74071	Phascolosoma sp. 'California'	cytochrome c oxidase subunit 1	248	72
3635	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	121	87
3636	R13556	Homo sapiens	Protein encoded downstream of htc_M oncoprotein.	128	65
3637	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	124	63
3638	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	139	51
3639	X65582	Mus musculus	alpha-2 collagen	102	53
3640	AF090942	Homo sapiens	PRO0657	97	76
3641	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	146	69
3642	G02338	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	118	55
3643	X14576	Murine leukemia virus	gag p15 protein	134	44
3644	AF130051	Homo sapiens	PRO0898	177	48
3646	G03064	Homo sapiens	Human secreted protein, SEQ ID NO: 7145.	120	59
3647	AK000385	Homo sapiens	unnamed protein product	105	40
3648	V00662	Homo sapiens	cytochrome oxidase 1	533	83
3649	AF090944	Homo sapiens	PRO0663	129	73
3650	AF090944	Homo sapiens	PRO0663	129	73
3651	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	88	60
3652	AF090930	Homo sapiens	PRO0478	92	57
3653	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	148	73
3654	AB018440	Echinococcus multilocularis	NADH dehydrogenase subunit 2	100	32
3655	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	165	68
3656	AF161356	Homo sapiens	HSPC093	106	48
3657	AF090930	Homo sapiens	PRO0478	158	85
3658	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	128	82
3659	U93374	Homo sapiens	putative p150	117	44
3660	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	149	51
3661	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	67	70
3662	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	99	62
3663	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	154	45
3664	Y27571	Homo sapiens	Human secreted protein encoded by gene No. 5.	136	77
3665	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	128	59
3666	U47855	Araneus diadematus	fibrin-3	109	39
3667	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	604	88
3668	K02401	Homo sapiens	chorionic somatomammotropin	636	93



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3669	AF083929	Mus musculus	ES18	133	46
3670	J01415	Homo sapiens	MTND4	620	87
3671	AK025047	Homo sapiens	unnamed protein product	160	60
3672	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	106	31
3673	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	766	94
3674	U74612	Homo sapiens	hepatocyte nuclear factor-3/fork head homolog 11A	113	69
3675	U80447	Caenorhabditis elegans	coded for by C. elegans cDNA yk187f6.5; coded for by C. elegans cDNA yk187f6.3; coded for by C. elegans cDNA yk146f11.5	113	39
3676	R63235	Homo sapiens	CNS neural thread protein HB4.	197	68
3677	U52077	Homo sapiens	mariner transposase	500	74
3678	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	174	97
3679	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	191	86
3680	AC003113	Arabidopsis thaliana	F24O1.6	102	83
3681	AF005370	Alcelaphine herpesvirus 1	putative immediate early protein	153	42
3682	G01502	Homo sapiens	Human secreted protein, SEQ ID NO: 5583.	111	62
3683	AP002543	Arabidopsis thaliana	gblAAD23015.1-gene_id:F15M7.16-similar to unknown protein	131	40
3684	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	146	64
3685	U93572	Homo sapiens	putative p150	158	43
3686	Y34068	Homo sapiens	Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).	98	43
3687	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	106	54
3688	L26953	Homo sapiens	chromosomal protein	128	76
3689	D38112	Homo sapiens	cytochrome c oxidase subunit 1	563	87
3690	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	109	67
3691	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	122	75
3692	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	165	85
3693	M20789	Homo sapiens	alpha-1 type I collagen	141	43
3694	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	50
3695	AF210651	Homo sapiens	NAG18	124	67
3696	AF130079	Homo sapiens	PRC2852	94	53
3697	Y19192	Taipa europaea	cytochrome oxidase subunit 1	618	85
3698	D38112	Homo sapiens	NADH dehydrogenase subunit 2	414	86
3699	D38112	Homo sapiens	cytochrome c oxidase subunit 1	487	76
3700	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	109	42
3701	AF217374	Acanthaster planci	cytochrome oxidase subunit I	563	85
3702	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	106	48
3703	D38112	Homo sapiens	cytochrome c oxidase subunit 1	522	79
3704	D67066	Bos taurus	N-WASP	219	42
3705	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	100	51
3706	G03798	Homo sapiens	Human secreted protein, SEQ ID NO:	115	44

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7879.		
3707	Z70684	Caenorhabditis elegans	F28D1.8	105	37
3708	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	74
3709	D38112	Homo sapiens	cytochrome c oxidase subunit 1	558	88
3710	AF217374	Acanthaster planci	cytochrome oxidase subunit I	512	85
3711	D38112	Homo sapiens	NADH dehydrogenase subunit 2	186	80
3712	AF197854	Melithreptus lunatus	cytochrome oxidase I	189	83
3713	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	95
3714	AB029027	Homo sapiens	KIAA1104 protein	141	81
3715	L26251	Trypanosoma brucei	CR5	73	31
3716	R95913	Homo sapiens	Neural thread protein.	117	44
3717	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	95	67
3718	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	108	81
3719	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	132	55
3720	M64923	Bos taurus	C10 protein	194	94
3721	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	115	75
3722	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	118	95
3723	AF302773	Homo sapiens	ninein-Lm isoform	157	57
3724	AK024455	Homo sapiens	FLJ00047 protein	134	59
3725	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	161	80
3726	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	121	52
3727	AF220264	Homo sapiens	MOST-1	86	88
3728	L27428	Homo sapiens	reverse transcriptase	316	62
3729	U83303	Homo sapiens	line-1 reverse transcriptase	112	46
3730	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	145	68
3731	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	118	56
3732	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	131	65
3733	AF090930	Homo sapiens	PRO0478	148	71
3734	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	140	72
3735	U93569	Homo sapiens	putative p150	270	59
3736	U93568	Homo sapiens	putative p150	151	38
3737	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	124	82
3738	X92485	Plasmodium vivax	pva1	101	44
3739	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	146	51
3740	AF090944	Homo sapiens	PRO0663	124	56
3741	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	94	47
3742	AF118086	Homo sapiens	PRO1992	124	61
3743	AF083929	Mus musculus	ES18	108	35
3744	L34685	Arabidopsis	cell wall protein	120	34

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		thaliana			
3745	AF090931	Homo sapiens	PRO0483	117	54
3746	AF090930	Homo sapiens	PRO0478	136	75
3747	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	154	59
3748	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	92	44
3749	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	98	42
3750	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	165	73
3751	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	87
3752	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	96	58
3753	U93574	Homo sapiens	putative p150	157	60
3754	X56015	Crithidia oncopelti	NADH dehydrogenase subunit 5	103	30
3755	M80613	Homo sapiens	putative	114	26
3756	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	119	54
3757	D38112	Homo sapiens	NADH dehydrogenase subunit 2	210	89
3758	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	91	58
3759	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	110	46
3760	M13100	Rattus norvegicus	unknown protein	119	46
3761	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	135	52
3762	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	84
3763	M11900	Mus musculus	15-kDa proline-rich salivary protein	125	40
3764	U63542	Homo sapiens	FAP protein	131	72
3765	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	143	76
3766	X92485	Plasmodium vivax	pval	119	54
3767	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	81	56
3768	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	98	65
3769	AB005216	Homo sapiens	Nck, Ash and phospholipase C gamma-binding protein NAP4	487	90
3770	AF026211	Caenorhabditis elegans	Similar to cuticular collagen	102	37
3771	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	91	55
3772	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	128	76
3773	AK024455	Homo sapiens	FLJ00047 protein	138	66
3774	AF090895	Homo sapiens	PRO0117	152	60
3775	AF130051	Homo sapiens	PRO0898	122	78
3776	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	100	63
3777	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	187	75
3778	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	130	56

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3779	X55685	Lycopersicon esculentum	extensin (class I)	132	38
3780	L27428	Homo sapiens	reverse transcriptase	116	53
3781	Y71066	Homo sapiens	Human membrane transport protein, MTRP-11.	188	86
3782	AL390114	Leishmania major	extremely cysteine/valine rich protein	122	67
3783	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	462	75
3784	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	127	67
3785	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	129	36
3786	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	152	78
3787	S80119	Rattus sp.	reverse transcriptase homolog	143	40
3788	AF090942	Homo sapiens	PRO0657	134	67
3789	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	63
3790	AF116661	Homo sapiens	PRO1438	128	45
3791	K03205	Homo sapiens	salivary proline-rich protein precursor	130	38
3792	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	127	74
3793	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	101	48
3794	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	175	46
3795	K03205	Homo sapiens	salivary proline-rich protein precursor	117	40
3796	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	185	88
3797	D38112	Homo sapiens	cytochrome c oxidase subunit 3	610	84
3798	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	136	56
3799	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	71	52
3800	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	127	77
3801	AF130079	Homo sapiens	PRO2852	164	54
3802	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	118	45
3803	U42580	Paramecium bursaria Chlorella virus 1	Pro-rich, PAK (20X); similar to Arabidopsis anter-specific Pro-rich protein, corresponds to Swiss-Prot Accession Number P40602	101	36
3804	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	173	87
3805	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	126	72
3806	D38112	Homo sapiens	NADH dehydrogenase subunit 4	225	85
3807	U88587	Nicotiana glauca	120 kDa style glycoprotein	118	38
3808	D38112	Homo sapiens	cytochrome c oxidase subunit 1	129	82
3809	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	122	67
3810	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	213	97
3811	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	106	63
3812	AF169974	Homo sapiens	serine racemase	153	56
3813	L27428	Homo sapiens	reverse transcriptase	175	43
3814	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	109	43

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3815	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	176	78
3816	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	112	65
3817	AF119901	Homo sapiens	PRO2831	113	55
3818	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	99	89
3819	AL160371	Leishmania major	probable (hvh-5) u1102, variant a DNA, complete virion genome	91	66
3820	X92485	Plasmodium vivax	pval	108	46
3821	AK024453	Homo sapiens	FLJ00047 protein	79	59
3822	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	178	87
3823	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	99	50
3824	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	86	94
3825	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	138	53
3826	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	88
3827	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	77	61
3828	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	139	51
3829	K03208	Homo sapiens	salivary proline-rich protein precursor	161	41
3830	U44838	Glycine max	extensin	108	47
3831	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	136	71
3832	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	205	84
3833	AL163912	Arabidopsis thaliana	glycine-rich protein atGRP-7	117	37
3834	AF130089	Homo sapiens	PRO2550	138	45
3835	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	92	76
3836	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	70
3837	X56010	Sorghum bicolor	hydroxyproline-rich glycoprotein	98	37
3838	X68249	Xenopus laevis	Proline rich protein	92	66
3839	U12690	Homo sapiens	cytochrome oxidase subunit II	262	92
3840	R63235	Homo sapiens	CNS neural thread protein HB4.	186	100
3841	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	103	64
3842	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HN1FO29.	116	62
3843	AF164614	Homo sapiens	envelope protein	508	77
3844	AF130051	Homo sapiens	PRO0898	130	73
3845	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	144	74
3846	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	119	68
3847	M13100	Rattus norvegicus	unknown protein	129	46
3848	X97675	Homo sapiens	plakophilin 2b	145	67
3849	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	141	65
3850	K03206	Homo sapiens	salivary proline-rich protein precursor	114	42

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3851	U93574	Homo sapiens	putative p150	165	82
3852	AF090931	Homo sapiens	PRO0483	97	78
3853	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	279	80
3854	U93570	Homo sapiens	putative p150	135	38
3855	M13100	Rattus norvegicus	unknown protein	100	57
3856	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	166	63
3857	Y48576	Homo sapiens	Human breast tumour-associated protein 37.	117	49
3858	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	147	45
3859	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	150	71
3860	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	165	69
3861	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	131	83
3862	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	171	81
3863	AK000241	Homo sapiens	unnamed protein product	100	48
3864	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	121	80
3865	AK024455	Homo sapiens	FLJ00047 protein	124	69
3866	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	87	64
3867	AF116712	Homo sapiens	PRO2738	92	48
3868	R13556	Homo sapiens	Protein encoded downstream of hnc_M oncoprotein.	165	62
3869	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	128	62
3870	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	94	75
3871	AK024455	Homo sapiens	FLJ00047 protein	83	72
3872	AJ242540	Volvox carterii f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	147	44
3873	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	113	51
3874	AF090930	Homo sapiens	PRO0478	120	63
3875	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	145	70
3876	D88674	Homo sapiens	antizyme inhibitor	147	75
3877	AF263744	Homo sapiens	crbb2-interacting protein ERBIN	212	37
3878	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	140	82
3879	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	82	35
3880	Y01181	Homo sapiens	Polypeptide fragment encoded by gene 12.	144	60
3881	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	122	60
3882	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	134	75
3883	M81321	Macaca fascicularis	proline-rich protein	101	41
3884	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	109	56
3885	AF013214	Bos taurus	acidic ribosomal phosphoprotein PO	177	94
3886	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	162	77

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4484.		
3887	Y59860	Homo sapiens	Human normal uterus tissue derived protein 23.	137	72
3888	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	147	72
3889	M64792	Rattus norvegicus	salivary proline-rich protein	104	40
3890	AF156228	Drosophila melanogaster	salivary gland secretion protein	104	35
3891	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCAC81.	90	47
3892	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	138	38
3893	D38112	Homo sapiens	NADH dehydrogenase subunit 5	146	65
3894	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	34
3895	X02873	Daucus carota	put. precursor	104	48
3896	AF090942	Homo sapiens	PRO0657	135	50
3897	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	195	77
3898	X92485	Plasmodium vivax	pval	111	62
3899	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	107	70
3900	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	94	93
3901	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	163	83
3902	AF090942	Homo sapiens	PRO0657	134	65
3903	AF220264	Homo sapiens	MOST-1	74	59
3904	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	131	53
3905	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	129	85
3906	AK025047	Homo sapiens	unnamed protein product	127	73
3907	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	135	86
3908	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	134	72
3909	X77816	Rattus norvegicus	PR-Vbeta1	104	62
3910	G02654	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.	114	70
3911	AK024455	Homo sapiens	FLI00047 protein	135	61
3912	U93567	Homo sapiens	putative p150	233	63
3913	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	96	40
3914	X94976	Brassica napus	cell wall-plasma membrane linker protein	104	36
3915	P92219	Homo sapiens (human)	CR1 protcin.	125	73
3916	X92485	Plasmodium vivax	pval	94	64
3917	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	105	52
3918	AF118086	Homo sapiens	PRO1992	130	87
3919	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	125	80
3920	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 162	162	79

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4493.		
3921	AF090930	Homo sapiens	PRO0478	128	64
3922	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	114	75
3923	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	130	65
3924	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	134	71
3925	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	102	58
3926	D63487	Homo sapiens	The KIAA0153 gene product is related to a putative C.elegans gene encoded in cosmid F42A8.	141	100
3927	U21123	Drosophila melanogaster	ena polypeptide	117	37
3928	X58438	Mus musculus	proline rich protein	136	36
3929	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	152	71
3930	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	132	73
3931	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	86	48
3932	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	110	65
3933	X92485	Plasmodium vivax	pval	116	36
3934	X97675	Homo sapiens	plakophilin 2b	129	82
3935	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	84	58
3937	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	107	56
3938	AF090895	Homo sapiens	PRO0117	166	68
3939	K02550	Oncorhynchus mykiss	70-kilodalton heat shock protein	104	38
3940	AK024455	Homo sapiens	FLJ00047 protein	112	74
3941	L26953	Homo sapiens	chromosomal protein	92	67
3942	U63542	Homo sapiens	FAP protein	135	75
3943	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	139	80
3944	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	141	67
3945	AK024455	Homo sapiens	FLJ00047 protein	123	76
3946	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	92	52
3947	W48927	Homo sapiens	Schwannin-binding protein C-terminal fragment.	103	56
3948	AF252293	Homo sapiens	PAR3	161	44
3949	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	125	47
3950	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	59
3951	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	174	87
3952	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	152	75
3953	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	168	64
3954	R95913	Homo sapiens	Neural thread protein.	110	54
3955	AF130089	Homo sapiens	PRO2550	122	63
3956	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	48



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3957	Y36203	Homo sapiens	Human secreted protein #75.	121	75
3958	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	177	61
3959	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	131	69
3960	U93563	Homo sapiens	putative p150	227	62
3961	D86853	Catharanthus roseus	extensin	100	40
3962	U112390	Cloning vector pSport1	beta-galactosidase alpha peptide	101	41
3963	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	107	80
3964	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	121	42
3965	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	66
3966	M11901	Rattus norvegicus	proline-rich salivary protein	101	34
3967	AF229126	Homo sapiens	acetylcholinesterase collagen-like tail subunit isoform VII	108	36
3968	AJ006770	Cicer arietinum	extensin	86	29
3969	AF130089	Homo sapiens	PRO2550	128	82
3970	U93563	Homo sapiens	putative p150	99	48
3971	AK000496	Homo sapiens	unfamed protein product	134	71
3972	Z70684	Caenorhabditis elegans	F28D1.8	108	42
3973	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	137	72
3974	AK024455	Homo sapiens	FLJ00047 protein	132	65
3975	AK024455	Homo sapiens	FLJ00047 protein	128	85
3976	X01918	Drosophila melanogaster	salivary gland glue protein	99	40
3977	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	136	46
3978	AF229067	Homo sapiens	PADI-H protein	107	87
3979	M64793	Rattus norvegicus	salivary proline-rich protein	189	48
3980	S80119	Rattus sp.	reverse transcriptase homolog	134	49
3981	AF090901	Homo sapiens	PRO0195	106	94
3982	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	111	42
3983	X92485	Plasmodium vivax	pva1	102	39
3984	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	127	64
3985	AB012162	Homo sapiens	APCL protein	190	42
3986	AB016099	Mus musculus	endonuclease/reverse transcriptase	139	65
3987	U93570	Homo sapiens	putative p150	170	71
3988	D38112	Homo sapiens	NADH dehydrogenase subunit 5	202	73
3989	D38112	Homo sapiens	NADH dehydrogenase subunit 5	244	85
3990	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	420	92
3991	D38112	Homo sapiens	NADH dehydrogenase subunit 4	272	85
3992	L38908	Nicotiana tabacum	extensin	114	40
3993	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	64
3994	AF090944	Homo sapiens	PRO0663	99	39
3995	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	150	75
3996	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	574	87
3997	D38112	Homo sapiens	NADH dehydrogenase subunit 4	488	76

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3998	U52077	Homo sapiens	mariner transposase	475	70
3999	U93570	Homo sapiens	p40	111	34
4000	U15647	Mus musculus	reverse transcriptase	137	43
4001	AF116712	Homo sapiens	PRO2738	105	52
4002	AF113685	Homo sapiens	PRO0974	125	53
4003	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	78
4004	AF116715	Homo sapiens	PRO2829	115	73
4005	D38112	Homo sapiens	NADH dehydrogenase subunit 2	288	80
4006	D38112	Homo sapiens	cytochrome c oxidase subunit 1	614	86
4007	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	106	45
4008	U90268	Homo sapiens	Krit1	152	52
4009	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	472	96
4010	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	304	100
4011	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	472	98
4012	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	102	50
4013	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	124	73
4014	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	118	47
4015	U12690	Homo sapiens	cytochrome oxidase subunit II	522	81
4016	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	147	52
4017	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	106	57
4018	AB003476	Homo sapiens	gravin	549	91
4019	D38112	Homo sapiens	NADH dehydrogenase subunit 4	391	93
4020	U44949	Xenopus laevis	zona pellucida A glycoprotein homolog	143	32
4021	D38113	Pan troglodytes	cytochrome c oxidase subunit I	571	88
4022	D38113	Pan troglodytes	cytochrome c oxidase subunit I	554	87
4023	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	165	88
4024	AL390114	Leishmania major	extremely cysteine/valine rich protein	131	38
4025	D38113	Pan troglodytes	cytochrome c oxidase subunit I	583	86
4026	AF090895	Homo sapiens	PRO0117	104	49
4027	AF130056	Homo sapiens	PRO1367	80	60
4028	X97675	Homo sapiens	plekophilin 2b	157	83
4029	X67337	Homo sapiens	Human pre-mRNA cleavage factor I 68 kDa subunit	114	35
4030	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	110	74
4031	D38112	Homo sapiens	ATPase subunit 6	395	80
4032	S70718	Hemicentrotus pulcherrimus-sea urchins, tests, Peptide, 632 aa	fibrillar collagen alpha 120 and 140 chains	104	33
4033	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	355	66
4034	AC004497	Homo sapiens	MX2	464	58
4035	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	151	61
4036	AF117888	Homo sapiens	myosin-Ixa	113	34
4038	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	100	48
4039	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	153	73

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4040	D38112	Homo sapiens	NADH dehydrogenase subunit 4	338	86
4041	AF116661	Homo sapiens	PRO1438	136	53
4042	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	120	84
4043	D38112	Homo sapiens	cytochrome c oxidase subunit 3	493	85
4044	M90516	Homo sapiens	glutamine:fructose-6-phosphate amidotransferase	261	72
4045	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	102	64
4046	AF130089	Homo sapiens	PRO2550	143	78
4047	AF090942	Homo sapiens	PRO0657	119	41
4048	R95913	Homo sapiens	Neural thread protein.	138	47
4049	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	111	59
4050	X77962	Tetrahymena thermophila	fibrillarin	105	49
4051	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	144	71
4052	X02794	Friend murine leukemia virus	Pr65	107	37
4053	Y00994	Homo sapiens	Human CSR3 protein sequence.	109	38
4054	AL121585	Homo sapiens	bA504H3.1 (SNX5 (sorting nexin 5))	299	74
4055	U00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	314	80
4056	C03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	65	54
4057	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	187	67
4058	AF205385	Pan troglodytes	NADH dehydrogenase subunit 5	202	89
4059	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	187	100
4060	U63542	Homo sapiens	FAP protein	142	73
4061	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	158	50
4062	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	123	44
4063	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	76	65
4064	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	165	46
4065	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	147	93
4066	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	76
4067	AB035523	Gallus gallus	avenaIII	101	48
4068	AC079829	Arabidopsis thaliana	Pto kinase interactor, putative	105	43
4069	AF210651	Homo sapiens	NAG18	97	77
4070	M64793	Rattus norvegicus	salivary proline-rich protein	111	43
4071	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	158	65
4072	K02576	Homo sapiens	salivary proline-rich protein 1	131	43
4073	AF038007	Homo sapiens	FIC1	153	96
4074	M35228	Trypanosoma brucei	ATPase 6	103	37
4075	U54788	Mus musculus	Wiskott-Aldrich Syndrome Protein	119	46
4076	M81321	Macaca fascicularis	proline-rich protein	104	36
4077	X52235	Homo sapiens	ORFII	192	39
4078	G00328	Homo sapiens	Human secreted protein, SEQ ID NO:	126	83

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4409.		
4079	AB026542	Homo sapiens	WASP-family protein	98	41
4080	L17318	Rattus norvegicus	proline-rich proteoglycan	105	42
4081	AF130051	Homo sapiens	PRO0898	117	42
4082	AF130089	Homo sapiens	PRO2550	85	79
4083	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	117	48
4084	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	89	40
4085	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	163	80
4086	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	144	74
4087	AF085691	Homo sapiens	multidrug resistance-associated protein 3A	197	49
4088	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	109	62
4089	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	139	51
4090	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	103	65
4091	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	159	68
4092	X92485	Plasmodium vivax	pval	95	38
4093	U93569	Homo sapiens	p40	205	40
4094	L16864	African swine fever virus	cd2 homologue	98	45
4095	X71413	Homo sapiens	ELE1	675	98
4096	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	149	60
4097	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	116	70
4098	AF090930	Homo sapiens	PRO0478	149	78
4099	AF090942	Homo sapiens	PRO0657	124	56
4100	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	139	62
4101	L26953	Homo sapiens	chromosomal protein	104	54
4102	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	128	70
4103	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	94	58
4104	U73199	Mus musculus	Rho-guanine nucleotide exchange factor	370	56
4105	AF090931	Homo sapiens	PRO0483	104	90
4106	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	133	72
4107	AF118082	Homo sapiens	PRO1902	145	49
4108	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	116	50
4109	U93564	Homo sapiens	p40	539	91
4110	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	144	54
4111	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	138	65
4112	AF217536	Homo sapiens	truncated mevalonate kinase	91	73
4113	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	120	36
4114	M17522	Paracoccus	cytochrome c1 precursor (EC 1.10.2.2)	101	41

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		denitrificans			
4115	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	121	59
4116	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	148	73
4117	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	80	85
4118	X04758	Homo sapiens	pro- alpha (V)collagen (AA 1099)	106	39
4119	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	122	47
4120	AF130089	Homo sapiens	PRO2550	132	68
4121	AF090942	Homo sapiens	PRO0657	136	48
4122	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone 11NHFO29.	115	66
4123	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	72	48
4124	X92485	Plasmodium vivax	pva1	104	54
4125	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	59
4126	AK024455	Homo sapiens	PLJ00047 protein	86	61
4127	AF119855	Homo sapiens	PRO1847	99	68
4128	S80119	Rattus sp.	reverse transcriptase homolog	129	39
4129	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	156	62
4130	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	135	72
4131	R86406	Homo sapiens	Human matrix metalloprotease MMP1a.	108	83
4132	L16461	Chlamydomonas reinhardtii	structural wall protein	87	37
4133	Y30713	Homo sapiens	Amino acid sequence of a human secreted protein.	232	95
4134	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	121	69
4135	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	135	70
4136	K02576	Homo sapiens	salivary proline-rich protein 1	134	42
4137	Y15173	Human papillomavirus type 75	E4 protein	101	38
4138	AF130089	Homo sapiens	PRO2550	130	35
4139	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	38
4140	Y36203	Homo sapiens	Human secreted protein #75.	120	48
4141	AF130089	Homo sapiens	PRO2550	139	36
4142	S80119	Rattus sp.	reverse transcriptase homolog	170	47
4143	U54636	Staphylococcus aureus	protein A	135	35
4144	AL390114	Leishmania major	extremely cysteine/valine rich protein	157	55
4145	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	112	54
4146	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	117	37
4147	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hbcn) gene product.	98	61
4148	AF130051	Homo sapiens	PRO0898	124	88
4149	G00673	Homo sapiens	Human secreted protein, SEQ ID NO:	133	67

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4754.		
4150	Z29481	Homo sapiens	3-hydroxyanthranilic acid dioxygenase	244	62
4151	M81321	Macaca fascicularis	proline-rich protein	172	50
4152	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	129	66
4153	AF119851	Homo sapiens	PRO1722	128	62
4154	AB037826	Homo sapiens	KIAA1405 protein	194	60
4155	M12099	Mus musculus	proline-rich protein	124	37
4156	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	46
4157	M11901	Rattus norvegicus	proline-rich salivary protein	124	41
4158	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	134	83
4159	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	141	74
4160	M76546	Helianthus annuus	hydroxyproline-rich protein	135	39
4161	U35730	Mus musculus	jerky	116	31
4162	Z81525	Caenorhabditis elegans	contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=35.5, E-value=4e-07, N=2	130	50
4163	AF113685	Homo sapiens	PRO0974	129	45
4164	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	168	71
4165	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	137	70
4166	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	175	72
4167	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	86	45
4168	AB000505	Daucus carota	unnamed protein product	101	43
4169	U87607	Rattus norvegicus	putative RNA binding protein 1	113	30
4170	AF119900	Homo sapiens	PRO2822	154	59
4171	AE001381	Plasmodium falciparum	hypothetical protein	106	33
4172	AE000034	Mycoplasma pneumoniae	bifunctional threonine dehydrogenase; galactosyltransferase	100	28
4173	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	100	47
4174	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	142	68
4175	AK024455	Homo sapiens	FLJ00047 protein	116	60
4176	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	94	44
4177	AK024455	Homo sapiens	FLJ00047 protein	102	59
4178	AY007557	Mycobacterium avium subsp. paratuberculosis	fibronectin-attachment protein FAP-P	98	42
4179	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	115	69
4180	M12100	Mus musculus	proline-rich protein MP-3	132	44
4181	AF090930	Homo sapiens	PRO0478	138	63
4182	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	152	75
4183	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	84

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4184	K03205	Homo sapiens	salivary proline-rich protein precursor	150	43
4185	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	128	51
4186	AF090944	Homo sapiens	PRO0663	124	49
4187	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	93	62
4188	D38112	Homo sapiens	ATPase subunit 6	439	78
4189	AF130051	Homo sapiens	PRO0898	89	57
4190	AF090930	Homo sapiens	PRO0478	137	83
4191	K03205	Homo sapiens	salivary proline-rich protein precursor	100	35
4192	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	212	91
4193	Y13247	Homo sapiens	FB19 protein	142	46
4194	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	268	93
4195	AF124729	Mus musculus	acinus <sup>5</sup>	140	42
4196	AJ277425	Globodera pallida	putative cuticular collagen	156	43
4197	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	77
4198	Z70684	Caenorhabditis elegans	F28D1.8	97	45
4199	M64793	Rattus norvegicus	salivary proline-rich protein	119	36
4200	X62379	Mus musculus	formin, isoform IV	115	48
4201	D38113	Pan troglodytes	NADH dehydrogenase subunit 4	224	93
4202	M14820	Trypanosoma brucei	ORF2 bases 1807-2850; first start codon at 2032; putative	103	29
4203	U93572	Homo sapiens	p40	182	34
4204	D82026	Silene latifolia	glycine-rich protein	98	49
4205	AF003151	Caenorhabditis elegans	contains similarity to an RNA recognition motif	107	40
4206	L07545	Leishmania tarentolae	A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression	101	35
4207	K03205	Homo sapiens	salivary proline-rich protein precursor	104	38
4208	AF229126	Homo sapiens	acetylcholinesterase collagen-like tail subunit isoform VII	96	75
4209	AF090895	Homo sapiens	PRO0117	142	68
4210	X92485	Plasmodium vivax	pval	104	35
4211	G02828	Homo sapiens	Human secreted protein, SEQ ID NO: 6909.	173	73
4212	G02828	Homo sapiens	Human secreted protein, SEQ ID NO: 6909.	151	69
4213	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	122	43
4214	AF090944	Homo sapiens	PRO0663	97	39
4215	X12544	Homo sapiens	3 HLA-DR B protein precursor (AA - 29 to 267)	111	60
4216	M69065	human herpesvirus 2	ORF1	89	38
4217	AF090895	Homo sapiens	PRO0117	133	78
4218	B01372	Homo sapiens	Neuron-associated protein.	135	46
4219	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	71	47
4220	U93567	Homo sapiens	p40	170	35
4221	D00570	Mus musculus	open reading frame (251 AA)	108	28
4222	X97675	Homo sapiens	plakophilin 2b	122	47
4223	AF270937	Plutella xylostella	PxORF73 peptide	99	54

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		granulovirus			
4224	AF130089	Homo sapiens	PRO2550	144	69
4225	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	125	82
4226	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	99	62
4227	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	172	59
4228	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	161	74
4229	AL049537	Homo sapiens	dJ1164110.1 (brefeldin A-inhibited guanine nucleotide-exchange protein 2)	212	90
4230	AF118086	Homo sapiens	PRO1992	150	69
4231	M81321	Macaca fascicularis	proline-rich protein	130	41
4232	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	138	68
4233	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	132	56
4234	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	110	52
4235	R13556	Homo sapiens	Protein encoded downstream of hhcm oncoprotein.	124	32
4236	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	119	42
4237	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	368	56
4238	R05913	Homo sapiens	Neural thread protein.	139	55
4239	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	146	63
4240	X97675	Homo sapiens	plakophilin 2b	108	78
4241	Y36156	Homo sapiens	Human secreted protein #28.	137	65
4242	AK000385	Homo sapiens	unnamed protein product	131	33
4243	AJ252253	human herpesvirus 2	glycoprotein G-2	107	36
4244	Y99447	Homo sapiens	Human PRO1556 (UNQ764) amino acid sequence SEQ ID NO:372.	597	100
4245	Y05398	Homo sapiens	Human TIE ligand NL8 protein sequence.	424	84
4246	L00016	Homo sapiens	urfa	222	90
4247	AF134579	Zea mays	arabinogalactan protein	134	39
4248	Z34465	Zea mays	extensin-like protein	123	33
4249	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	128	62
4250	J02695	Plasmodium yoelii	circumsporozoite protein	110	33
4251	AK024455	Homo sapiens	FLJ00047 protein	136	65
4252	U02570	Homo sapiens	CDC42 GTPase-activating protein	566	93
4253	D38112	Homo sapiens	cytochrome c oxidase subunit I	449	85
4254	R13556	Homo sapiens	Protein encoded downstream of hhcm oncoprotein.	111	63
4255	M61143	Bovine herpesvirus 1	latency-related open reading frame 2; putative	101	42
4256	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	43
4257	Y06294	Homo sapiens	Human transcription regulator MOP6 partial sequence.	410	79
4258	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	112	61
4259	D90252	Human papillomavirus type 5b	E4 protein	110	32



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4260	X90569	Homo sapiens	elastic titin	660	95
4261	AF090930	Homo sapiens	PRO0478	114	71
4262	AF132209	Homo sapiens	prepro-major basic protein homolog	422	72
4263	AF043102	Pneumocystis carinii	surface glycoprotein A	121	29
4264	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	132	55
4265	AF090895	Homo sapiens	PRO0117	159	62
4266	AF090930	Homo sapiens	PRO0478	143	50
4267	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	119	34
4268	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	106	61
4269	D23660	Homo sapiens	ribosomal protein	493	73
4270	AF130089	Homo sapiens	PRO2550	119	39
4271	U93564	Homo sapiens	putative p150	121	37
4272	AB033615	Mus musculus	phospholipase C-L2	485	79
4273	AF006082	Homo sapiens	Arp2	488	83
4274	Y12293	Mus musculus	lun	104	33
4275	X54289	Bos taurus	cGMP-dependent protein kinase (isoform 1 beta)	561	81
4276	AF119855	Homo sapiens	PRO1847	155	71
4277	J01415	Homo sapiens	MTND4	372	63
4278	AB021078	Plasmodium falciparum	ybbA	101	30
4279	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	110	73
4280	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	110	73
4281	AF119851	Homo sapiens	PRO1722	110	60
4282	D38116	Pan paniscus	NADH dehydrogenase subunit 1	346	92
4283	Y15908	Homo sapiens	DIA-12C protein	109	52
4284	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	122	76
4285	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	121	42
4286	AK024455	Homo sapiens	FLJ00047 protein	135	57
4287	Y11525	Homo sapiens	CCAAT/enhancer binding protein alpha	100	32
4288	AF033122	Homo sapiens	non-p53 regulated PA26-T1 nuclear protein	128	81
4289	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	111	39
4290	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	140	58
4291	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	132	34
4292	X60432	Zea mays	prolin rich protein	118	42
4293	U09567	Homo sapiens	zinc finger protein ZNF136	461	60
4294	AF038960	Homo sapiens	SKD1 homolog	146	82
4295	AL390114	Leishmania major	extremely cysteine/valine rich protein	128	54
4296	U66561	Homo sapiens	kruppel-related zinc finger protein	512	89
4297	AF043706	Caenorhabditis elegans	contains similarity to granulins	104	55
4298	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	65
4299	AF152510	Homo sapiens	protocadherin gamma A3 short form protein	520	87

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4300	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	142	72
4301	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	109	50
4302	AL035440	Arabidopsis thaliana	putative protein	103	31
4303	L05500	Homo sapiens	adenyl cyclase	655	96
4304	AF116712	Homo sapiens	PRO2738	140	54
4305	D13757	Homo sapiens	amidophosphoribosyltransferase	182	92
4306	L20450	Mus musculus	DNA-binding protein	470	64
4307	AF213386	Mus musculus	ATP-binding cassette protein	175	97
4308	X76850	Mus musculus	MAP kinase-activated protein kinase 2	154	69
4309	S80119	Rattus sp.	reverse transcriptase homolog	123	55
4310	X67337	Homo sapiens	Human pre-mRNA cleavage factor 1 68 kDa subunit	110	32
4311	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	96	58
4312	Z46236	Ovis aries	keratinocyte growth factor	210	75
4313	AB020700	Homo sapiens	KIAA0893 protein	569	87
4314	AF124727	Homo sapiens	aclnus5	498	88
4315	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	88	32
4316	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	122	53
4317	AF119900	Homo sapiens	PRO2822	135	58
4318	U74612	Homo sapiens	hepatocyte nuclear factor-3/fork head homolog 11A	104	70
4319	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	117	51
4320	AB026054	Homo sapiens	brain finger protein	412	90
4321	AF090944	Homo sapiens	PRO0663	133	71
4322	AF165513	Homo sapiens	vacuolar protein sorting 45 isoform	712	97
4323	Y99418	Homo sapiens	Human PRO1317 (UNQ783) amino acid sequence SEQ ID NO:277.	532	97
4324	AF163772	Leishmania major	7138.7	142	37
4325	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	128	59
4326	W40054	Homo sapiens	P300/CBP-associated transcriptional cofactor P/CAF C-terminus.	175	94
4327	AF217411	Homo sapiens	neuregulin 3 isoform HNL3	549	84
4328	U94836	Homo sapiens	ERPROT 213-21	175	87
4329	Y20763	Homo sapiens	Human neurofilament-M mutant protein fragment 45.	501	87
4330	AB037745	Homo sapiens	KIAA1324 protein	1014	99
4331	M91563	Rattus norvegicus	NMDA receptor subtype 2C	116	39
4332	G03704	Homo sapiens	Human secreted protein, SEQ ID NO: 7785.	286	76
4333	AC006841	Arabidopsis thaliana	Mutator-like transposase	130	70
4334	AP000373	Arabidopsis thaliana	jasmonate inducible protein; myrosinase binding protein-like	130	53
4335	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	377	90
4336	AJ277426	Globodera pallida	putative cuticular collagen	112	37

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4337	U16802	Rattus norvegicus	Ca <sup>2+</sup> -dependent activator protein; calcium-dependent actin-binding protein	560	79
4338	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	118	56
4339	AB024520	Homo sapiens	notch4	93	33
4340	AF128406	Homo sapiens	nuclear prelamin A recognition factor	241	100
4341	W19771	Homo sapiens	Beta-1 integrin modulator B171.	169	100
4342	AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2 Antigen)	666	88
4343	D50312	Homo sapiens	uKATP-1	542	80
4344	U84487	Homo sapiens	CX3C chemokine precursor	371	78
4345	U93569	Homo sapiens	putative p150	111	47
4346	AL161755	Streptomyces coelicolor A3(2)	putative serine/threonine protein kinase	102	30
4347	AK026162	Homo sapiens	unnamed protein product	377	98
4348	AF221759	Homo sapiens	Mam1	314	47
4349	AF165926	Homo sapiens	NUP155	147	84
4351	U50185	Rattus norvegicus	PP-1M	144	52
4352	D50455	Rattus norvegicus	phospholipase C delta4	196	70
4353	X54131	Homo sapiens	protein-tyrosine phosphatase	261	87
4354	AF151850	Homo sapiens	CG1-92 protein	255	92
4355	G03996	Homo sapiens	Human secreted protein, SEQ ID NO: 8077.	105	95
4356	U93564	Homo sapiens	putative p150	171	72
4357	AP001507	Bacillus halodurans	unknown conserved protein	159	34
4358	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	153	60
4359	AF072697	Mus musculus	SHYC	177	97
4360	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	129	69
4361	M98776	Homo sapiens	keratin 1	449	77
4362	AK024436	Homo sapiens	FLJ00026 protein	671	91
4363	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	155	49
4364	D13896	Rattus norvegicus	cytoplasmic dynein heavy chain	327	92
4365	X79389	Homo sapiens	glutathione transferase T1	164	96
4366	AB006458	Mus musculus	alpha-D-mannosidase	177	56
4367	X01060	Homo sapiens	put. transferrin receptor (aa 1-760)	160	96
4368	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	103	54
4369	AL353715	Homo sapiens	bK3184A7.3.1 (helicase-like protein NHL)	485	100
4370	AF001631	Oryctolagus cuniculus	glucose-regulated protein GRP94	118	92
4371	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	113	80
4372	AL121741	Schizosaccharomyces pombe	putative negative regulator of vesicle formation	200	41
4373	M96982	Homo sapiens	U2 snRNP auxiliary factor small subunit	279	70
4374	U47741	Homo sapiens	CREB-binding protein	123	96
4375	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	127	75
4376	Y12781	Homo sapiens	transducin (beta) like 1 protein	1056	90

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4377	W69424	Homo sapiens	Human secreted protein bg140_1.	183	97
4378	AL096700	Homo sapiens	dj499B10.2 (phosphorylase kinase, alpha 2 (liver) (PYK))	639	86
4379	AF177390	Manduca sexta	antennal specific membrane protein AMP	378	51
4380	X97675	Homo sapiens	plakophilin 2b	156	75
4381	R33713	Homo sapiens	Pg1101.	104	100
4382	AB015473	Arabidopsis thaliana	gene_id:MCM23.1~unknown protein	113	61
4383	AF116715	Homo sapiens	PRO2829	133	50
4384	AL357472	Homo sapiens	VP533B	676	99
4385	AF090931	Homo sapiens	PRO0483	155	58
4386	U92645	Gecarcinus lateralis	alpha-1-tubulin	511	75
4387	Y36095	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 480.	202	90
4388	M64923	Bos taurus	C10 protein	218	95
4389	X98264	Homo sapiens	M-phase phosphoprotein 4	197	100
4390	AK000264	Homo sapiens	unnamed protein product	239	73
4391	M12937	Homo sapiens	ferritin heavy subunit	662	84
4392	P92219	Homo sapiens (human)	CR1 protein.	116	80
4393	X16135	Homo sapiens	L protein (AA 1-558)	759	99
4394	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	148	58
4395	AC005591	Homo sapiens	PkB-like	170	97
4396	AF161426	Homo sapiens	HSPC308	313	77
4397	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	146	61
4398	AF104921	Homo sapiens	succinyl-CoA synthetase alpha subunit	679	88
4399	AF257330	Homo sapiens	COBW-like protein	586	90
4400	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	116	65
4401	AF119851	Homo sapiens	PRO1722	101	79
4402	M55542	Homo sapiens	guanylate binding protein isoform I	230	76
4403	Y07752	Volvox carteri	pherophorin-S	459	88
4404	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	113	44
4405	U07786	Sus scrofa	beta actin	519	90
4406	A06977	Homo sapiens	albumin	586	88
4407	L20755	Cuscuta reflexa	hybrid proline-rich protein;cytokinin-induced;haustoria	112	41
4408	AB002299	Homo sapiens	KIAA0301	612	98
4409	AB001424	Mus musculus	KIF17	104	47
4410	M88108	Homo sapiens	p62	574	92
4411	AL121673	Homo sapiens	bA305P22.2 (novel protein)	415	71
4412	AF064553	Mus musculus	NSD1 protein	224	64
4413	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	107	36
4414	A06977	Homo sapiens	albumin	505	82
4415	A06977	Homo sapiens	albumin	596	90
4416	Y87116	Homo sapiens	Human secreted protein sequence SEQ ID NO:155.	123	50
4417	AL359782	Trypanosoma brucei	possible (hly-6) u1102, variant a dna, complete virion genome.	103	85
4418	G03053	Homo sapiens	Human secreted protein, SEQ ID NO: 7134.	100	54
4419	AF049606	Mus musculus	transcription factor NF-A1c isoform b	114	90

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4420	Z11190_cdl	Homo sapiens	11-DEC-1998 Interleukin-3 coding sequence from b2HFLS20W cDNA library.	354	97
4421	W64469	Homo sapiens	Human secreted protein from clone CW795_2.	203	100
4422	M12523	Homo sapiens	albumin Venezia	350	94
4423	AF130077	Homo sapiens	PRO2619	561	89
4424	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	161	64
4425	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	393	91
4426	A09561	synthetic construct	human serum albumin	651	96
4427	AL133215	Homo sapiens	bA108L7.5 (novel protein similar to Plasmodium POM1 and C. elegans F46G1.1.1 (Tr:Q20485))	392	100
4428	W33663	Homo sapiens	Human puromycin-sensitive aminopeptidase (PSA)-68.	172	96
4429	AB021654	Homo sapiens	DD2/bile acid-binding protein/AKR1C2/3alpha-hydroxysteroid dehydrogenase type 3	184	81
4430	W63683	Homo sapiens	Human secreted protein 3.	114	42
4431	AY008763	Homo sapiens	sentrin/SUMO-specific protease	447	96
4432	U52965	Homo sapiens	ENX-1	176	94
4433	AF180470	Mus musculus	Kiaa0575	423	77
4434	X17206	Homo sapiens	put. LLRep3 protein (AA I-221)	581	99
4435	Y70929	Homo sapiens	Human zilla4 splice variant protein.	621	100
4436	C00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	135	71
4437	A06977	Homo sapiens	albumin	610	97
4438	A00279	synthetic construct	Human serum albumin	621	94
4439	L29028	Chlamydomonas eugametos	amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 .. 109, 128 .. 130, 132 .. 134, 158 .. 160, 163 .. 165; amino acid feature: Rod protein domain, aa 169 .. 340; amino acid feature: globular protein domain, aa 32 .. 168	105	36
4440	AK024455	Homo sapiens	FLJ00047 protein	112	65
4441	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	133	69
4442	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	142	60
4443	AF113685	Homo sapiens	PRO0974	101	54
4444	W03627	Homo sapiens	Human follicle stimulating hormone GPR N-terminal sequence.	181	42
4445	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	132	76
4446	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	141	54
4447	L02867	Homo sapiens	paraneoplastic antigen	136	78
4448	D38435	Homo sapiens	homologue of yeast PMS1	108	66
4449	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	122	65
4450	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	68
4451	AF220264	Homo sapiens	MOST-1	101	40
4452	AF130079	Homo sapiens	PRO2852	97	59
4453	AF116715	Homo sapiens	PRO2829	139	69

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4454	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	144	53
4455	AF130087	Homo sapiens	PRO2411	108	73
4456	AF279891	Homo sapiens	dead box protein 15	108	58
4457	L08258	Strongylocentrotus purpuratus	kinesin light chain isoform 4	176	94
4458	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	116	78
4460	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	146	74
4461	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	156	52
4462	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	118	72
4463	AF119900	Homo sapiens	PRO2822	144	80
4464	M15530	Homo sapiens	B-cell growth factor	92	76
4465	Y17833	Human endogenous retrovirus K	env protein	107	62
4466	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	132	78
4467	AF090895	Homo sapiens	PRO0117	112	79
4468	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	146	64
4469	X97675	Homo sapiens	plakophilin 2b	119	78
4470	AF118081	Homo sapiens	PRO1900	119	74
4471	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	121	60
4472	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	63
4473	Y86248	Homo sapiens	Human secreted protein HCHPP68, SEQ ID NO: 163.	205	73
4474	AF130114	Homo sapiens	PRO2459	121	67
4475	AF178534	Homo sapiens	talin	213	67
4476	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	122	92
4477	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	99	66
4478	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	142	62
4479	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	153	55
4480	AF217374	Acanthaster planci	cytochrome oxidase subunit I	130	100
4481	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	110	57
4482	Y20983	Homo sapiens	Human glial fibrillary acidic protein GFAP wild type fragment 9.	110	63
4483	AF221552	Oryza sativa	proline-rich protein RiP-15	119	33
4484	L25941	Homo sapiens	integral nuclear envelope inner membrane protein	110	84
4485	AF130089	Homo sapiens	PRO2550	161	81
4486	U39742	Caenorhabditis elegans	coded for by C. elegans cDNA yk25e5.3; coded for by C. elegans cDNA yk25e5.5; similar to repeat guanylate kinase domain of D. melanogaster lethal(1) discs large-1 tumor suppressor protein (SP:DLG1_DROME, P31007) and R. norvegicus postsynaptic density protein	98	72

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			95 (PSD-95) (SP:PSD9_RAT, P31016)		
4487	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	89	81
4488	X97675	Homo sapiens	plakophilin 2b	127	88
4489	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	105	71
4490	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	160	64
4491	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	122	77
4492	U83280	Leishmania donovani	39 kDa antigen	107	76
4493	AF023142	Homo sapiens	pre-mRNA splicing SR protein rA4	141	40
4494	K02576	Homo sapiens	salivary proline-rich protein 1	119	40
4495	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	98	45
4496	AF130089	Homo sapiens	PRO2550	132	75
4497	AF090930	Homo sapiens	PRO0478	160	76
4498	AF119900	Homo sapiens	PRO2822	158	55
4499	AF116661	Homo sapiens	PRO1438	126	44
4500	AF116661	Homo sapiens	PRO1438	118	42
4501	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	113	48
4502	M81321	Macaca fascicularis	proline-rich protein	154	44
4503	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	96
4504	D44596	Saccharomyces cerevisiae	Mdjlp heat shock protein	93	42
4505	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	163	76
4506	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	207	93
4507	U93564	Homo sapiens	p40	520	86
4508	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	135	55
4509	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	77
4510	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	146	66
4511	L27428	Homo sapiens	reverse transcriptase	143	87
4512	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	80
4513	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	97	75
4514	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	60
4515	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	73
4516	AF130051	Homo sapiens	PRO0898	141	86
4517	U12690	Homo sapiens	cytochrome oxidase subunit II	185	94
4518	G02597	Homo sapiens	Human secreted protein, SEQ ID NO: 6678.	130	100
4519	AK024455	Homo sapiens	FLJ00047 protein	152	68
4520	AF210651	Homo sapiens	NAG18	161	88
4521	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	140	68
4522	AF217374	Acanthaster planci	cytochrome oxidase subunit I	131	76

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4523	U72520	Mus musculus	mena protein	102	42
4524	J01415	Homo sapiens	cytochrome oxidase subunit 3	129	75
4525	AL160493	Leishmania major	probable (bhv-6) u1102, variant a DNA, complete virion genome	108	84
4526	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	139	76
4527	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	89
4528	AF090931	Homo sapiens	PRO0483	91	88
4529	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	51
4530	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	130	92
4531	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	123	64
4532	L26953	Homo sapiens	chromosomal protein	102	79
4533	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	88	54
4534	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	122	40
4535	AF090944	Homo sapiens	PRO0663	113	53
4536	U15647	Mus musculus	expressed in select embryonal carcinoma cells and testicular cells; similar to Swiss-Prot Accession Number P11260	119	35
4537	L13858	Homo sapiens	guanine nucleotide exchange factor	150	81
4538	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	138	68
4539	AF090930	Homo sapiens	PRO0478	104	53
4540	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	112	64
4541	K02401	Homo sapiens	chorionic somatomammotropin	672	96
4542	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	171	67
4543	J04208	Homo sapiens	inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	455	92
4544	K02401	Homo sapiens	chorionic somatomammotropin	397	88
4545	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	155	66
4546	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	161	68
4547	R24056	Homo sapiens	hGH variant #8 - 172Arg 174Thr 176Tyr 178His.	117	62
4548	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	111	68
4549	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	124	65
4550	AF119855	Homo sapiens	PRO1847	152	68
4551	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	153	70
4552	M59217	Homo sapiens	alpha-1 type XIII collagen	98	57
4553	R83119	Homo sapiens	Human cisplatin resistance protein.	136	96
4554	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	72
4555	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	91	60
4556	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	70
4557	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y	101	44



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			isoform		
4558	AF130089	Homo sapiens	PRO2550	150	85
4559	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	161	56
4560	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	81	64
4561	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	115	55
4562	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	106	82
4563	AF090931	Homo sapiens	PRO0483	145	73
4564	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	358	77
4565	AF130089	Homo sapiens	PRO2550	175	85
4566	Z93244	Homo sapiens	bK116F5.2 (PUTATIVE RhoGAP (CDC42 GTPase Activating Protein) LIKE protein)	125	61
4567	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	142	56
4568	AF130089	Homo sapiens	PRO2550	125	75
4569	AF130089	Homo sapiens	PRO2550	172	82
4570	AF225961	Rattus norvegicus	RhoGEF glutamate transport modulator GTRAP48	149	78
4571	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	143	64
4572	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	157	70
4573	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	91	73
4574	X92485	Plasmodium vivax	pwal	111	52
4575	U93567	Homo sapiens	p40	151	71
4576	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	90	57
4577	AC007508	Arabidopsis thaliana	FIK23.4	143	42
4578	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	145	53
4579	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	175	73
4580	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	142	76
4581	AF130079	Homo sapiens	PRO2852	117	70
4582	AF090930	Homo sapiens	PRO0478	109	57
4583	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	134	79
4584	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	149	62
4585	AF118090	Homo sapiens	PRO2044	175	97
4586	AL080243	Homo sapiens	E1A binding protein p300; match: proteins: Sw:Q09472 Sw:Q92793 Sw:P45481 Wp:CE00571 Wp:CE21117 Tr:O01368 Wp:CE08856 Wp:CE00570 Wp:CE08453 Tr:O44076	144	93
4587	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICE1) protein sequence.	140	62
4588	AJ131245	Homo sapiens	Sec24B protein	151	81
4589	W02105	Homo sapiens	Human L-asparaginase.	559	100
4590	L26953	Homo sapiens	chromosomal protein	146	71
4591	M16976	Glycine max	N-75	125	36

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4592	AF119851	Homo sapiens	PRO1722	118	61
4593	AF090931	Homo sapiens	PRO0483	99	85
4594	M20789	Homo sapiens	alpha-1 type I collagen	103	41
4595	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	97	72
4596	AF130089	Homo sapiens	PRO2550	124	71
4597	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	143	65
4598	AF118082	Homo sapiens	PRO1902	122	64
4599	AK023034	Homo sapiens	unnamed protein product	156	100
4600	AF118082	Homo sapiens	PRO1902	148	62
4601	AF119855	Homo sapiens	PRO1847	130	50
4602	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	99	77
4603	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	162	65
4604	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	135	54
4605	AL160371	Leishmania major	probable (nhv-6) u1102, variant a DNA, complete virion genome	123	75
4606	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	127	74
4607	V00672	Pan troglodytes	reading frame protein 4	194	72
4608	X86791	Sus scrofa	beta-globin	156	87
4609	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	130	88
4610	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	90
4611	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	149	68
4612	AB029309	Homo sapiens	Npw38-binding protein NpwBP	120	38
4613	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	148	53
4614	AK024372	Homo sapiens	unnamed protein product	124	63
4615	AC005360	Homo sapiens	FAA	175	91
4616	D38113	Pan troglodytes	ATPase subunit 6	204	69
4617	R13556	Homo sapiens	Protein encoded downstream of hbc_M oncoprotein.	122	45
4618	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	118	81
4619	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	99	90
4620	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	125	50
4621	S79410	Mus musculus	nuclear localization signal binding protein	107	45
4622	AF126163	Homo sapiens	HLA3 protein	124	75
4623	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	109	69
4624	U38184	Trypanosoma cruzi	ATPase subunit 6	102	45
4625	U01849	Trypanosoma brucei	ORF1	97	36
4626	G03058	Homo sapiens	Human secreted protein, SEQ ID NO: 7139.	95	57
4627	M33228	Trypanosoma brucei	ATPase 6	126	37
4628	AF118086	Homo sapiens	PRO1992	113	60
4629	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	149	41

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4630	X12544	Homo sapiens	3 HLA-DR B protein precursor (AA - 29 to 267)	108	48
4631	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	46
4632	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	124	60
4633	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	151	60
4634	J01415	Homo sapiens	cytochrome oxidase subunit 3	138	100
4635	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	135	56
4636	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	100
4637	X67320	Rattus norvegicus	H1d-Histone	122	40
4638	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	181	76
4639	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	96	73
4640	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	136	54
4641	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	70
4642	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	190	56
4643	M29580	Homo sapiens	zinc finger protein 7 (ZFP7)	103	38
4645	U47741	Homo sapiens	CREB-binding protein	207	94
4646	AL035461	Homo sapiens	dJ967N21.5 (novel MCM2/3/5 family member)	213	80
4647	G03435	Homo sapiens	Human secreted protein, SEQ ID NO: 7516.	76	60
4648	AF227948	Homo sapiens	HBV pX associated protein-8; XAP-8	402	86
4649	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	143	86
4650	U93574	Homo sapiens	putative p150	121	33
4651	A02739	synthetic construct	chloramphenicol acetyltransferase	622	99
4652	AF190449	Mus musculus	putative transcription factor ALF-4	274	83
4653	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	108	76
4654	X15187	Homo sapiens	precursor polypeptide (AA -21 to 782)	763	98
4655	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	91
4656	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	169	77
4657	B01372	Homo sapiens	Neuron-associated protein.	135	83
4658	AK024455	Homo sapiens	FLJ00047 protein	151	60
4659	AC004850	Homo sapiens	vacuolar assembly protein VPS41 homolog (S53)	187	92
4660	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	181	92
4661	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	138	58
4662	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	154	78
4663	M69180	Homo sapiens	nonmuscle myosin heavy chain-A	106	84
4664	AF130089	Homo sapiens	PRO2550	117	65
4665	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	91

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4666	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	62
4667	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	111	78
4668	AF113695	Homo sapiens	PRO1365	82	71
4669	AF003540	Homo sapiens	Krueppel family zinc finger protein	111	64
4670	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	49
4671	AL109658	Homo sapiens	dJ776F14.1 (ortholog of mouse I47)	110	100
4672	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	129	62
4673	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	138	60
4674	X51591	Homo sapiens	beta-myosin heavy chain (1151 AA)	442	97
4675	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	148	76
4676	D86971	Homo sapiens	no similarities to reported gene products	133	100
4677	K02576	Homo sapiens	salivary proline-rich protein 1	142	43
4678	AF044205	Gossypium hirsutum	proline-rich protein precursor	117	39
4679	D38116	Pan paniscus	NADH dehydrogenase subunit 4	243	98
4680	AF113685	Homo sapiens	PRO0974	117	74
4681	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	193	90
4682	L26163	Mus musculus	histone H1c	111	37
4683	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	145	78
4684	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	53
4685	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	110	60
4686	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	153	72
4687	D38112	Homo sapiens	NADH dehydrogenase subunit 6	165	100
4688	W50922	Homo sapiens	Amino acid sequence of a heterogenous ribonucleotide protein.	139	100
4689	Y00281	Homo sapiens	precursor	789	100
4690	AF210651	Homo sapiens	NA G18	142	65
4691	L26953	Homo sapiens	chromosomal protein	124	72
4692	L26953	Homo sapiens	chromosomal protein	124	72
4693	U12690	Homo sapiens	cytochrome oxidase subunit II	166	80
4694	L27428	Homo sapiens	reverse transcriptase	144	87
4695	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	74
4696	W29474	Homo sapiens	Human histone H1 isoform H1S-1.	93	41
4697	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	126	56
4698	S79410	Mus musculus	nuclear localization signal binding protein	138	62
4699	G00413	Homo sapiens	Human secreted protein, SEQ ID NO: 4494.	141	54
4700	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	162	70
4701	AF003540	Homo sapiens	Krueppel family zinc finger protein	112	88
4702	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	159	59
4703	AF241242	Mus musculus	T-cell-specific T-box transcription factor T-bet	294	75
4704	Y86248	Homo sapiens	Human secreted protein HCHPF68,	152	80

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SEQ ID NO:163.		
4705	AF038963	Homo sapiens	RNA helicase	102	70
4706	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	148	63
4707	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	145	70
4708	AF289099	Maackia amurensis	ENOD2f	113	42
4709	AF130087	Homo sapiens	PRO2411	124	57
4710	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	188	86
4711	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	86
4712	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	143	78
4713	AF273133	Ochotona macrotis	NADH dehydrogenase subunit 4	154	76
4714	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	104	48
4715	Z18361	Ovis aries	trichohyalin	120	33
4716	AF130089	Homo sapiens	PRO2550	152	75
4717	AF119851	Homo sapiens	PRO1722	143	60
4718	K03205	Homo sapiens	salivary proline-rich protein precursor	145	45
4719	K02401	Homo sapiens	chorionic somatomammotropin	619	96
4720	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	114	52
4721	J03756	Homo sapiens	hGH-V2	515	74
4722	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	194	93
4723	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	128	56
4724	D49490	Homo sapiens	protein disulfide isomerase-related protein (PDIR)	213	55
4725	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	138	66
4726	K02401	Homo sapiens	chorionic somatomammotropin	657	98
4727	D87459	Homo sapiens	Similar to Volvox carteri extensin (S22697)	162	80
4728	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	99	34
4729	AF090944	Homo sapiens	PRO0663	151	63
4730	M32305	Human papillomavirus type 47	E1/E4 fusion protein	106	40
4731	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	133	57
4732	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	76
4733	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	114	43
4734	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	72
4735	M76546	Helianthus annuus	hydroxyproline-rich protein	113	43
4736	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	99	59
4737	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	92	47
4738	AP000616	Oryza sativa	similar to RING-H2 finger protein	133	73

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			RHA1a (AF078683)		
4739	AF044205	Gossypium hirsutum	proline-rich protein precursor	105	42
4740	S78854	Oryctolagus cuniculus	alpha-tropomyosin	159	87
4741	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	151	79
4742	B01372	Homo sapiens	Neuron-associated protein.	159	85
4743	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	122	100
4744	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	82
4745	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	78
4746	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	164	80
4747	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	100
4748	AL359782	Trypanosoma brucei	probable similar to ring-l2 finger protein rha1a.	117	53
4749	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	208	93
4750	AF155232	Pisum sativum	extensin	172	40
4751	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	76
4752	AF130079	Homo sapiens	PRO2852	104	70
4753	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	154	50
4754	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	167	50
4755	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	138	100
4756	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	163	66
4757	M11901	Rattus norvegicus	proline-rich salivary protein	102	45
4758	D38112	Homo sapiens	NADH dehydrogenase subunit 5	242	94
4759	AF046935	Homo sapiens	PCF11p homolog	244	94
4760	M76546	Helianthus annuus	hydroxyproline-rich protein	165	41
4761	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	115	60
4762	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	178	84
4763	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	134	84
4764	R95913	Homo sapiens	Neural thread protein.	136	70
4765	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	139	69
4766	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	102	56
4767	U63159	Mus musculus	transaldolase	218	100
4768	AF230279	Caenorhabditis elegans	SWI5-like protein; PSA-1	106	38
4769	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	116	56
4770	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	136	67
4771	X92485	Plasmodium	pva1	85	64

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
4772	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	95	80
4773	AC002398	Homo sapiens	F25965_3	96	39
4774	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	75
4775	AF120151	Homo sapiens	cytokine receptor-like molecule 9	112	100
4776	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	141	74
4777	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	108	75
4778	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	117	55
4779	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	101	55
4780	AB007860	Homo sapiens	KIAA0400	119	88
4781	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	122	88
4782	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	98	84
4783	M22334	Homo sapiens	unknown protein	611	93
4784	Y36203	Homo sapiens	Human secreted protein #75.	350	76
4785	K02401	Homo sapiens	chorionic somatomammotropin	188	97
4786	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	152	64
4787	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	102	67
4788	M38451	Homo sapiens	growth hormone	264	94
4789	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	77
4790	K02401	Homo sapiens	chorionic somatomammotropin	250	96
4791	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	127	88
4792	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	125	78
4793	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	131	51
4794	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	124	57
4795	M18095	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	103	34
4796	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	131	69
4797	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	160	77
4798	AL132841	Caenorhabditis elegans	Y15E3A.3	120	51
4799	AL009146	Drosophila melanogaster	alternatively spliced form	79	94
4800	S74221	Homo sapiens	IK factor=cytokine down-regulating HLA class II	108	80
4801	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	121	100
4802	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	94	90
4803	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	101	90

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4804	R95913	Homo sapiens	Neural thread protein.	139	71
4805	X61045	Hydra sp.	mini-collagen	126	68
4806	X12544	Homo sapiens	3 HLA-DR B protein precursor (AA - 29 to 267)	114	56
4807	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	160	84
4808	D38112	Homo sapiens	NADH dehydrogenase subunit 6	277	94
4809	L26953	Homo sapiens	chromosomal protein	90	60
4810	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	76
4811	L26953	Homo sapiens	chromosomal protein	121	62
4812	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	124	71
4813	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	78	46
4814	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	100	78
4815	AF152961	Homo sapiens	chromatin-specific transcription elongation factor FACT 140 kDa subunit	152	96
4816	U93569	Homo sapiens	putative p150	334	82
4817	AB014575	Homo sapiens	KIAA0675 protein	125	67
4818	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	114	90
4819	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	129	45
4820	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein thala.	134	48
4821	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	129	61
4822	R96800	Homo sapiens	Human histocyte-secreted factor HSF.	137	83
4823	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	126	55
4824	AF113685	Homo sapiens	PRO0974	110	54
4825	U63542	Homo sapiens	FAP protein	136	70
4826	X83413	Human herpesvirus 6	U88	130	54
4827	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	152	76
4828	U76609	Homo sapiens	ribosomal L5 protein	134	89
4829	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	110	57
4830	AC006161	Arabidopsis thaliana	putative CENP-B/ARS-binding protein-like protein	141	31
4831	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	143	71
4832	U94189	Rattus norvegicus	Duo	158	79
4833	J04031	Homo sapiens	MDMCSF (EC 1.5.1.5; EC 3.5.4.9; EC 6.3.4.3)	193	97
4834	Y13397	Homo sapiens	Amino acid sequence of protein PRO334.	654	97
4835	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	107	53
4836	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	464	93
4837	AF272833	Homo sapiens	misato	413	87
4838	AF130089	Homo sapiens	PRO2550	132	71
4839	G00333	Homo sapiens	Human secreted protein, SEQ ID NO:	116	54



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4414.		
4840	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	89	80
4841	W77354	Homo sapiens	Human telomere repeat binding factor 2 truncated protein.	106	100
4842	AF090942	Homo sapiens	PRO0657	160	75
4843	AF090944	Homo sapiens	PRO0663	202	80
4844	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	167	81
4845	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	166	74
4846	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	228	97
4847	U12690	Homo sapiens	cytochrome oxidase subunit II	198	95
4848	AB023485	Mus musculus	transcription factor CA150b	118	42
4849	Z70684	Caenorhabditis elegans	F28D1.8	98	42
4850	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	106	45
4851	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	179	92
4852	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	145	82
4853	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	123	77
4854	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	112	55
4855	U66464	Homo sapiens	hematopoietic progenitor kinase	110	81
4856	AC011708	Azobidopsis thaliana	putative RING zinc finger protein	121	43
4857	M81321	Macaca fascicularis	proline-rich protein	126	35
4858	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	104	40
4859	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	75
4860	X65165	Volvox carteri	extensin	248	55
4861	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	106	79
4862	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	185	92
4863	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	75
4864	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
4865	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	163	63
4866	AB023229	Homo sapiens	KIAA1012 protein	208	92
4867	R96800	Homo sapiens	Human histocyte-secreted factor HSF.	144	80
4868	L26953	Homo sapiens	chromosomal protein	126	70
4869	U63542	Homo sapiens	FAP protein	134	40
4870	D86853	Catharanthus roseus	extensin	102	48
4871	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	69
4872	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	55
4873	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	156	84

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4874	Y17832	Human endogenous retrovirus K	env protein	219	67
4875	AF217517	Homo sapiens	uncharacterized bone marrow protein BM041	81	38
4876	L27428	Homo sapiens	reverse transcriptase	105	91
4877	M64792	Rattus norvegicus	salivary proline-rich protein	146	46
4878	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	99	38
4879	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	105	77
4880	R58816	Homo sapiens	Human c-myc far upstream element (FUSE) binding protein (FBP) variant from PBL clone 31-10.	87	39
4881	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	150	67
4882	AF175223	Drosophila melanogaster	SANT domain protein SMRTER	84	89
4883	AF174482	Homo sapiens	polycomb 3	136	57
4884	Y34324	Homo sapiens	Amino acid sequence of a human gastric cancer antigen protein.	147	66
4885	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	141	71
4886	U55376	Caenorhabditis elegans	F16H11.2 gene product	95	100
4887	AF261918	Homo sapiens	disintegrin metalloproteinase with thrombospondin repeats	262	72
4888	J02459	bacteriophage lambda	K (tail component;199)	610	100
4889	Y95435	Homo sapiens	Human calcium channel SOC-2/CRAC-1.	219	89
4890	B01372	Homo sapiens	Neuron-associated protein.	134	80
4891	X64712	Gallus gallus	collagen-alpha-3 type IX	112	41
4892	K02401	Homo sapiens	chorionic somatomammotropin	556	87
4893	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	108	55
4894	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	62
4895	L26953	Homo sapiens	chromosomal protein	93	81
4896	AJ277740	Homo sapiens	RPB11b1beta protein	102	66
4897	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	145	87
4898	AL359782	Trypanosoma brucei	possible (hvh-6) u1102, variant a dna, complete virion genome.	131	67
4899	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	153	64
4900	U90304	Homo sapiens	iroquois-class homeodomain protein IRX-2a	109	41
4901	D29956	Homo sapiens	This gene is similar to tre oncogene(X63547).	120	73
4902	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	116	70
4903	Y69166	Homo sapiens	A mature human N-acetylglucosaminyl transferase protein.	102	82
4904	AF119900	Homo sapiens	PRO2822	157	57
4905	U93565	Homo sapiens	putative p150	146	55
4906	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	120	67
4907	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	160	76
4908	Y86248	Homo sapiens	Human secreted protein HCHPF68.	136	55

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SEQ ID NO:163.		
4909	AF155232	Pisum sativum	extensin	98	43
4910	U15647	Mus musculus	reverse transcriptase	196	50
4911	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	144	56
4912	AF225419	Homo sapiens	HSCARG	248	61
4913	M76546	Helianthus annuus	hydroxyproline-rich protein	110	47
4914	AL117382	Homo sapiens	dJ881L22.2 (novel protein)	312	100
4915	AB037814	Homo sapiens	KIAA1393 protein	192	68
4916	D38112	Homo sapiens	NADH dehydrogenase subunit 4	169	89
4917	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	90
4918	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	86
4919	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	132	100
4920	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	183	65
4921	AF090944	Homo sapiens	PRO0663	141	57
4922	AF090931	Homo sapiens	PRO0483	159	55
4923	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	81
4924	U09500	Homo sapiens	cytochrome b	276	94
4925	AB002377	Homo sapiens	KIAA0379 protein	304	98
4926	M22334	Homo sapiens	unknown protein	201	62
4927	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	65
4928	AF130089	Homo sapiens	PRO2550	116	82
4929	U21123	Drosophila melanogaster	ena polypeptide	94	41
4930	W75159	Homo sapiens	Human secreted protein encoded by gene 43 clone HITD54.	294	82
4931	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	96	74
4932	G02460	Homo sapiens	Human secreted protein, SEQ ID NO: 6541.	101	57
4933	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	142	70
4934	AF130087	Homo sapiens	PRO2411	137	80
4935	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	132	56
4936	AB032604	Mus musculus	MIWI (piwi)	313	50
4937	X74987	Homo sapiens	2'-5' oligoadenylate binding protein	144	96
4938	AF054658	Homo sapiens	kappa 1 immunoglobulin light chain variable region	120	87
4939	R96800	Homo sapiens	Human histocyte-secreted factor HSF.	134	67
4940	U22230	Felis catus	ribosomal protein S17	118	100
4941	AB028956	Homo sapiens	KIAA1033 protein	527	88
4942	G00429	Homo sapiens	Human secreted protein, SEQ ID NO: 4510.	281	86
4943	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	71
4944	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	108	95
4945	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	170	76
4946	AF090895	Homo sapiens	PRO0117	125	65
4947	D13866	Homo sapiens	alpha-catenin	575	100
4948	L01664	Homo sapiens	lysophospholipase	166	96

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4949	AF118085	Homo sapiens	PRO1975	572	96
4950	AK024455	Homo sapiens	FLJ00047 protein	95	81
4951	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	58
4952	AB011142	Homo sapiens	KIAA0570 protein	120	88
4953	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	108	39
4954	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	175	69
4955	AK024455	Homo sapiens	FLJ00047 protein	119	64
4956	AF116715	Homo sapiens	PRO2829	142	75
4957	M31520	Homo sapiens	ribosomal protein S24	158	100
4958	D38113	Pan troglodytes	ATPase subunit 8	98	64
4959	AF130089	Homo sapiens	PRO2550	156	75
4960	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	136	95
4961	S61950	Oryctolagus cuniculus	alpha 2(I) procollagen, alpha 2(I) {C-terminal}	159	93
4962	AF070540	Homo sapiens	putative nuclear protein	513	93
4963	S61950	Oryctolagus cuniculus	alpha 2(I) procollagen, alpha 2(I) {C-terminal}	159	93
4964	AF146191	Homo sapiens	FRG1	343	92
4965	Y16624	Homo sapiens	Human phosphoprotein 32 (pp32) protein sequence.	114	100
4966	X67813	Canis familiaris	signal recognition particle, 72 kDa subunit	127	100
4967	S79410	Mus musculus	nuclear localization signal binding protein	127	63
4968	U83303	Homo sapiens	line-1 reverse transcriptase	117	69
4969	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	101	80
4970	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	173	69
4971	D38112	Homo sapiens	ATPase subunit 6	112	91
4972	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	209	97
4973	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	162	80
4974	AL050399	Arabidopsis thaliana	putative proline-rich protein	75	91
4975	L11668	Bos taurus	cyclophilin-40	134	100
4976	M55169	Homo sapiens	tripeptidyl peptidase II	385	90
4977	AF090944	Homo sapiens	PRO0663	154	88
4978	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	102	62
4979	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	128	70
4980	G00721	Homo sapiens	Human secreted protein, SEQ ID NO: 4802.	104	95
4981	R54656	Homo sapiens	Prostaglandin I2 production stimulating protein B.	101	100
4982	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	124	38
4983	AF273053	Homo sapiens	CTCL tumor antigen se89-1	281	96
4984	M15530	Homo sapiens	B-cell growth factor	117	58
4985	D13641	Homo sapiens	mitochondrial outer membrane protein 19	534	94
4986	L11316	Mus musculus	ect2	528	92
4987	X51755	Homo sapiens	open reading frame (458 AA)	108	90
4988	M61877	Homo sapiens	erythroid alpha spectrin	129	87

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4989	X57316	Saccharomyces cerevisiae	carboxypeptidase s	134	50
4990	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	151	78
4991	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO 163.	173	61
4992	M34019	Bos taurus	beta-adrenergic receptor kinase	172	100
4993	L26953	Homo sapiens	chromosomal protein	135	86
4994	X97675	Homo sapiens	plakophilin 2b	124	63
4995	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	153	77
4996	AF130089	Homo sapiens	PRO2550	175	48
4997	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	95	68
4998	Y86214	Homo sapiens	Nuclear transport protein clone hfb341 protein sequence.	312	98
4999	G03681	Homo sapiens	Human secreted protein, SEQ ID NO: 7762.	100	95
5000	AF152961	Homo sapiens	chromatin-specific transcription elongation factor FACT 140 kDa subunit	127	96
5001	U70063	Homo sapiens	acid ceramidase	315	96
5002	AF041373	Rattus norvegicus	clathrin assembly protein short form	163	63
5003	AK001841	Homo sapiens	unnamed protein product	468	83
5004	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	143	61
5005	S79410	Mus musculus	nuclear localization signal binding protein	116	47
5006	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	107	55
5007	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	151	76
5008	Z15005	Homo sapiens	CENP-E	281	84
5009	AF130089	Homo sapiens	PRO2550	122	75
5010	AL049698	Homo sapiens	dJ470B24.1.1 (myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6) (isoform 1))	77	33
5011	G02382	Homo sapiens	Human secreted protein, SEQ ID NO: 6463.	90	62
5012	AL023780	Schizosaccharomyces pombe	DNA binding protein	145	36
5013	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	93	46
5014	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	104	43
5015	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	55
5016	U15647	Mus musculus	expressed in select embryonal carcinoma cells and testicular cells; similar to Swiss-Prot Accession Number P11260	119	35
5017	B10545	Homo sapiens	Human aspartate protease psn-like4 protein.	649	98
5018	AF089745	Homo sapiens	FK506-binding protein	656	98
5019	AF081484	Homo sapiens	alpha-tubulin isoform 1	634	97
5020	AF081484	Homo sapiens	alpha-tubulin isoform 1	603	92
5021	AF081484	Homo sapiens	alpha-tubulin isoform 1	623	94
5022	AF081484	Homo sapiens	alpha-tubulin isoform 1	671	100

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SEQ ID No:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5023	AF130089	Homo sapiens	PRO25 50	109	71
5024	AB013452	Homo sapiens	ATPaseII	208	77
5025	R27654	Homo sapiens	Human calcium channel 27980/16.	183	100
5026	Y36156	Homo sapiens	Human secreted protein #78.	114	64
5027	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	74
5028	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	149	59
5029	S74728	Homo sapiens	antiquitin=26g turgor protein homolog	652	98
5030	L41498	Homo sapiens	longation factor 1-alpha I	592	87
5031	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N-acetylglactosaminyltransferase	454	70
5032	AJ223948	Homo sapiens	RNA helicase	574	84
5033	AF021935	Rattus norvegicus	myotonic dystrophy kinase-related Cdc42-binding kinase	670	97
5034	AF150755	Mus musculus	microtubule-actin crosslinking factor	526	80
5035	AF150755	Mus musculus	microtubule-actin crosslinking factor	602	89
5036	AF081484	Homo sapiens	alpha-tubulin isoform I	598	89
5037	U09823	Oryctolagus cuniculus	elongation factor I alpha	708	96
5038	AE003621	Drosophila melanogaster	CG13384 gene product	279	45
5039	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	107	68
5040	AF047469	Homo sapiens	arsenite translocating ATPase	650	94
5041	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	109	41
5042	AJ007798	Homo sapiens	stromal antigen 3, (STAG3)	288	100
5043	L26953	Homo sapiens	chromosomal protein	124	67
5044	AB005047	Homo sapiens	SH3 binding protein	105	88
5045	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	143	78
5046	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	164	83
5047	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	121	63
5048	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	153	64
5049	Y01158	Homo sapiens	Secreted protein encoded by gene I8 clone HCAC181.	120	59
5050	Z25535	Homo sapiens	nuclear pore complex protein hnupI53	115	88
5051	J03176	Bradyrhizobium japonicum	cytochrome b/c1 precursor	97	35
5052	X85995	Homo sapiens	immunoglobulin light chain	200	100
5053	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	164	76
5054	B01372	Homo sapiens	Neuron-associated protein.	109	80
5055	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	209	54
5056	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	110	51
5057	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	93	39
5058	X92474	Homo sapiens	ch-TOG	147	100
5059	L27428	Homo sapiens	reverse transcriptase	264	75
5060	S79410	Mus musculus	nuclear localization signal binding protein	119	44
5061	L25616	Homo sapiens	CG1 protein'	119	77
5062	G03790	Homo sapiens	Human secreted protein, SEQ ID NO:	99	62

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7871.		
5063	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	164	59
5064	AF118082	Homo sapiens	PRO1902	175	53
5065	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	84	51
5066	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	100
5067	AF155232	Pisum sativum	extensin	137	45
5068	X63005	Mus musculus	proline-rich protein	98	35
5069	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	307	56
5070	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	173	89
5071	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	153	68
5072	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	164	73
5073	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	109	73
5074	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	121	80
5075	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	113	72
5076	U12690	Homo sapiens	cytochrome oxidase subunit II	151	88
5077	AF090944	Homo sapiens	PRO0663	138	78
5078	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	150	74
5079	X97675	Homo sapiens	plakophilin 2b	179	93
5080	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	123	76
5081	AF240630	Mus musculus	IQ motif containing GTPase activating protein 1	176	59
5082	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	100	54
5083	S79410	Mus musculus	nuclear localization signal binding protein	99	59
5084	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	101	57
5085	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	118	77
5086	AB047600	Macaca fascicularis	hypothetical protein	93	69
5087	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	88	80
5088	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	112	57
5089	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	87	61
5090	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	74	61
5091	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	83	78
5092	AF065484	Homo sapiens	sorting nexin 1A	172	81
5093	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	139	90
5094	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	78
5095	U02113	Mus musculus	protein kinase	147	84

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5096	R13556	Homo sapiens	Protein encoded downstream of ihc_M oncogene.	129	67
5097	U64849	Caenorhabditis elegans	Contains similarity to Pfam domain: PF00646 (F-box), Score=28.7, E-value=4.3e-05, N=1	197	39
5098	AF006010	Homo sapiens	progesterone induced protein	174	86
5099	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	119	55
5100	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	132	82
5101	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	159	77
5102	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	99	70
5103	J02459	bacteriophage lambda	J (tail: host specificity; 1132)	485	96
5104	J02459	bacteriophage lambda	H (tail component; 853)	823	98
5105	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	106	42
5106	AF130089	Homo sapiens	PRO2550	121	35
5107	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	135	81
5108	P92219	Homo sapiens (human)	CR1 protein.	123	88
5109	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	83	78
5110	U41751	Mus musculus	EI24	560	83
5111	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	69
5112	AF130089	Homo sapiens	PRO2550	164	88
5113	G03084	Homo sapiens	Human secreted protein, SEQ ID NO: 7165.	160	72
5114	AF052831	Trypanosoma cruzi	unknown	107	70
5115	AL359782	Trypanosoma brucei	possible (hiv-6) u1102, variant a dna; complete virion genome.	128	68
5116	X55684	Lycopersicon esculentum	extensin (class I)	60	29
5117	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	124	64
5118	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	115	60
5119	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	112	79
5120	X65718	Prunus dulcis	extensin	94	33
5121	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
5122	AJ007714	Homo sapiens	lysine-ketoglutarate reductase /saccharopine dehydrogenase	154	96
5123	AJ007714	Homo sapiens	lysine-ketoglutarate reductase /saccharopine dehydrogenase	158	80
5124	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	109	44
5125	AF130089	Homo sapiens	PRO2550	112	46
5126	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	129	60
5127	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	99	68



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5128	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	143	57
5129	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	140	55
5130	J02459	bacteriophage lambda	H (tail component;853)	378	100
5131	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	123	78
5132	J04088	Homo sapiens	DNA topoisomerase II (EC 5.99.1.3)	163	96
5133	AL132841	Caenorhabditis elegans	Y15E3A.3	147	85
5134	D90827	Escherichia coli	Serine/Threonine protein phosphatase (EC 3.1.3.16).	329	46
5135	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	159	62
5136	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	161	91
5137	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	136	96
5138	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	129	67
5139	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	93	31
5140	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	141	46
5141	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	166	67
5142	AF003535	Homo sapiens	ORF2-like protein	168	50
5143	AF259792	Homo sapiens	SWIILbeta protein	684	98
5144	Y36203	Homo sapiens	Human secreted protein #75.	130	63
5145	AF130089	Homo sapiens	PRO2550	151	76
5146	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	52
5147	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	129	85
5148	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	101	67
5149	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	118	56
5150	AF130051	Homo sapiens	PRO0898	80	72
5151	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	165	63
5152	X56832	Homo sapiens	muscle specific enolase	573	90
5153	X76930	Homo sapiens	hepatocyte nuclear factor 4	544	91
5154	U12919	Mus musculus	adenylyl cyclase type VII	156	75
5155	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	91	76
5156	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	133	50
5157	Y08387	Homo sapiens	mu-adaptin-related protein 2	252	86
5158	R13556	Homo sapiens	Protein encoded downstream of hhcm oncoprotein.	126	66
5159	AF090942	Homo sapiens	PRO0657	139	77
5160	AF090942	Homo sapiens	PRO0657	120	70
5161	D67066	Bos taurus	N-WASP	135	42
5162	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	115	73
5163	AF044496	Canis familiaris	acidic ribosomal phosphoprotein P0	112	78
5164	W48351	Homo sapiens	Human breast cancer related protein	106	58

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2.		
5165	AJ250095	Bordetella bronchiseptica	pertactin (P.68)	119	64
5166	U96411	Mus musculus	otogelin; MLEMP	609	90
5167	AF116238	Homo sapiens	pseudouridine synthase 1	237	87
5168	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	151	78
5169	AL050342	Homo sapiens	dJ655K7.1 (novel protein)	263	100
5170	AK024455	Homo sapiens	FLJ00047 protein	177	72
5171	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	94	100
5172	L38908	Nicotiana tabacum	extensin	101	47
5173	AF055904	Myxococcus xanthus	unknown	107	36
5174	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	143	59
5175	Y00337	Homo sapiens	Human secreted protein encoded by gene 81.	123	85
5176	AJ010957	Hippopotamus amphibius	NADH1	212	90
5177	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	84	76
5178	U83280	Leishmania donovani	39 kDa antigen	128	90
5179	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	183	45
5180	L27428	Homo sapiens	reverse transcriptase	106	46
5181	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	144	45
5182	R83119	Homo sapiens	Human cisplatin resistance protein.	142	96
5183	R95530	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 1 TU).	475	71
5184	AF090930	Homo sapiens	PRC0478	121	57
5185	AF193613	Homo sapiens	cell recognition molecule Caspr2	338	50
5186	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	102	36
5187	AL031118	Homo sapiens	dJ153G14.3 (novel C2H2 type Zinc Finger protein)	465	62
5188	AF183144	Mus musculus	left-right dynein	199	83
5189	J02459	bacteriophage lambda	J (tail: host specificity;1132)	748	95
5190	AF193613	Homo sapiens	cell recognition molecule Caspr2	229	50
5191	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	135	65
5192	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	84
5193	Y00311	Homo sapiens	Human secreted protein encoded by gene 54.	112	49
5194	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	126	56
5195	AF104261	Mus musculus	Pax transcription activation domain interacting protein PTIP	487	72
5196	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	132	65
5197	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	130	80
5198	X55777	Homo sapiens	52kD protein	106	30
5199	AF092170	Homo sapiens	polycystic kidney disease 2 related	122	91

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5200	AF092170	Homo sapiens	protein polycystic kidney disease 2 related protein	138	96
5201	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	107	67
5202	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	81
5203	R95913	Homo sapiens	Neural thread protein.	96	61
5204	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	83	55
5205	AF319476	Homo sapiens	GKAP42	705	100
5206	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	78	62
5207	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	119	75
5208	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	166	50
5209	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	139	39
5210	AF090931	Homo sapiens	PRO0483	94	90
5211	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	114	74
5212	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	116	70
5213	U53209	Homo sapiens	transformer-2 alpha	124	95
5214	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	130	58
5215	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	151	49
5216	L26953	Homo sapiens	chromosomal protein	95	52
5217	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	66
5218	AF220264	Homo sapiens	MOST-1	151	65
5219	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	125	53
5220	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	138	65
5221	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	129	66
5222	AF194537	Homo sapiens	NAG13	120	60
5223	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	115	60
5224	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	144	58
5225	AF000996	Homo sapiens	ubiquitous TPR motif, Y isoform	164	70
5226	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	125	73
5227	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	164	69
5228	M34451	Caenorhabditis elegans	collagen (rol-6)	100	41
5229	X16396	Homo sapiens	precursor polypeptide (AA -29 to 315)	306	88
5230	AI.359782	Trypanosoma brucei	possible (hly-6) u1102, variant a dna, complete virion genome.	112	69
5231	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	157	75
5232	D86982	Homo sapiens	similar to human ankyrin 1(S08275)	201	100
5233	AF116712	Homo sapiens	PRO2738	135	49
5234	AI.049758	Homo sapiens	dJ437M21.1 (novel protein)	184	70

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5235	AB014527	Homo sapiens	KIAA0627 protein	164	100
5236	AF194537	Homo sapiens	NAG13	183	64
5237	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	170	43
5238	AF135439	Mus musculus	formin binding protein 11	230	100
5239	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	137	69
5240	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	168	63
5241	AF116661	Homo sapiens	PRO1438	152	58
5242	L27428	Homo sapiens	reverse transcriptase	193	53
5243	AF130089	Homo sapiens	PRO2550	141	60
5244	AF118086	Homo sapiens	PRO1992	135	71
5245	AJ228863	Mus musculus	CLIP-115	195	97
5246	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	81
5247	AC007887	Arabidopsis thaliana	F15O4.29	76	93
5248	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	151	75
5249	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	66
5250	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	70
5251	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	80
5252	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	54
5253	AF090944	Homo sapiens	PRO0663	177	62
5254	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	132	57
5255	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	129	74
5256	D38112	Homo sapiens	NADH dehydrogenase subunit 2	157	91
5257	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	160	78
5258	U16296	Homo sapiens	TIAM1 protein	133	100
5259	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	92	93
5260	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	324	78
5261	AK024455	Homo sapiens	FLJ00047 protein	100	50
5262	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	217	100
5263	AB047600	Macaca fascicularis	hypothetical protein	125	57
5264	U83246	Homo sapiens	copine I	199	86
5265	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	72
5266	U91329	Homo sapiens	kinesin-like motor protein KIF1C	132	93
5267	J00672	Oryctolagus cuniculus	beta-myosin	109	100
5268	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	74	43
5269	AF119851	Homo sapiens	PRO1722	96	61
5270	AF090930	Homo sapiens	PRO0478	113	91
5271	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	123	62
5272	B01372	Homo sapiens	Neuron-associated protein.	122	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5273	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	116	78
5274	AF090931	Homo sapiens	PRO0483	144	67
5275	AL160493	Leishmania major	probable (hhrv-6) u1102, variant a DNA, complete virion genome	117	68
5276	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	111	58
5277	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	67
5278	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	67
5279	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	69
5280	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	196	45
5281	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	115	73
5282	A18812	Brassica napus	extensin	120	38
5283	Z68747	Homo sapiens	imogen 38	291	75
5284	X77816	Rattus norvegicus	PR-Vbeta1	97	37
5285	AF130089	Homo sapiens	PRO2550	181	73
5286	AF130089	Homo sapiens	PRO2550	147	67
5287	AF090942	Homo sapiens	PRO0657	90	50
5288	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	116	74
5289	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	143	64
5290	D86972	Homo sapiens	similar to E.coli hypothetical 29.6 KD protein(P1:YIGW_ECOLI)	111	100
5291	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	145	57
5292	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	65
5293	Y08061	Homo sapiens	Human c-myc protein fragment.	213	76
5294	AF090895	Homo sapiens	PRO0117	134	52
5295	AF017635	Homo sapiens	DCHT	145	100
5296	G02558	Homo sapiens	Human secreted protein, SEQ ID NO: 6639.	136	60
5297	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	67
5298	AK024455	Homo sapiens	FLJ00047 protein	67	80
5299	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	164	75
5300	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	55
5301	R14643	Homo sapiens	Gamma interferon receptor.	107	82
5302	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	238	90
5303	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	205	68
5304	AF130089	Homo sapiens	PRO2550	100	77
5305	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncogene.	117	44
5306	X92485	Plasmodium vivax	pva1	128	61
5307	G02597	Homo sapiens	Human secreted protein, SEQ ID NO: 6678.	77	57
5308	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	140	42
5309	Y91577	Homo sapiens	Human secreted protein sequence	489	78

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded by gene 2 SEQ ID NO:250.		
5310	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	65
5311	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	129	65
5312	AF119851	Homo sapiens	PRO1722	97	65
5313	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	160	90
5314	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	113	81
5315	AF071310	Mus musculus	OPA-containing protein 1	228	53
5316	AF090942	Homo sapiens	PRO0657	162	70
5317	U83303	Homo sapiens	line-1 reverse transcriptase	109	83
5318	AF090894	Homo sapiens	PRO0113	125	63
5319	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	129	66
5320	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	130	75
5321	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	138	81
5322	L27428	Homo sapiens	reverse transcriptase	139	52
5323	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	109	83
5324	AF118082	Homo sapiens	PRO1902	107	70
5325	M81321	Macaca fascicularis	proline-rich protein	114	37
5326	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	112	79
5327	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	99	72
5328	AF090930	Homo sapiens	PRO0478	152	73
5329	L27428	Homo sapiens	reverse transcriptase	267	65
5330	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	140	82
5331	AL160493	Leishmania major	probable (hgv-6) u1102, variant a DNA, complete virion genome	164	54
5332	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	135	52
5333	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	124	76
5334	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	97	56
5335	AP000060	Aeropyrum pernix	103aa long hypothetical protein	71	50
5336	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	75
5337	Z93784	Homo sapiens	dJ398C22.1 (novel protein, ortholog of mouse brain protein E46)	280	68
5338	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	132	64
5339	AF210651	Homo sapiens	NAG18	160	56
5340	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	133	80
5341	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	151	75
5342	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	105	50
5343	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	103	75
5344	G03021	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	132	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7102.		
5345	Y87103	Homo sapiens	Human secreted protein sequence SEQ ID NO:142.	92	48
5346	AL121891	Homo sapiens	dJ1187M17.2 (KLAA0552 protein)	148	43
5347	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	130	33
5348	AF090944	Homo sapiens	PRO0663	205	72
5349	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	135	57
5350	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	101	37
5351	AF265578	Homo sapiens	orphan neurotransmitter transporter NTT5	121	39
5352	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	105	75
5353	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	167	69
5354	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	97	60
5355	G00590	Homo sapiens	Human secreted protein, SEQ ID NO: 4671.	113	80
5356	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	123	67
5357	W88609	Homo sapiens	Secreted protein encoded by gene 76 clone HKIXL73.	94	79
5358	AC004450	Arabidopsis thaliana	putative extensin	110	37
5359	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	79
5360	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	199	74
5361	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	174	97
5362	AB017437	Gallus gallus	avena	98	44
5363	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	93
5364	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	181	70
5365	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	159	68
5366	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	94	60
5367	X52022	Homo sapiens	collagen type VI, alpha 3 chain	150	33
5368	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	120	77
5369	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	145	75
5370	X97675	Homo sapiens	plakophilin 2b	170	85
5371	AF130079	Homo sapiens	PRO2852	103	95
5372	L26953	Homo sapiens	chromosomal protein	117	54
5373	AF210651	Homo sapiens	NAG18	137	67
5374	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	106	76
5375	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	109	70
5376	AL109819	Arabidopsis thaliana	extensin-like protein	123	34
5377	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	127	79
5378	AF036170	Dictyostelium	homeobox-containing protein Warai	93	83

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		discoideum			
5379	AF130089	Homo sapiens	PRO2550	134	75
5380	AF161384	Homo sapiens	HSPC266	663	96
5381	AF130051	Homo sapiens	PRO0898	147	77
5382	AF090944	Homo sapiens	PRO0663	118	83
5383	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	129	55
5384	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	110	68
5385	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	53
5386	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	145	96
5387	U54788	Mus musculus	Wiskott-Aldrich Syndrome Protein	108	51
5388	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	104	89
5389	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	70
5390	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	103	72
5391	AL359782	Trypanosoma brucei	possible (hvh-6) u1102, variant a dna, complete virion genome.	119	85
5392	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	120	65
5393	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	131	78
5394	G01552	Homo sapiens	Human secreted protein, SEQ ID NO: 5633.	159	90
5395	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	110	65
5396	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	85	59
5397	X86681	Homo sapiens	HNP36 protein	248	71
5398	L27428	Homo sapiens	reverse transcriptase	133	62
5399	R13556	Homo sapiens	Protein encoded downstream of hbc_M oncogene.	132	54
5400	AL080196	Homo sapiens	hypothetical protein	164	96
5401	D38112	Homo sapiens	NADH dehydrogenase subunit 5	119	75
5402	AF090944	Homo sapiens	PRO0663	99	64
5403	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	93	58
5404	U42471	Mus musculus	Wiskott-Aldrich Syndrome protein homolog.	103	37
5405	W05278	Homo sapiens	Tumour necrosis factor-related gene product CL6.5.40.	137	80
5406	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	102	69
5407	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	102	69
5408	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	142	69
5409	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	139	63
5410	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	65	47
5411	AF181626	Drosophila melanogaster	BcDNA.GH03694	171	53
5412	U93565	Homo sapiens	putative p150	195	70
5413	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	170	64



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5414	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	126	61
5415	X83572	Homo sapiens	ARSD	133	100
5416	D86853	Catharanthus roseus	extensin	113	41
5417	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	139	60
5418	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	175	77
5419	R32010	Homo sapiens	Rp15-TIA-1.	140	83
5420	D67066	Bos taurus	N-WASP	153	41
5421	U42391	Homo sapiens	myosin-IXb	203	100
5422	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	116	74
5423	AF220264	Homo sapiens	MOST-1	94	78
5424	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	128	63
5425	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	131	57
5426	AF130089	Homo sapiens	PRO2550	120	58
5427	Z70204	Caenorhabditis elegans	contains similarity to Pfam domain: PF00628 (PHD-finger), Score=63.1, E-value=1.9e-15, N=1-cDNA EST EMBL:T00556 comes from this gene-cDNA EST yk344f7.5 comes from this gene	131	55
5428	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	158	51
5429	AF130089	Homo sapiens	PRO2550	112	73
5430	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	161	52
5431	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	131	72
5432	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	152	79
5433	AF090942	Homo sapiens	PRO0657	109	67
5434	AE003588	Drosophila melanogaster	CG2839 gene product	141	50
5435	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	154	79
5436	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	128	41
5437	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	143	63
5438	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	117	84
5439	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	112	76
5440	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	42
5441	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	124	64
5442	AL160493	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	193	56
5443	X07495	Homo sapiens	translated region (AA 1-264)	108	41
5444	C02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	135	62
5445	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	130	41
5446	SS8722	Homo sapiens	X-linked retinopathy protein [C-terminal, clone XEH.8c]	136	71

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5447	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHF029.	123	62
5448	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	101	45
5449	U13866	unidentified cloning vector	non-functional lacZ alpha peptide	106	57
5450	X01469	Plasmodium lophurae	histidine-rich protein	162	56
5451	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	130	88
5452	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	155	68
5453	AF119900	Homo sapiens	PRO2822	162	63
5454	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHF029.	120	51
5455	AC007204	Homo sapiens	BC273239 1	1483	69
5456	L27428	Homo sapiens	reverse transcriptase	122	41
5457	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	141	39
5458	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	68
5459	AF090930	Homo sapiens	PRO0478	144	64
5460	AF130089	Homo sapiens	PRO2550	124	60
5461	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	135	69
5462	X97675	Homo sapiens	plakophilin 2b	103	72
5463	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	137	69
5464	AF229067	Homo sapiens	PADI-H protein	146	65
5465	AF116715	Homo sapiens	PRO2829	83	71
5466	AF090930	Homo sapiens	PRO0478	146	52
5467	U93574	Homo sapiens	putative p150	203	52
5468	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	89	50
5469	AF191838	Homo sapiens	TANK binding kinase TBK1	121	95
5470	AF130079	Homo sapiens	PRO2852	146	69
5471	AF090944	Homo sapiens	PRO0663	90	66
5472	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	106	63
5473	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	60
5474	AF064553	Mus musculus	NSD1 protein	269	100
5475	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	132	65
5476	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	130	86
5477	U11271	Homo sapiens	thromboxane A2 receptor	118	67
5478	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	143	60
5479	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	113	75
5480	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	119	74
5481	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	103	85
5482	AF238235	Entamoeba histolytica	diaphanous protein	108	35
5483	AF090930	Homo sapiens	PRO0478	120	55
5484	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	84

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5485	M61883	<i>Sus scrofa</i>	apomucin	252	55
5486	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	107	77
5487	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	110	46
5488	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	88	62
5489	AF025467	<i>Caenorhabditis elegans</i>	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	124	47
5490	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	220	71
5491	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	65
5492	M76546	<i>Helianthus annuus</i>	hydroxyproline-rich protein	116	38
5493	AF118086	Homo sapiens	PRO1992	135	82
5494	AF090930	Homo sapiens	PRO0478	105	74
5495	Y94451	Homo sapiens	Human inflammation associated protein #8.	170	61
5496	G03465	Homo sapiens	Human secreted protein, SEQ ID NO: 7546.	72	65
5497	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	152	78
5498	X56123	<i>Mus musculus</i>	talin	594	88
5499	AL035652	Homo sapiens	dJ1J6.1 (topoisomerase (DNA) I)	105	86
5500	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
5501	Y45389	Homo sapiens	Human secreted protein fragment encoded from gene 31.	161	93
5502	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	119	60
5503	X03145	Homo sapiens	pot. ORF I	215	79
5504	AF240630	<i>Mus musculus</i>	IQ motif containing GTPase activating protein 1	180	61
5505	AL390212	Homo sapiens	dJ29M10B.1.2 (protein kinase C binding protein 1 (isoform 2))	1282	93
5506	AF118086	Homo sapiens	PRO1992	146	61
5507	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	116	74
5508	U42471	<i>Mus musculus</i>	Wiscott-Aldrich Syndrome protein homolog	165	50
5509	D38112	Homo sapiens	NADH dehydrogenase subunit 5	211	95
5510	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	114	69
5511	AF090944	Homo sapiens	PRO0663	125	58
5512	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	125	53
5513	Y36156	Homo sapiens	Human secreted protein #28.	110	68
5514	AF118086	Homo sapiens	PRO1992	128	76
5515	Z22866	<i>Mus musculus</i>	skelemin	218	95
5516	Z22866	<i>Mus musculus</i>	skelemin	218	95
5517	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	127	71
5518	AL133380	Homo sapiens	dJ86P8.3 (Similar to MAP3K10 (mitogen-activated protein kinase kinase kinase 10))	603	77
5519	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	187	78
5520	AF090901	Homo sapiens	PRO0195	115	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5521	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	180	53
5522	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	155	73
5523	W90847	Homo sapiens	Human lymphocyte targeted peptide #15.	149	100
5524	X97675	Homo sapiens	plakophilin 2b	153	70
5525	D37793	Mus musculus	synaptotagminII/TP4BP	651	84
5526	M32319	Homo sapiens	HLA protein allele B51	754	94
5527	AF130051	Homo sapiens	PRO0898	93	64
5528	X92485	Plasmodium vivax	pva1	88	66
5529	AJ131890	Homo sapiens	DNA polymerase lambda	205	100
5530	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	132	68
5531	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	87	59
5532	AF090931	Homo sapiens	PRO0483	133	75
5533	AF090942	Homo sapiens	PRO0657	122	66
5534	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	145	56
5535	D38112	Homo sapiens	NADH dehydrogenase subunit 5	569	91
5536	K02401	Homo sapiens	chorionic somatomammotropin	375	98
5537	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	136	68
5538	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	130	44
5539	S62928	Homo sapiens	PRB1M protein precursor	104	40
5540	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	127	70
5541	AE000463	Escherichia coli K12	putative glycosidase	254	100
5542	J02459	bacteriophage lambda	H (tail component;853)	761	100
5543	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICE1) protein sequence.	119	58
5544	U59185	Homo sapiens	putative monocarboxylate transporter	233	87
5545	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	187	65
5546	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	556	84
5547	X92485	Plasmodium vivax	pva1	110	67
5548	AB023233	Homo sapiens	KIAA1016 protein	246	97
5549	U16359	Rattus norvegicus	nitric oxide synthase	95	64
5550	AC002044	Homo sapiens	Alpha-fetoprotein enhancer binding protein (3' partial)	111	38
5551	AF026802	Homo sapiens	alpha-3 type IX collagen	117	47
5552	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	85	88
5553	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	91	88
5554	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	104	71
5555	AF130089	Homo sapiens	PRO2550	172	86
5556	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	105	72
5557	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	160	61

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5558	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	131	68
5559	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	112	67
5560	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	159	73
5561	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	141	67
5562	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	150	71
5563	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	146	80
5564	AF090942	Homo sapiens	PRO0657	157	73
5565	M64793	Rattus norvegicus	salivary proline-rich protein	169	43
5566	AL035526	Arabidopsis thaliana	extensin-like protein	103	40
5567	AF130089	Homo sapiens	PRO2550	132	67
5568	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	129	83
5569	X67337	Homo sapiens	Human pre-mRNA cleavage factor I 68 kDa subunit	153	42
5570	AF068266	Homo sapiens	EHT protein	169	91
5571	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	113	42
5572	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	68
5573	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	122	71
5574	L20450	Mus musculus	DNA-binding protein	283	61
5575	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	95
5576	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	140	71
5577	Y20648	Homo sapiens	Human neurofilament-L wild type protein fragment 38.	66	37
5578	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	112	41
5579	AL339782	Trypanosoma brucei	possible (hly-5) u1102, variant a dna, complete virion genome.	142	74
5580	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	142	77
5581	AF153606	Homo sapiens	angiopoietin-related protein	737	95
5582	AF090930	Homo sapiens	PRO0478	149	77
5583	X52493	Glycine max	DNA-directed RNA polymerase	140	46
5584	M76546	Helianthus annuus	hydroxyproline-rich protein	101	51
5585	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	66	47
5586	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	130	72
5587	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	148	56
5588	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	148	66
5589	AC006014	Homo sapiens	similar to KIAA0618 and nuclear envelope protein POM 121; alternatively spliced product; similar to PID:g3327050 and P52591 (PID:g1709213)	108	84
5590	R13556	Homo sapiens	Protein encoded downstream of hhc_M	122	84

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			oncoprotein.		
5591	AB001684	Chlorella vulgaris	ORF74	61	47
5592	AF090930	Homo sapiens	PRO0478	123	70
5593	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	120	57
5594	W80406	Homo sapiens	A. secreted protein encoded by clone dh40_3.	124	59
5595	L26953	Homo sapiens	chromosomal protein	116	62
5596	L26953	Homo sapiens	chromosomal protein	115	67
5597	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	157	55
5598	Y71213	Homo sapiens	Human irritable bowel disease related polypeptide IMX39.	131	44
5599	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	125	45
5600	AF130089	Homo sapiens	PRO2550	142	62
5601	AY014404	Homo sapiens	kinesin-like protein RBKIN2	297	98
5602	AF210651	Homo sapiens	NAG18	113	71
5603	AF090931	Homo sapiens	PRO0483	129	71
5604	X01060	Homo sapiens	put. transferrin receptor (aa 1-760)	226	80
5605	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	455	75
5606	M64793	Rattus norvegicus	salivary proline-rich protein	119	42
5607	A31039	Nicotiana glauca	PRP3	92	36
5608	AF090944	Homo sapiens	PRO0663	147	64
5609	G00552	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	64	46
5610	X01065	Calina moschata	histone H5	88	40
5611	U03413	Dictyostelium discoideum	calcium binding protein	104	40
5612	AL160493	Leishmania major	probable (hmv-6) u1102, variant a DNA, complete virion genome	144	37
5613	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	127	65
5614	G01218	Homo sapiens	Human secreted protein, SEQ ID NO: 5299.	196	97
5615	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	122	68
5616	AB029309	Homo sapiens	Npw38-binding protein NpwBP	312	78
5617	X03145	Homo sapiens	pot. ORF III	101	80
5618	AF090930	Homo sapiens	PRO0478	159	78
5619	D88461	Rattus rattus	N-WASP	107	40
5620	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	104	38
5621	Y36156	Homo sapiens	Human secreted protein #28.	134	50
5622	AF090894	Homo sapiens	PRO0113	119	65
5623	AF130089	Homo sapiens	PRO2550	130	69
5624	AF130089	Homo sapiens	PRO2550	140	78
5625	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	162	49
5626	AF130089	Homo sapiens	PRO2550	152	80
5627	AF151837	Homo sapiens	CGI-79 protein	127	78
5628	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	122	84
5629	AJ237981	Vitis vinifera	putative proline-rich cell wall protein	93	50
5630	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	110	52

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5631	AF130089	Homo sapiens	PRO2550	151	62
5632	U47661	Lupinus luteus	proline-rich protein PRP2 precursor	67	28
5633	Y08061	Homo sapiens	Human c-myb protein fragment.	93	61
5634	AL133215	Homo sapiens	bA108L7.6 (semaphorin 4G (sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain))	323	100
5635	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	138	67
5636	AF090942	Homo sapiens	PRO0657	184	67
5637	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	95	80
5638	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	139	83
5639	AF119900	Homo sapiens	PRO2822	143	62
5640	AL390114	Leishmania major	extremely cysteine/valine rich protein	151	61
5641	Y36243	Homo sapiens	Human secreted protein encoded by gene 20.	118	72
5642	AF090895	Homo sapiens	PRO0117	140	56
5643	Y51611	Homo sapiens	Human HSGT1 protein.	611	96
5644	AF162692	Homo sapiens	putative voltage-gated calcium channel gamma-4 subunit	172	73
5645	Z98883	Homo sapiens	c407A10.1 (GPII (N-acetylglucosaminyl transferase component))	229	100
5646	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	117	80
5647	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	159	78
5648	AF217517	Homo sapiens	uncharacterized bone marrow protein BM041	97	49
5649	AF210651	Homo sapiens	NAG18	149	58
5650	AK000385	Homo sapiens	unnamed protein product	125	36
5651	U02313	Mus musculus	protein kinase	143	96
5652	AF090944	Homo sapiens	PRO0663	95	43
5653	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	61
5654	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	100	58
5655	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	157	70
5656	AP000516	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	100
5657	M64793	Rattus norvegicus	salivary proline-rich protein	123	47
5658	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	159	46
5659	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	163	60
5660	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	46
5661	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	125	71
5662	D87744	Mus musculus	DRPLA protein	89	40
5663	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	65
5664	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	87	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5665	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	71	44
5666	A18812	Brassica napus	extensin	98	41
5667	AF130089	Homo sapiens	PRO2550	128	74
5668	AF090930	Homo sapiens	PRO0478	136	54
5669	X52634	Mus musculus	tlm protein	169	59
5670	AB001684	Chlorella vulgaris	ORF49b	70	62
5671	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	153	66
5672	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	123	78
5673	AF090942	Homo sapiens	PRO0657	150	60
5674	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	123	78
5675	M22332	Homo sapiens	unknown protein	121	43
5676	W40353	Homo sapiens	Human unspecified protein from US5702907.	128	72
5677	AL049868	Homo sapiens	dJ927M24.2 (KIAA1219)	403	95
5678	U31785	Human papillomavirus type 36	putative	103	44
5679	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	101	73
5680	AF068229	Homo sapiens	lysyl hydroxylase 3	148	92
5681	Y00358	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	209	81
5682	AB008515	Homo sapiens	RanBPM	142	100
5683	AB010692	Arabidopsis thaliana	contains similarity to endo-beta-N-acetylglucosaminidase-gene_id:K1812.3.27	143	45
5684	J02459	bacteriophage lambda	J (tail:host specificity;1132)	746	100
5685	AL359782	Trypanosoma brucei	possible (hly-6) u1102, variant a dna, complete virion genome.	194	69
5686	AB049054	Homo sapiens	brain link protein-1	160	100
5687	AF229067	Homo sapiens	PADI-H protein	144	68
5688	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	120	70
5689	AP001313	Arabidopsis thaliana	contains similarity to pherophorin-gene_id:T5M7.14	106	47
5690	M76976	Drosophila melanogaster	dorsal-ventral patterning protein	167	37
5691	L24559	Homo sapiens	DNA polymerase alpha	175	100
5692	AF071777	Mus musculus	IRE1	604	85
5693	AF061741	Homo sapiens	retinal short-chain dehydrogenase/reductase retSDR1	704	99
5694	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	178	66
5695	AF092092	Homo sapiens	AP-3 adaptor complex mu3A subunit	653	92
5696	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	106	86
5697	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	132	75
5698	M64793	Rattus norvegicus	salivary proline-rich protein	116	40
5699	AF161361	Homo sapiens	HSPC098	128	56
5700	U21123	Drosophila melanogaster	ena polypeptide	106	57



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5701	AF119901	Homo sapiens	PRO2831	113	76
5702	K02576	Homo sapiens	salivary proline-rich protein 1	101	49
5703	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	105	78
5704	AF130089	Homo sapiens	PRO2550	122	75
5705	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	136	72
5706	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	113	75
5707	AF229067	Homo sapiens	PADI-H protein	134	81
5708	W40353	Homo sapiens	Human unspecified protein from US5702907.	129	65
5709	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	137	81
5710	AK024455	Homo sapiens	FLJ00047 protein	108	54
5711	Y76381	Homo sapiens	Fragment of human secreted protein encoded by gene 75.	247	93
5712	AF116715	Homo sapiens	PRO2829	118	75
5713	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	154	71
5714	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	141	79
5715	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	91	80
5716	AF090944	Homo sapiens	PRO0663	136	56
5717	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	153	65
5718	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	109	70
5719	AF130089	Homo sapiens	PRO2550	140	86
5720	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	144	67
5721	AF130089	Homo sapiens	PRO2550	146	58
5722	AF118086	Homo sapiens	PRO1992	130	58
5723	D21230	Homo sapiens	alpha 1(XV) collagen chain	390	78
5724	AL049569	Homo sapiens	dJ37C10.5 (KIAA0445)	266	93
5725	X04412	Homo sapiens	plasma gelsolin	761	95
5726	A21853	synthetic construct	serine protease inhibitor	206	100
5727	Y16610	Homo sapiens	paraplegin	218	95
5728	AF132021	Homo sapiens	myosin X	613	87
5729	AL163491	Arabidopsis thaliana	putative protein	236	46
5730	L19704	Homo sapiens	alternative first exon	561	86
5731	D83703	Homo sapiens	peroxisome assembly factor-2	240	84
5732	AB007936	Homo sapiens	KIAA0467 protein	189	77
5733	L38622	Mus musculus	mSin3B gene product	280	94
5734	AF051944	Gallus gallus	Xin	460	68
5735	B07857	Homo sapiens	Amino acid sequence of Smad1 interactor protein clone S1+12-5.	172	67
5736	Z14020	Nicotiana tabacum	Pistil extensin like protein, partial CDS only	105	44
5737	L17308	Gossypium hirsutum	proline-rich cell wall protein	145	34
5738	Y76141	Homo sapiens	Human secreted protein encoded by gene 18.	109	72
5739	AF178534	Homo sapiens	talin	583	82
5740	D13435	Homo sapiens	PIG-F	143	100
5741	AC005578	Homo sapiens	F20887_1, partial CDS	584	86

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5742	AC005578	Homo sapiens	F20887_1, partial CDS	470	85
5743	AJ010479	Homo sapiens	kinesin-like protein	102	23
5744	M19419	Mus musculus	proline-rich salivary protein	107	42
5745	U29577	Caenorhabditis elegans	lysine-rich	97	44
5746	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	90	67
5747	D84223	Homo sapiens	leucyl tRNA synthetase	165	83
5748	J04990	Homo sapiens	cathepsin G	165	100
5749	Y36203	Homo sapiens	Human secreted protein #75.	122	77
5750	V00488	Homo sapiens	alpha globin	181	94
5751	M18642	Homo sapiens	lactoferrin	122	96
5752	W15286	Homo sapiens	Soluble type I insulin-like growth factor receptor.	481	87
5753	Z98595	Schizosaccharomyces pombe	coronin-like protein	192	38
5754	AL035683	Homo sapiens	dJ1063B2.1 (Beta-1,4-galactosyltransferase)	259	100
5755	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	170	61
5756	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	105	61
5757	D49490	Homo sapiens	protein disulfide isomerase-related protein (PDIR)	669	96
5758	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	175	72
5759	X61451	Mus musculus	F41	130	100
5760	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	91	61
5761	AL160493	Leishmania major	probable (hbfv-6) u1102, variant a DNA, complete virion genome	130	76
5762	AF130079	Homo sapiens	PRO2852	126	61
5763	AF143946	Homo sapiens	transcriptional activator SRCAP	288	40
5764	M80627	Homo sapiens	helix-loop-helix protein	127	88
5765	AF038007	Homo sapiens	FIC1	290	47
5766	G01881	Homo sapiens	Human secreted protein, SEQ ID NO: 5962.	427	97
5767	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	172	75
5768	B12884	Homo sapiens	Human alpha-bradeion protein sequence.	465	70
5769	Y66645	Homo sapiens	Membrane-bound protein PRO1310.	347	100
5770	AB033158	Mus musculus	nuclear protein ZAP	115	39
5771	X83575	Cricetulus griseus	CHO1 antigen	113	57
5772	AF135422	Homo sapiens	GDP-mannose pyrophosphorylase A	764	91
5773	L38644	Rattus norvegicus	karyopherin beta	121	68
5774	AB020746	Arabidopsis thaliana	protein kinase-like protein	107	33
5775	Y17920	Drosophila melanogaster	CALO protein	128	31
5776	AK000309	Homo sapiens	unnamed protein product	988	98
5777	AF010404	Homo sapiens	ALR	469	97
5778	AB045131	Homo sapiens	NAD(P)H-dependent retinol dehydrogenase/reductase	126	92
5779	AF197927	Homo sapiens	AF5q31 protein	530	95
5780	X79198	Homo sapiens	host cell factor	119	74
5781	X69838	Homo sapiens	G9a	157	41

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5782	Y94450	Homo sapiens	Human inflammation associated protein #7.	227	44
5783	AF216804	Rattus norvegicus	nuclear matrix transcription factor	1539	98
5784	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	638	91
5785	AF000149	Mus musculus	ATP-binding cassette transporter	292	41
5786	D89974	Homo sapiens	glycosylphosphatidyl inositol anchored protein GPI-80	490	78
5787	AF090942	Homo sapiens	PRO0657	132	63
5788	X56932	Homo sapiens	23 kD highly basic protein	286	100
5789	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	114	63
5790	Z97211	Schizosaccharomyces pombe	kinesin-like protein	346	60
5791	AF134707	Homo sapiens	disintegrin and metalloproteinase domain 19	144	95
5792	Z19550	Homo sapiens	N-acetyllactosaminide beta-1,6-N-acetylglucosaminyltransferase	547	76
5793	AF090930	Homo sapiens	PRO0478	103	80
5794	Y59879	Homo sapiens	Human normal uterus tissue derived protein 42.	407	97
5795	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	149	72
5796	AF077208	Homo sapiens	HSPC022	682	100
5797	D42138	Homo sapiens	PIG-B	597	86
5798	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	151	75
5799	M29487	Homo sapiens	integrin alpha subunit precursor	160	80
5800	D87438	Homo sapiens	Similar to a C.elegans protein in cosmid C14H10	354	85
5801	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSSL.	195	97
5802	AB030176	Homo sapiens	peptidylarginine deiminase type II	107	100
5803	D38441	Homo sapiens	acylamino acid-releasing enzyme	156	71
5804	Y55939	Homo sapiens	Human GEK2 protein.	157	96
5805	X89626	Bos taurus	240K protein of rod photoreceptor cng-channel	92	42
5806	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	177	38
5807	Y86275	Homo sapiens	Human secreted protein HSRGW16, SEQ ID NO:190.	436	77
5808	D50577	Mesocricetus auratus	carboxylesterase precursor	328	55
5809	AF272148	Homo sapiens	KRAB zinc finger protein	593	68
5810	W37260	Homo sapiens	Human semaphorin Y.	651	96
5811	AF202893	Mus musculus	Kif21b	491	82
5812	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	219	38
5813	AB017114	Homo sapiens	AD 3	142	57
5814	AC007954	Homo sapiens	unknown	678	100
5815	AF124726	Homo sapiens	acinusL	790	93
5816	AB015330	Homo sapiens	HRHFB2007	167	36
5817	AB020684	Homo sapiens	KIAA0877 protein	699	57
5818	Z15025	Homo sapiens	Bat2	172	49
5819	X95761	Mus musculus	new;Rhobin	549	79
5820	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	166	68
5821	X55126	Mus musculus	Zfp-29	633	93
5822	Y99366	Homo sapiens	Human PRO1475 (UNQ746) amino	452	98

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			acid sequence SEQ ID NO:88.		
5823	AB040801	Homo sapiens	SREB3	611	95
5824	M27878	Homo sapiens	DNA binding protein	462	64
5825	Y13620	Homo sapiens	BCL9	140	40
5826	AF152510	Homo sapiens	protocadherin gamma A3 short form protein	525	92
5827	M23451	Achlya ambisexualis	steroid receptor	337	61
5828	AJ011305	Homo sapiens	guanine nucleotide exchange factor, delta subunit	132	100
5829	Y85565	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/2) sequence.	710	96
5830	U03277	Drosophila melanogaster	cloned by ability to arrest the cell cycle when expressed in the fission yeast Schizosaccharomyces pombe	258	46
5831	AF193342	Mus musculus	GCN2alpha	469	85
5832	AF279265	Homo sapiens	putative anion transporter 1	240	91
5833	AK023998	Homo sapiens	unnamed protein product	687	97
5834	AK023998	Homo sapiens	unnamed protein product	674	96
5835	AF071059	Mus musculus	zinc finger RNA binding protein	243	100
5836	AF178534	Homo sapiens	talín	463	62
5837	J04569	Homo sapiens	glial fibrillary acidic protein	102	55
5838	AF068625	Mus musculus	DNA cytosine-5 methyltransferase 3A	130	89
5839	AB037739	Homo sapiens	KIAA1318 protein	644	97
5840	R86865	Homo sapiens	Human protocadherin pc3.	660	96
5841	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	117	84
5842	X51486	Gallus gallus	cNFI-A1 protein (AA 1-522)	590	86
5843	U65785	Homo sapiens	150 kDa oxygen-regulated protein ORP150	200	95
5844	U16126	Homo sapiens	EEA4	679	97
5845	AL035071	Homo sapiens	dJ1085F17.1.3 (ortholog of mouse DNMT3B (DNA Cytosine-5 Methyltransferase 3B3) (isoform 3))	717	100
5846	Y13620	Homo sapiens	BCL9	505	81
5847	AC004812	Homo sapiens	similar to human HsGCN1 U7700 (PID:g2282576); similar to yeast translation activator GCN1 (PID:g462168)	316	100
5848	M77246	Rattus norvegicus	beta-chain clathrin associated protein complex AP-2	611	89
5849	AF007833	Homo sapiens	kruppel-related zinc finger protein hKrox	569	79
5850	AF056617	Homo sapiens	BWSCR2 associated zinc-finger protein BAZ1	175	32
5851	D38548	Homo sapiens	The ha0936 gene product is novel.	409	65
5852	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	166	55
5853	D87071	Homo sapiens	similar to C.elegans protein encoded in cosmid T20D3 (Z68220).	188	76
5854	M64979	Homo sapiens	glial factor-1	557	83
5855	G01480	Homo sapiens	Human secreted protein, SEQ ID NO: 5561.	400	82
5856	X06345	Xenopus laevis	lamin A (AA 1-265)	109	68
5857	AB017499	Oryctolagus cuniculus	Lipoprotein Receptor Related Protein 5	196	40
5858	D43633	Oryzias latipes	G protein-coupled seven-transmembrane receptor	281	50
5859	AF067165	Homo sapiens	zinc finger protein 3	669	87

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5860	AI.031118	Homo sapiens	dJ153G14.3 (novel C2H2 type Zinc Finger protein)	218	38
5861	U13897	Homo sapiens	homolog of Drosophila discs large protein, isoform 1	130	35
5862	M74002	Homo sapiens	arginine rich nuclear protein	80	23
5863	X67855	Oryctolagus cuniculus	brain calcium channel BII-1	147	66
5864	U35376	Homo sapiens	repressor transcriptional factor	475	67
5865	AF251038	Homo sapiens	GAP-like protein	325	58
5866	L46815	Mus musculus	DNA binding protein Rc	409	66
5867	S68944	Rattus sp.	Na+/Cl(-)-dependent neurotransmitter transporter	582	95
5868	X97675	Homo sapiens	phakophilin 2b	159	93
5869	AF152478	Homo sapiens	protocadherin alpha 13 short form protein	680	100
5870	AF118082	Homo sapiens	PRO1902	130	48
5871	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	149	49
5872	A61971	unidentified	MCSP	621	82
5873	Z54206	Bovine herpesvirus 1	UL51	104	33
5874	AF069765	Homo sapiens	signal recognition particle 72	674	97
5875	AF179428	Homo sapiens	DNA polymerase zeta catalytic subunit variant 1	692	100
5876	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	119	48
5877	Y94990	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	446	98
5878	L08811	Drosophila melanogaster	adherin	264	42
5879	D86983	Homo sapiens	similar to D.melanogaster peroxidase(U11052)	429	100
5880	AF152508	Homo sapiens	protocadherin gamma A2 short form protein	664	100
5881	AF152508	Homo sapiens	protocadherin gamma A2 short form protein	660	98
5882	AF190018	Mus musculus	K-Cl cotransporter	199	88
5883	AB023229	Homo sapiens	KIAA1012 protein	107	83
5884	U53420	Rattus norvegicus	sodium-calcium exchanger form 3	595	98
5885	AF039019	Homo sapiens	zinc finger DNA binding protein 89 kDa	608	92
5886	AF207661	Homo sapiens	sodium bicarbonate cotransporter-like protein	701	100
5887	AF130051	Homo sapiens	PRO0898	115	74
5888	AF152508	Homo sapiens	protocadherin gamma A2 short form protein	720	100
5889	AF251079	Homo sapiens	heptacellular carcinoma novel gene-3 protein	741	98
5890	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	118	51
5891	AF157326	Homo sapiens	TIP120 protein	571	85
5892	AF129170	Homo sapiens	apolipoprotein E receptor 2	630	99
5893	X05561	Homo sapiens	alpha-I chain precursor (AA -27 to 917) (2953 is 2nd base in codon)	197	45
5894	AJ238374	Homo sapiens	putative protein TH1	641	96
5895	X63526	Homo sapiens	homologue to elongation factor 1-gamma from A.salina	709	97
5896	Y11651	Homo sapiens	phosphate cyclase	521	80

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5897	Y18448	Homo sapiens	Bassoon protein	681	100
5898	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	138	63
5899	AF152473	Homo sapiens	protocadherin alpha C1 short form protein	733	100
5900	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	133	66
5901	R06463	Homo sapiens	Derived protein of clone 1CA13 (ATCC 40553).	522	99
5902	X12928	Triticum aestivum	HMW glutenin subunit 5 (AA 1-848)	169	25
5903	X61048	Hydra sp.	mini-collagen	88	33
5904	AF118082	Homo sapiens	PRO1902	247	60
5905	A00279	synthetic construct	Human serum albumin	482	84
5906	T14722_cd1	Homo sapiens	01-DEC-1992 Human CD27 antigen cDNA.	431	94
5907	Y73475	Homo sapiens	Human secreted protein clone ye7.1 protein sequence SEQ ID NO:172.	271	94
5908	AF175265	Homo sapiens	vacuolar sorting protein 35	645	92
5909	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	125	50
5910	G00560	Homo sapiens	Human secreted protein, SEQ ID NO: 4441.	115	58
5911	W88762	Homo sapiens	Polypeptide fragment encoded by gene 20.	152	50
5912	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	154	68
5913	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	209	71
5914	AB046048	Macaca fascicularis	unnamed portein product	143	49
5915	S80644	Sus scrofa	glutaminase; GA	338	85
5916	AF213393	Mus musculus	ATP-binding cassette protein	92	95
5917	X52622	Mus musculus	integrase (409 AA)	425	45
5918	U49973	Homo sapiens	ORF2: function unknown	114	64
5919	S71403	Mus musculus	m33-A isoform	120	42
5920	AF090931	Homo sapiens	PRO0483	94	89
5921	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	99	36
5922	AJ006770	Cicer arietinum	extensin	96	32
5923	AJ250193	Mus musculus	muscle protein 637	730	72
5924	AF229067	Homo sapiens	PADI-H protein	278	63
5925	X92485	Plasmodium vivax	pva1	99	50
5926	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	84	66
5927	AF130089	Homo sapiens	PRO2550	114	64
5928	J00126	Homo sapiens	MHC factor B	237	100
5929	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	251	79
5930	AF090895	Homo sapiens	PRO0117	63	62
5931	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	147	37
5932	U83857	Homo sapiens	Aac11	209	80
5933	AF068294	Homo sapiens	HDCMB45P	144	50
5934	X92485	Plasmodium vivax	pva1	135	69
5935	L07545	Leishmania tarentolae	A 'c' was inserted after nt 369 (-nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to	127	36

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gel compression		
5936	R95913	Homo sapiens	Neural thread protein.	276	58
5937	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	130	65
5938	Y16781	Homo sapiens	Human secreted protein (clone bh157.7).	1258	100
5939	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	167	68
5940	U93570	Homo sapiens	putative p150	103	41
5941	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	189	74
5942	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	110	47
5943	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	122	90
5944	AF130089	Homo sapiens	PRO2550	101	48
5945	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	162	86
5946	X92485	Plasmodium vivax	pva1	104	70
5947	M29622	Mus musculus	open reading frame 2	132	64
5948	AF130089	Homo sapiens	PRO2550	131	60
5949	AF130089	Homo sapiens	PRO2550	151	60
5950	AF130079	Homo sapiens	PRO2852	117	52
5951	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	185	62
5952	U49973	Homo sapiens	ORF2: function unknown	160	62
5953	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	145	55
5954	M22332	Homo sapiens	unknown protein	169	41
5955	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	133	72
5956	U70935	Peromyscus maniculatus	reverse transcriptase	100	36
5957	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	105	63
5958	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	112	48
5959	Z49944	Canis familiaris	CDC42 GTP-binding protein	120	40
5960	AF118082	Homo sapiens	PRO1902	158	61
5961	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	91	65
5962	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	121	62
5963	AF118082	Homo sapiens	PRO1902	113	60
5964	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	65
5965	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	120	57
5966	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	306	77
5967	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	80	41
5968	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	109	75
5969	AF119855	Homo sapiens	PRO1847	162	72
5970	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	146	46
5971	M19155	Plasmodium falciparum	S-antigen precursor	122	37
5972	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	121	66

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5973	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	107	60
5974	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	83	68
5975	G00497	Homo sapiens	Human secreted protein, SEQ ID NO: 4578.	111	47
5976	U93572	Homo sapiens	p40	112	33
5977	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	107	58
5978	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	120	70
5979	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	106	54
5980	M64792	Rattus norvegicus	salivary proline-rich protein	105	31
5981	X66285	Mus musculus	HCl ORF	86	36
5982	M64793	Rattus norvegicus	salivary proline-rich protein	110	43
5983	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	131	60
5984	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	110	60
5985	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	107	47
5986	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	160	77
5987	AF130079	Homo sapiens	PRO2852	272	77
5988	U93570	Homo sapiens	putative p150	87	46
5989	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	202	89
5990	AF130089	Homo sapiens	PRO2550	238	74
5991	AF118082	Homo sapiens	PRO1902	119	41
5992	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	60
5993	L27428	Homo sapiens	reverse transcriptase	110	60
5994	S79410	Mus musculus	nuclear localization signal binding protein	98	45
5995	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	90
5996	X58236	Homo sapiens	36/8-8 fusion protein with epitope for anti-lectin antibody	78	68
5997	Y08061	Homo sapiens	Human c-myc protein fragment.	97	63
5998	AP002460	Arabidopsis thaliana	gene_id:F1D9_26-unknown protein	100	38
5999	U93569	Homo sapiens	p40	103	52
6000	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	100	63
6001	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	121	51
6002	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	115	64
6003	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	105	40
6004	AF130089	Homo sapiens	PRO2550	122	63
6005	R95913	Homo sapiens	Neural thread protein.	235	56
6006	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	173	58
6007	X92485	Plasmodium vivax	pva1	96	53



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6008	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	236	62
6009	Y17832	Human endogenous retrovirus K	env protein	103	66
6010	AF119900	Homo sapiens	PRO2822	91	50
6011	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	155	55
6012	Y86248	Homo sapiens	Human secreted protein HCHPP68, SEQ ID NO:163.	201	91
6013	Y36156	Homo sapiens	Human secreted protein #28.	253	70
6014	AF130079	Homo sapiens	PRO2852	119	36
6015	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	137	63
6016	AF130089	Homo sapiens	PRO2550	110	40
6017	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	57
6018	AF116661	Homo sapiens	PRO1438	147	69
6019	AF130089	Homo sapiens	PRO2550	169	71
6020	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	208	60
6021	AF119851	Homo sapiens	PRO1722	147	65
6022	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	139	47
6023	AF130089	Homo sapiens	PRO2550	142	66
6024	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	91	76
6025	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	103	48
6026	D86853	Catharanthus roseus	extensin	97	46
6027	AF130089	Homo sapiens	PRO2550	95	47
6028	X92485	Plasmodium vivax	pval	102	61
6029	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	149	53
6030	G00643	Homo sapiens	Human secreted protein, SEQ ID NO: 4724.	96	76
6031	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	144	44
6032	AB011483	Arabidopsis thaliana	contains similarity to root cap protein-gene id:MUF9.16	117	37
6033	X92485	Plasmodium vivax	pval	85	40
6034	AF118082	Homo sapiens	PRO1902	112	58
6035	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	121	59
6036	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	65
6037	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	107	71
6038	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	140	65
6039	X92485	Plasmodium vivax	pval	84	78
6040	AF130051	Homo sapiens	PRO0898	107	69
6041	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	113	58
6042	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	209	75

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6043	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	98	56
6044	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	126	43
6045	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	65
6046	Y36156	Homo sapiens	Human secreted protein #28.	93	62
6047	AF130079	Homo sapiens	PRO2852	205	83
6048	R95913	Homo sapiens	Neural thread protein.	148	45
6049	D38112	Homo sapiens	cytochrome c oxidase subunit 3	234	86
6050	D38113	Pan troglodytes	NADH dehydrogenase subunit 5	403	61
6051	M11901	Rattus norvegicus	proline-rich salivary protein	96	42
6052	AF130089	Homo sapiens	PRO2550	348	73
6053	AF119851	Homo sapiens	PRO1722	109	68
6054	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	168	66
6055	AF161356	Homo sapiens	HSPC093	83	58
6056	X92485	Plasmodium vivax	pva1	155	55
6057	G04000	Homo sapiens	Human secreted protein, SEQ ID NO: 8081.	520	100
6058	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	148	65
6059	W03626	Homo sapiens	Human thyrotropin GPR N-terminal sequence.	163	53
6060	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	300	68
6061	U93563	Homo sapiens	putative p150	389	37
6062	AF090895	Homo sapiens	PRO0117	66	78
6063	X92485	Plasmodium vivax	pva1	110	86
6064	AF130089	Homo sapiens	PRO2550	166	71
6065	M22332	Homo sapiens	unknown protein	188	48
6066	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	101	52
6067	AF010144	Homo sapiens	neuronal thread protein AD7c-N1P	107	41
6068	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	99	75
6069	M22332	Homo sapiens	unknown protein	153	80
6070	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	109	82
6071	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	123	73
6072	AF130079	Homo sapiens	PRO2852	143	60
6073	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	132	55
6074	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	158	65
6075	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	157	68
6076	AF116712	Homo sapiens	PRO2738	102	41
6077	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	102	69
6078	G00554	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	109	60
6079	AF118082	Homo sapiens	PRO1902	196	61
6080	AF118082	Homo sapiens	PRO1902	165	59
6081	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	153	66

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6082	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	188	71
6083	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	109	60
6084	V00672	Pan troglodytes	reading frame protein 4	185	85
6085	AF130051	Homo sapiens	PRO0898	307	67
6086	AF130079	Homo sapiens	PRO2852	96	72
6087	D38112	Homo sapiens	NADH dehydrogenase subunit 1	171	82
6088	AF090895	Homo sapiens	PRO0117	110	67
6089	L43360	Peromyscus maniculatus	reverse transcriptase	101	46
6090	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	114	36
6091	Y02925	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	111	46
6092	G00366	Homo sapiens	Human secreted protein, SEQ ID NO: 4447.	137	54
6093	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	176	59
6094	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	199	50
6095	U70935	Peromyscus maniculatus	reverse transcriptase	216	44
6096	X71442	Rattus norvegicus	ORF 1; putative	109	53
6097	AF119855	Homo sapiens	PRO1847	88	71
6098	L27428	Homo sapiens	reverse transcriptase	104	45
6099	AF090895	Homo sapiens	PRO0117	119	61
6100	U52077	Homo sapiens	mariner transposase	295	67
6101	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	156	73
6102	M22332	Homo sapiens	unknown protein	132	44
6103	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	140	56
6104	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	64	47
6105	M64791	Rattus norvegicus	salivary proline-rich protein	123	41
6106	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	139	69
6107	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	75	58
6108	AF068294	Homo sapiens	HDCMB45P	141	43
6109	AF118086	Homo sapiens	PRO1992	160	77
6110	M63819	Plasmodium falciparum	malaria antigen	62	46
6111	G03093	Homo sapiens	Human secreted protein, SEQ ID NO: 7174.	130	65
6112	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	282	70
6113	AF119851	Homo sapiens	PRO1722	156	63
6114	AF229067	Homo sapiens	PADI-H protein	134	48
6115	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	143	44
6116	D38112	Homo sapiens	cytochrome c oxidase subunit 1	201	80
6117	AF285567	Microcebus griseorufus	cytochrome b	185	58
6118	AL138656	Arabidopsis thaliana	extensin precursor-like protein	141	28
6119	X92485	Plasmodium vivax	pva1	165	61

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6120	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	164	84
6121	M13100	Rattus norvegicus	unknown protein	176	49
6122	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	177	50
6123	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	83	71
6124	AF130089	Homo sapiens	PRO2550	109	85
6125	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	129	70
6126	AF144054	Homo sapiens	apoptosis related protein APR-4	149	54
6127	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	138	70
6128	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	236	77
6129	U93564	Homo sapiens	putative p150	152	53
6130	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	129	57
6131	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	127	56
6132	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	195	67
6133	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	92	42
6134	AK000496	Homo sapiens	unnamed protein product	158	59
6135	X92485	Plasmodium vivax	pval	146	55
6136	Y36203	Homo sapiens	Human secreted protein #75.	133	57
6137	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	148	68
6138	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	106	36
6139	AF130051	Homo sapiens	PRO0898	77	65
6140	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	222	73
6141	AF119851	Homo sapiens	PRO1722	107	63
6142	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	117	57
6143	R95913	Homo sapiens	Neural thread protein.	114	70
6144	AF068294	Homo sapiens	HDCMB45P	123	56
6145	AF118082	Homo sapiens	PRO1902	113	32
6146	AF010144	Homo sapiens	neuronal thread protein AD7c-NTIP	105	42
6147	Y30731	Homo sapiens	Amino acid sequence of a human secreted protein.	938	100
6148	U93574	Homo sapiens	putative p150	99	47
6149	AF090894	Homo sapiens	PRO0113	145	55
6150	AF130079	Homo sapiens	PRO2852	125	49
6151	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	91	48
6152	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	89	60
6153	Y01398	Homo sapiens	Secreted protein encoded by gene 16 clone HNGFR75.	90	82
6154	X92485	Plasmodium vivax	pval	110	42
6155	S79410	Mus musculus	nuclear localization signal binding protein	118	48
6156	G01495	Homo sapiens	Human secreted protein, SEQ ID NO:	170	89

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			5576.		
6157	X92485	Plasmodium vivax	pva1	157	52
6158	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	108	58
6159	U36794	Coturnix japonica	Cytochrome oxidase subunit I	70	73
6160	AF118082	Homo sapiens	PRO1902	119	66
6161	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	154	64
6162	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	107	37
6163	M22332	Homo sapiens	unknown protein	125	51
6164	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	163	59
6165	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	235	64
6166	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	108	36
6167	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	139	59
6168	D38112	Homo sapiens	cytochrome c oxidase subunit 3	562	85
6169	D58113	Pan troglodytes	NADH dehydrogenase subunit 4	296	51
6170	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	95	85
6171	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	329	73
6172	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	136	53
6173	K03206	Homo sapiens	salivary proline-rich protein precursor	104	36
6174	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	75
6175	U93569	Homo sapiens	p40	192	40
6176	X70343	Nicotiana glauca	extensin	94	35
6177	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	140	81
6178	AF119855	Homo sapiens	PRO1847	114	43
6179	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	98	68
6180	X03717	Homo sapiens	pot. unidentified reading frame	112	42
6181	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	204	76
6182	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	110	73
6183	D38112	Homo sapiens	NADH dehydrogenase subunit 3	240	88
6184	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	102	47
6185	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	99	49
6186	Y36156	Homo sapiens	Human secreted protein #28.	196	75
6187	AF169387	Mus musculus	alpha 3 collagen IV	111	38
6188	AF194537	Homo sapiens	NAG13	138	37
6189	X91836	Vigna unguiculata	extensin class 1 protein	167	33
6190	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	175	63
6191	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	123	46
6192	X92485	Plasmodium	pva1	115	54

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
6193	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	345	65
6194	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	82	54
6195	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	214	56
6196	Y19767	Homo sapiens	SEQ ID NO 485 from WO922243.	87	79
6197	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	118	41
6198	X62691	Homo sapiens	ribosomal protein homologous to yeast S24	215	73
6199	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	100	46
6200	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	143	73
6201	Y00711	Mus musculus	cytochrome oxidase I	435	92
6202	U93572	Homo sapiens	putative p150	99	63
6203	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	109	45
6204	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	163	39
6205	M15530	Homo sapiens	B-cell growth factor	113	60
6206	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	128	50
6207	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	181	72
6208	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	75
6209	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	120	62
6210	Y36203	Homo sapiens	Human secreted protein #75.	169	81
6211	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	130	52
6212	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	123	48
6213	D86854	Catharanthus roseus	extensin	120	44
6214	G02754	Homo sapiens	Human secreted protein, SEQ ID NO: 6835.	117	100
6215	W33698	Homo sapiens	AL-2-long (AL-2l) protein.	262	100
6216	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	102	62
6217	U40342	Mus musculus	ninein	77	72
6218	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	174	49
6219	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	234	54
6220	X92485	Plasmodium vivax	pva1	107	46
6221	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	104	40
6222	X86029	Vigna unguiculata	extensin-like protein	140	35
6223	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	216	59
6224	AF068294	Homo sapiens	HDCMB45P	164	60
6225	Y50797	Homo sapiens	Human calmodulin/NEF protein binding inhibitor 2	135	50
6226	AE003859	Xylella fastidiosa	hypothetical protein	139	41
6227	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	103	58

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4718.		
6228	AF130089	Homo sapiens	PRO2550	126	43
6229	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	190	88
6230	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	77
6231	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	174	79
6232	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	78
6233	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	164	67
6234	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2. SEQ ID NO:250.	288	94
6235	AF113685	Homo sapiens	PRO0974	114	46
6236	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	150	40
6237	AL096844	Streptomyces coelicolor A3(2)	putative integral membrane protein	88	39
6238	AF130079	Homo sapiens	PRO2852	167	50
6239	AF130089	Homo sapiens	PRO2550	365	85
6240	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	212	69
6241	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	102	54
6242	AF109907	Homo sapiens	S164	146	90
6243	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	132	52
6244	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	138	52
6245	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	113	32
6246	AF130089	Homo sapiens	PRO2550	154	77
6247	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	91	40
6248	Y36156	Homo sapiens	Human secreted protein #28.	105	43
6249	AF116661	Homo sapiens	PRO1438	131	60
6250	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	132	68
6251	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	70	73
6252	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	106	42
6253	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	247	68
6254	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	75
6255	V00662	Homo sapiens	cytochrome oxidase I	355	78
6256	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	131	65
6257	D38112	Homo sapiens	cytochrome c oxidase subunit I	176	86
6258	AF061340	Artibeus jamaicensis	cytochrome c oxidase subunit III	308	63
6259	AF016099	Mus musculus	endonuclease/reverse transcriptase	114	43
6260	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	179	78
6261	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	192	75
6262	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	71
6263	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	114	37
6264	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	88	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6265	U49974	Homo sapiens	mariner transposase	206	71
6266	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	71	72
6267	AF097473	Mus musculus	ORF1	86	40
6268	X70343	Nicotiana sylvestris	extensin	95	33
6269	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	84
6270	L27428	Homo sapiens	reverse transcriptase	132	48
6271	AF118082	Homo sapiens	PRO1902	153	53
6272	U12690	Homo sapiens	cytochrome oxidase subunit II	222	91
6273	X03145	Homo sapiens	pot. ORF V	89	35
6274	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	90	71
6275	U93572	Homo sapiens	p40	83	43
6276	AF058700	Bos taurus	ubiquitin-S27a fusion protein	148	70
6277	AF016099	Mus musculus	endonuclease/reverse transcriptase	96	65
6278	AF130079	Homo sapiens	PRO2852	179	86
6279	AF161356	Homo sapiens	HSEFC093	108	57
6280	X77816	Rattus norvegicus	PR-Vbeta1	109	51
6281	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	130	58
6282	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	81	69
6283	AF068294	Homo sapiens	HDCMB45P	98	37
6284	AF116715	Homo sapiens	PRO2829	112	68
6285	X92485	Plasmodium vivax	pva1	92	64
6286	U93570	Homo sapiens	p40	90	38
6287	Y36203	Homo sapiens	Human secreted protein #75.	225	62
6288	Z11793	Homo sapiens	selenoprotein P	220	65
6289	X92485	Plasmodium vivax	pva1	125	70
6290	X52634	Mus musculus	tlm protein	114	45
6291	M11901	Rattus norvegicus	proline-rich salivary protein	94	36
6292	AF116661	Homo sapiens	PRO1438	144	46
6293	L27428	Homo sapiens	reverse transcriptase	81	44
6294	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	152	51
6295	AF130089	Homo sapiens	PRO2550	137	35
6296	L27428	Homo sapiens	reverse transcriptase	96	53
6297	B01372	Homo sapiens	Neuron-associated protein.	134	69
6298	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	110	58
6299	AF130089	Homo sapiens	PRO2550	110	61
6300	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	136	63
6301	AF220264	Homo sapiens	MOST-1	172	90
6302	AF130079	Homo sapiens	PRO2852	311	71
6303	AF068294	Homo sapiens	HDCMB45P	136	53
6304	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	110	62
6305	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	113	45
6306	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	166	58



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6307	S85655	Homo sapiens	prohibitin	664	91
6308	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	155	64
6309	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	73
6310	AF119851	Homo sapiens	PRO1722	160	67
6311	L27428	Homo sapiens	reverse transcriptase	91	50
6312	AF130089	Homo sapiens	PRO2550	140	55
6313	AF130089	Homo sapiens	PRO2550	211	68
6314	X15917	Paramecium aurelia	ORF4 protein (AA 1-156)	97	38
6315	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	94	51
6316	Y36203	Homo sapiens	Human secreted protein #75.	124	65
6317	L27428	Homo sapiens	reverse transcriptase	117	56
6318	M11900	Mus musculus	15-kDa proline-rich salivary protein	105	41
6319	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	175	69
6320	U92673	Eurythene sp. 'AUS-3F'	cytochrome oxidase I	59	37
6321	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	283	72
6322	AK000496	Homo sapiens	unnamed protein product	206	70
6323	AB047934	Macaca fascicularis	hypothetical protein	173	68
6324	AB023485	Mus musculus	transcription factor CA150b	131	43
6325	AF020262	Bos taurus	general protein transport factor p16	76	67
6326	U22376	Homo sapiens	alternatively spliced product using exon 13A	98	57
6327	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	115	60
6328	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	100	57
6329	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	115	67
6330	U43360	Peromyscus maniculatus	reverse transcriptase	82	63
6331	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	138	57
6332	K01664	Drosophila melanogaster	Bkm-like protein	112	37
6333	M69297	Homo sapiens	ORF 3	70	43
6334	U15647	Mus musculus	reverse transcriptase	146	53
6335	AF090894	Homo sapiens	PRO0113	107	48
6336	AF130089	Homo sapiens	PRO2550	359	75
6337	AJ271872	Nicotiana glauca	extensin	134	32
6338	AJ132694	Homo sapiens	small GTPase rac1b	99	100
6339	AF119851	Homo sapiens	PRO1722	123	60
6340	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	215	56
6341	U83774	Peris apivorus	cytochrome oxidase I	193	80
6342	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	139	62
6343	X92485	Plasmodium vivax	pva1	104	81
6344	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	110	64
6345	U93572	Homo sapiens	p40	79	48
6346	X92485	Plasmodium	pva1	156	55

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
6347	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	104	85
6348	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	158	77
6349	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	89	64
6350	AF130089	Homo sapiens	PRO2550	187	69
6351	U56732	Rattus norvegicus	KRAB/zinc finger suppressor protein 1	161	64
6352	U70932	Peromyscus leucopus	reverse transcriptase	126	61
6353	X55687	Lycopersicon esculentum	extensin (class II)	89	44
6354	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	107	57
6355	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	88	76
6356	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	98	61
6357	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	165	51
6358	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	214	58
6359	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	75	88
6360	X07882	Homo sapiens	Po protein	151	47
6361	Z11592	Phytophthora parasitica	cytochrome c oxidase subunit 3	78	76
6362	AF090944	Homo sapiens	PRO0663	130	46
6363	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	39
6364	AF229067	Homo sapiens	PADI-H protein	155	75
6365	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	100	55
6366	AK024501	Homo sapiens	FLJ00110 protein	282	100
6367	AF118082	Homo sapiens	PRO1902	157	57
6368	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	151	63
6369	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	161	96
6370	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	124	63
6371	AF130079	Homo sapiens	PRO2852	297	77
6372	X92485	Plasmodium vivax	pva1	129	42
6373	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	122	63
6374	AF119851	Homo sapiens	PRO1722	251	65
6375	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	139	73
6376	X70343	Nicotiana sylvestris	extensin	104	35
6377	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	70	52
6378	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	97	69
6379	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	109	51
6380	Z38128	Mus musculus	histone H1	113	36
6381	U93573	Homo sapiens	p40	212	43

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6382	K02576	Homo sapiens	salivary proline-rich protein 1	109	40
6383	AL096744	Homo sapiens	hypothetical protein	164	49
6384	AF220264	Homo sapiens	MOST-1	119	56
6385	X92485	Plasmodium vivax	pva1	108	65
6386	X53581	Rattus norvegicus	ORF4	148	36
6387	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	116	52
6388	M13100	Rattus norvegicus	unknown protein	119	48
6389	AB047948	Macaca fascicularis	hypothetical protein	80	33
6390	X53581	Rattus norvegicus	ORF4	139	55
6391	AK025947	Homo sapiens	unnamed protein product	166	52
6392	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	244	75
6393	M22332	Homo sapiens	unknown protein	166	39
6394	AF229067	Homo sapiens	PADI-H protein	128	59
6395	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	80	70
6396	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	95	44
6397	M26361	Mus musculus	LINE/Ig H-chain fusion protein	97	61
6398	AF118082	Homo sapiens	PRO1902	93	48
6399	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	116	89
6400	U93570	Homo sapiens	putative p150	88	43
6401	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	147	61
6402	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	77	56
6403	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	156	47
6404	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	155	56
6405	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	88	39
6406	G00983	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	84	68
6407	G00560	Homo sapiens	Human secreted protein, SEQ ID NO: 4641.	244	90
6408	L27428	Homo sapiens	reverse transcriptase	108	42
6409	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	136	58
6410	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	106	44
6411	U70935	Peromyscus maniculatus	reverse transcriptase	154	40
6412	AF090931	Homo sapiens	PRO0483	99	85
6413	AL031186	Homo sapiens	bK984G1.1 (supported by FGENSE)	249	78
6414	AF130089	Homo sapiens	PRO2550	100	55
6415	AB047963	Macaca fascicularis	hypothetical protein	165	57
6416	M22332	Homo sapiens	unknown protein	111	42
6417	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	140	50
6418	AF016099	Mus musculus	endonuclease/reverse transcriptase	147	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6419	D38112	Homo sapiens	NADH dehydrogenase subunit 1	194	84
6420	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	144	81
6421	U49973	Homo sapiens	ORF2: function unknown	91	62
6422	G02754	Homo sapiens	Human secreted protein, SEQ ID NO: 6835.	135	96
6423	AF072508	Homo sapiens	envelope protein	128	49
6424	AK000385	Homo sapiens	unnamed protein product	161	54
6425	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	148	54
6426	X92485	Plasmodium vivax	pval	103	75
6427	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	183	80
6428	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	97	46
6429	AF016099	Mus musculus	endonuclease/reverse transcriptase	100	51
6430	Y36203	Homo sapiens	Human secreted protein #75.	139	58
6431	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	112	47
6432	X92485	Plasmodium vivax	pval	83	72
6433	Y35984	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 233.	121	59
6434	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	66	43
6435	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	152	51
6436	D89501	Homo sapiens	similar to salivary proline-rich protein P-B	88	38
6437	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	113	58
6438	X99467	Medicago truncatula	ENOD20	110	37
6439	Y86574	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:491.	129	58
6440	X92485	Plasmodium vivax	pval	114	46
6441	AK024455	Homo sapiens	FLJ00047 protein	173	57
6442	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	85	51
6443	Y36203	Homo sapiens	Human secreted protein #75.	104	56
6444	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	138	50
6445	M24732	Homo sapiens	lamin-like protein	71	45
6446	AF119851	Homo sapiens	PRO1722	163	69
6447	AF126163	Homo sapiens	HLA3 protein	98	53
6448	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	151	58
6449	AF200187	cercopithecine herpesvirus 15	EBNA2-like protein	125	38
6450	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	107	52
6451	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	114	54
6452	AF090942	Homo sapiens	PRO0657	129	65
6453	M119503	Homo sapiens	ORF1; putative	86	39
6455	X92485	Plasmodium vivax	pval	99	40

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6456	X86030	Vigna unguiculata	extensin-like protein	115	36
6457	Y08061	Homo sapiens	Human c-myc protein fragment.	113	61
6458	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	90	37
6459	AF119851	Homo sapiens	PRO1722	243	66
6460	J05497	Rattus norvegicus	snRNP-associated polypeptide N	101	31
6461	AF130089	Homo sapiens	PRO2550	183	76
6462	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	93	53
6463	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	122	72
6464	Y36156	Homo sapiens	Human secreted protein #28.	85	52
6465	AL160493	Leishmania major	probable (hlv-6) u1102, variant a DNA, complete virion genome	120	40
6466	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	94	36
6467	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	96	58
6468	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	121	67
6469	X92485	Plasmodium vivax	pval	89	72
6470	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	128	56
6471	AF130089	Homo sapiens	PRO2550	155	83
6472	U93569	Homo sapiens	putative p150	131	42
6473	AF130079	Homo sapiens	PRO2852	111	54
6474	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	115	51
6475	AF220264	Homo sapiens	MOST-1	111	58
6476	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	137	45
6477	AF016099	Mus musculus	endonuclease/reverse transcriptase	106	35
6478	X92485	Plasmodium vivax	pval	220	55
6480	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	112	61
6481	U49973	Homo sapiens	ORF2: function unknown	96	42
6482	U15647	Mus musculus	reverse transcriptase	111	61
6483	X92485	Plasmodium vivax	pval	181	49
6484	L27428	Homo sapiens	reverse transcriptase	135	50
6485	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	144	52
6486	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	174	63
6487	U93569	Homo sapiens	p40	176	53
6488	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO: 1051.	72	42
6489	L26953	Homo sapiens	chromosomal protein	93	33
6490	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	125	57
6491	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	155	70
6492	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	251	75
6493	U15647	Mus musculus	reverse transcriptase	100	40

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6494	AK027208	Homo sapiens	unnamed protein product	109	68
6495	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	52
6496	AF130089	Homo sapiens	PRO2550	230	69
6497	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	237	62
6498	AF090894	Homo sapiens	PRO0113	140	68
6499	Y03000	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	138	84
6500	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	123	69
6501	M69297	Homo sapiens	ORF 3	87	58
6502	M22332	Homo sapiens	unknown protein	81	44
6503	X92485	Plasmodium vivax	pval	111	52
6504	AF090895	Homo sapiens	PRO0117	131	60
6505	Y73932	Homo sapiens	Human prostate tumor EST fragment derived protein #119.	97	69
6506	U93568	Homo sapiens	putative p150	122	32
6507	X86029	Vigna unguiculata	extensin-like protein	177	32
6508	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	282	60
6509	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	142	61
6510	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	93	35
6511	U52077	Homo sapiens	mariner transposase	372	73
6512	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	81	50
6513	AF090928	Homo sapiens	PRO0470	97	39
6514	AF134827	Monodelphis domestica	small nuclear ribonucleoprotein B'	108	47
6515	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	82	44
6516	AF068754	Homo sapiens	heat shock factor binding protein 1 HSBP1	118	69
6517	AF130089	Homo sapiens	PRO2550	207	69
6518	M22332	Homo sapiens	unknown protein	154	55
6519	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	95	39
6520	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	65	37
6521	AK023563	Homo sapiens	unnamed protein product	268	58
6522	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	181	61
6523	AF210651	Homo sapiens	NAG18	85	85
6524	AF130079	Homo sapiens	PRO2852	127	51
6525	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	113	51
6526	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	85	62
6527	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	115	48
6528	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	86	60
6529	R59842	Homo sapiens	ApoE4L1 protease.	92	58
6530	R59842	Homo sapiens	ApoE4L1 protease.	135	77
6531	W48351	Homo sapiens	Human breast cancer related protein	88	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCR82.		
6532	AF119851	Homo sapiens	PRO1722	121	61
6533	AF063866	Melanoplus sanguinipes entomopoxvirus	ORF MSV233 hypothetical protein	85	35
6534	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	123	59
6535	R95913	Homo sapiens	Neural thread protein.	132	67
6536	AF130079	Homo sapiens	PRO2852	113	58
6537	AB047600	Macaca fascicularis	hypothetical protein	159	60
6538	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	279	68
6539	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	112	55
6540	AF130089	Homo sapiens	PRO2550	124	56
6541	U93574	Homo sapiens	putative p150	159	39
6542	AF118082	Homo sapiens	PRO1902	114	45
6543	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	78	50
6544	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	118	44
6545	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	138	62
6546	AF116661	Homo sapiens	PRO1438	162	59
6547	S62928	Homo sapiens	PRB1M protein precursor	116	48
6548	AB030192	Mus musculus	homologue of S70447 F1Fo-ATP synthase complex Fo membrane domain f subunit	174	63
6549	AK025116	Homo sapiens	unnamed protein product	136	56
6550	X92485	Plasmodium vivax	pval	105	56
6551	AF130079	Homo sapiens	PRO2852	172	91
6552	U70935	Peromyscus maniculatus	reverse transcriptase	84	42
6553	S79410	Mus musculus	nuclear localization signal binding protein	100	55
6554	M76546	Helianthus annuus	hydroxyproline-rich protein	110	39
6555	AF130089	Homo sapiens	PRO2550	205	64
6556	AF130079	Homo sapiens	PRO2852	165	48
6557	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	160	74
6558	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	133	49
6559	X92485	Plasmodium vivax	pval	121	78
6560	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	76	45
6561	AF217374	Acanthaster planci	cytochrome oxidase subunit 1	234	85
6562	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	61
6563	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	134	84
6564	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	66	47
6565	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	180	49

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6566	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	96	57
6567	X92485	Plasmodium vivax	pval	96	58
6568	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	103	73
6569	AF119851	Homo sapiens	PRO1722	81	60
6570	AF289098	Cladrastis kentukea	ENOD2	110	36
6571	AF118086	Homo sapiens	PRO1992	115	65
6572	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	142	57
6573	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	89	41
6574	M22332	Homo sapiens	unknown protein	95	34
6575	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	98	64
6576	AK021848	Homo sapiens	unnamed protein product	131	41
6577	AF161356	Homo sapiens	HSPC093	155	57
6578	AF116909	Homo sapiens	unknown	75	76
6579	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	95	53
6580	AF130089	Homo sapiens	PRO2550	276	74
6581	K02576	Homo sapiens	salivary proline-rich protein 1	119	33
6582	U49973	Homo sapiens	ORF2: function unknown	94	62
6583	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	90	65
6584	AJ249395	Globodera pallida	NADH-ubiquinone oxidoreductase subunit 4	99	41
6585	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	75	62
6586	U49973	Homo sapiens	ORF2: function unknown	134	58
6587	Y08061	Homo sapiens	Human c-myb protein fragment.	112	47
6588	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	217	53
6589	K02576	Homo sapiens	salivary proline-rich protein 1	147	41
6590	U43627	Arabidopsis thaliana	extensin	103	31
6591	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	71	34
6592	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	177	66
6593	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	100	72
6594	M69297	Homo sapiens	ORF 3	137	43
6595	X68101	Rattus norvegicus	trg	372	89
6596	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	81	62
6597	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	99	43
6598	Z99714	Homo sapiens	bK1048E9.5 (novel protein)	1642	98
6599	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	162	59
6600	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	132	65
6601	AK000385	Homo sapiens	unnamed protein product	187	74
6602	AF130051	Homo sapiens	PRO0898	137	54
6603	S58722	Homo sapiens	X-linked retinopathy protein (C-	88	48



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			terminal, clone XEH.8c}		
6604	X61047	Hydra sp.	mini-collagen	116	45
6605	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	109	71
6606	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	212	66
6607	AF232673	Homo sapiens	B17 long form	1272	99
6608	AF118082	Homo sapiens	PRO1902	77	52
6609	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	132	74
6610	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	70	61
6611	Y36203	Homo sapiens	Human secreted protein #75.	140	62
6612	X92485	Plasmodium vivax	pva1	157	72
6613	U52077	Homo sapiens	mariner transposase	260	67
6614	AF161392	Homo sapiens	HSPC274	138	45
6615	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	93	65
6616	AF119831	Homo sapiens	PRO1722	147	49
6617	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	101	63
6618	AL390114	Leishmania major	extremely cysteine/valine rich protein	117	39
6619	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	105	58
6620	U15647	Mus musculus	reverse transcriptase	106	38
6621	AF130089	Homo sapiens	PRO2550	171	52
6622	X92485	Plasmodium vivax	pva1	139	44
6623	AF090895	Homo sapiens	PRO0117	161	58
6624	M63730	Homo sapiens	BPAG2	107	32
6625	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	183	61
6626	AF078860	Homo sapiens	PTD007	69	73
6627	AL080253	Arabidopsis thaliana	putative snRNP protein	101	37
6628	AK000385	Homo sapiens	unnamed protein product	140	57
6629	W60652	Homo sapiens	Human DVic-1 (alternative transcript).	218	51
6630	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	152	66
6631	AB046048	Macaca fascicularis	unnamed protein product	118	65
6632	X92485	Plasmodium vivax	pva1	119	88
6633	X03145	Homo sapiens	pot. ORF V	98	39
6634	K02576	Homo sapiens	salivary proline-rich protein I	165	41
6635	X59448	Drosophila melanogaster	dynamitin	111	39
6636	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	162	50
6637	AF130089	Homo sapiens	PRO2550	141	75
6638	AF118082	Homo sapiens	PRO1902	108	63
6639	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	144	60
6640	Y19767	Homo sapiens	SEQ ID NO 485 from WO922243.	104	47
6641	AF118082	Homo sapiens	PRO1902	121	53
6642	AF118082	Homo sapiens	PRO1902	195	68
6643	R95913	Homo sapiens	Neural thread protein.	212	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6644	AF090928	Homo sapiens	PRO0470	81	65
6645	AF130079	Homo sapiens	PRO2852	151	69
6646	AF003535	Homo sapiens	ORF2-like protein	140	35
6647	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	169	61
6648	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	100	42
6649	M15530	Homo sapiens	B-cell growth factor	121	76
6650	AF090942	Homo sapiens	PRO0657	119	53
6651	AF118082	Homo sapiens	PRO1902	130	52
6652	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	143	87
6653	AF130089	Homo sapiens	PRO2550	143	63
6654	AF119851	Homo sapiens	PRO1722	285	70
6655	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	103	75
6656	AF119855	Homo sapiens	PRO1847	61	60
6657	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	107	36
6658	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	84	61
6659	AF119851	Homo sapiens	PRO1722	177	54
6660	X92485	Plasmodium vivax	pval	104	55
6661	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	116	57
6662	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	68
6663	L22029	Glycine max	hydroxyproline-rich glycoprotein	115	35
6664	D00570	Mus musculus	open reading frame (251 AA)	126	35
6665	AF130051	Homo sapiens	PRO0898	129	77
6666	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	108	42
6667	G02851	Homo sapiens	Human secreted protein, SEQ ID NO: 6932.	71	41
6668	AF130079	Homo sapiens	PRO2852	110	59
6669	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	113	66
6670	G00527	Homo sapiens	Human secreted protein, SEQ ID NO: 4608.	98	73
6671	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	80	51
6672	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	113	36
6673	V01201	Simian sarcoma virus	coding sequence of pol	143	47
6674	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	159	78
6675	G00648	Homo sapiens	Human secreted protein, SEQ ID NO: 4729.	64	56
6676	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	96	48
6677	AF130089	Homo sapiens	PRO2550	100	75
6678	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	94	68
6679	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	105	71
6680	G03812	Homo sapiens	Human secreted protein, SEQ ID NO: 7893.	218	53
6681	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 7893.	115	53

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4433.		
6682	AF161356	Homo sapiens	HSPC093	163	47
6683	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	78	72
6684	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	87	42
6685	S79410	Mus musculus	nuclear localization signal binding protein	98	43
6686	U93564	Homo sapiens	p40	96	41
6687	AF119855	Homo sapiens	PRO1847	137	67
6688	U52077	Homo sapiens	mariner transposase	268	81
6689	X92485	Plasmodium vivax	pva1	97	58
6690	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	133	56
6691	M63274	Plasmodium falciparum	malaria antigen	61	46
6692	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	147	80
6693	M11901	Rattus norvegicus	proline-rich salivary protein	115	40
6694	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	131	50
6695	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	174	66
6696	AF068294	Homo sapiens	HDCMB45P	154	59
6697	X55685	Lycopersicon esculentum	extensin (class I)	112	41
6698	M83293	Simian immunodeficiency virus	vpx protein	85	41
6699	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	169	88
6700	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	121	58
6701	AF118080	Homo sapiens	PRO1880	127	59
6702	X92485	Plasmodium vivax	pva1	106	58
6703	AF161356	Homo sapiens	HSPC093	155	53
6704	X92485	Plasmodium vivax	pva1	164	54
6705	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	172	59
6706	AK025326	Homo sapiens	unnamed protein product	146	50
6707	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	112	43
6708	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	119	71
6709	AF176531	Mus musculus	F-box protein FBX16	324	60
6710	X92485	Plasmodium vivax	pva1	96	64
6711	AF130089	Homo sapiens	PRO2550	203	67
6712	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	150	59
6713	AF090944	Homo sapiens	PRO0663	114	43
6714	AL390114	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	110	47
6715	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	131	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6716	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	103	65
6717	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	115	46
6718	G01222	Homo sapiens	Human secreted protein, SEQ ID NO: 5303.	54	100
6719	Y36203	Homo sapiens	Human secreted protein #75.	129	78
6720	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	107	64
6721	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICE1) protein sequence.	130	61
6722	Y36203	Homo sapiens	Human secreted protein #75.	167	72
6723	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	46
6724	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	133	42
6725	U80761	Homo sapiens	CTG26 alternate open reading frame	88	76
6726	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	218	61
6727	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2, SEQ ID NO:250.	399	81
6728	U01877	Homo sapiens	p300 protein	119	27
6729	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	107	51
6730	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	130	58
6731	X66285	Mus musculus	HC1 ORF	79	38
6732	K02576	Homo sapiens	salivary proline-rich protein 1	114	38
6733	AF057352	Homo sapiens	hepatocellular carcinoma autoantigen	148	81
6734	AF090895	Homo sapiens	PRO0117	152	57
6735	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	61
6736	X92485	Plasmodium vivax	pval	92	89
6737	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	112	49
6738	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	278	72
6739	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	191	47
6740	AF118082	Homo sapiens	PRO1902	83	49
6741	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	83	43
6742	Y36708	Homo sapiens	Fragment of human secreted protein encoded by gene 62.	71	64
6743	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	177	70
6744	Y91475	Homo sapiens	Human secreted protein sequence encoded by gene 25, SEQ ID NO:148.	159	50
6745	X92485	Plasmodium vivax	pval	112	39
6746	Z82268	Caenorhabditis elegans	predicted using Genefinder—contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=73.8, E-value=1.2e-18, N=2; PF01484 (Nematode cuticle collagen N-terminal domain), Score=37.5, E-value=1e-07, N=1—cDNA EST yk92f1.5 comes from this gene—cDNA EST yk55f6.5 comes from this gene—cDNA EST yk65b7.3 comes from this gene—cDNA EST	108	36

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			yk583.5 comes from this gene-cDNA EST yk72h5.5 comes from this gene-cDNA EST yk55c4.5 comes from this gene-cDNA EST yk58h1.5 comes from this gene-cDNA EST yk65a12.5 comes from this gene-cDNA EST yk94f4.5 comes from this gene		
6747	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	113	38
6748	R95913	Homo sapiens	Neural thread protein.	108	56
6749	U57747	Mus musculus	platelet-activating factor acetylhydrolase isoform Ib beta subunit	209	69
6750	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	159	65
6751	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	96	48
6752	AF090895	Homo sapiens	PRO0117	115	56
6753	AF217973	Homo sapiens	unknown	105	66
6754	AF119851	Homo sapiens	PRO1722	156	55
6755	AF119855	Homo sapiens	PRO1847	189	66
6756	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	163	55
6757	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	123	57
6758	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	156	70
6759	AF130051	Homo sapiens	PRO0898	98	68
6760	M36914	Zea mays	cell wall protein (put.); putative	75	28
6761	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	98	85
6762	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	88	62
6763	M19756	Homo sapiens	MHC HLA-Bw47 precursor	580	92
6764	AL359782	Trypanosoma brucei	possible (hlyv-6) u1102, variant a dna, complete virion genome.	115	52
6765	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	321	51
6766	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	124	59
6767	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	303	64
6768	AF061340	Artibeus jamaicensis	cytochrome c oxidase subunit II	213	67
6769	T71265_cdl	Homo sapiens	19-JAN-1996 Neuronal apoptosis inhibitor protein (NAIP) cDNA.	188	59
6770	E01390	Homo sapiens	Neuron-associated protein.	92	55
6771	AF017777	Drosophila melanogaster	la costa	114	50
6772	Z34955	Sus scrofa	protein phosphatase 2A 65 kDa regulatory subunit, alpha isoform	331	93
6773	X61296	Rattus norvegicus	open reading frame 2	101	37
6774	AL117345	Homo sapiens	dJ416F21.2 (novel protein)	639	91
6775	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	110	61
6776	AJ007798	Homo sapiens	stromal antigen 3, (STAG3)	238	76
6777	AB029065	Mus musculus	Scr/Thr kinase KKIAMRE-beta	165	66
6778	M37400	Homo sapiens	aspartate aminotransferase	208	68
6779	AF130089	Homo sapiens	PRO2550	127	52
6780	AF130079	Homo sapiens	PRO2852	332	81

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6781	AL049748	Homo sapiens	dJ41P2.2 (RNA binding motif protein 9 (isoform 1))	264	60
6782	L11007	Rattus norvegicus	cyclin-dependent kinase 4	239	75
6783	AF319938	Thermus thermophilus	competence factor ComEA	115	36
6784	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	119	44
6785	L16864	African swine fever virus	cd2 homologue	152	34
6786	Y36203	Homo sapiens	Human secreted protein #75.	99	44
6787	AF130087	Homo sapiens	PRO2411	172	65
6788	AF208846	Homo sapiens	BM-004	664	100
6789	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	90	83
6790	AP000059	Aeropyrum pernix	120aa long hypothetical protein	81	43
6791	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	53
6792	Y12961	Homo sapiens	Amino acid sequence of a human secreted peptide.	175	65
6793	Y73442	Homo sapiens	Human secreted protein clone ya66_1 protein sequence SEQ ID NO:106.	565	93
6794	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	136	50
6795	AC004022	Homo sapiens	serum paraoxonase/arylesterase 3	137	93
6796	AF009668	multiple sclerosis associated retrovirus	polyprotein	194	60
6797	R59842	Homo sapiens	ApoE4L1 protease.	121	92
6798	U88167	Caenorhabditis elegans	contains similarity to C2 domains	171	73
6799	AF293024	Homo sapiens	steroid receptor RNA activator isoform 1	767	97
6800	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	65
6801	B01203	Homo sapiens	Human GTPase associated protein-28.	313	87
6802	AL359782	Trypanosoma brucei	possible (hly-6) u1102, variant a dna, complete virion genome.	125	47
6803	AF078036	Homo sapiens	RelA associated inhibitor; NF-kappaB subunit p65 binding protein	1275	95
6804	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	131	53
6805	Y57946	Homo sapiens	Human transmembrane protein HTMPN-70.	1128	100
6806	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	81	81
6807	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	52
6808	AB046048	Macaca fascicularis	unnamed protein product	273	63
6809	K02401	Homo sapiens	chorionic somatomammotropin	446	95
6810	AF130089	Homo sapiens	PRO2550	150	56
6811	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	123	65
6812	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	93	38
6813	AF090930	Homo sapiens	PRO0478	103	65
6814	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	138	54

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6815	B24423	Homo sapiens	Human PRO1244 protein sequence SEQ ID NO:193.	484	95
6816	M11901	Rattus norvegicus	proline-rich salivary protein	105	43
6817	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	96	56
6818	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	102	48
6819	U82303	Homo sapiens	unknown	105	57
6820	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	113	45
6821	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	97	39
6822	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	146	86
6823	U52077	Homo sapiens	mariner transposase	192	78
6824	AC004237	Homo sapiens	KIF3	129	86
6825	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	138	66
6826	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	112	64
6827	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	108	68
6828	U49974	Homo sapiens	mariner transposase	103	86
6829	AF119851	Homo sapiens	PRO1722	115	53
6830	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	82	62
6831	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	94	73
6832	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	131	53
6833	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	74	50
6834	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	168	61
6835	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	140	60
6836	X92485	Plasmodium vivax	pval	99	58
6837	AB046048	Macaca fascicularis	unnamed portein product	147	42
6838	AB047600	Macaca fascicularis	hypothetical protein	134	52
6839	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	60
6840	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	126	73
6841	AF130089	Homo sapiens	PRO2550	167	63
6842	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	140	56
6843	AF090894	Homo sapiens	PRO0113	148	62
6844	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	119	51
6845	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	75	61
6846	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	65	44
6847	AF130089	Homo sapiens	PRO2550	160	76
6848	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	132	68
6849	AF116715	Homo sapiens	PRO2829	123	67
6850	Y01437	Homo sapiens	Secreted protein encoded by gene 55	142	96

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HLMBP18.		
6851	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	110	76
6852	AF068294	Homo sapiens	HDCMB45P	161	56
6853	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	111	57
6854	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	165	72
6855	AF130051	Homo sapiens	PRO0898	117	61
6856	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	138	72
6857	X55685	Lycopersicon esculentum	extensin (class I)	190	45
6858	AL359782	Trypanosoma brucei	possible (hvh-6) u1102, variant a dna, complete virion genome.	164	69
6859	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	90	52
6860	AF119851	Homo sapiens	PRO1722	331	73
6861	G00418	Homo sapiens	Human secreted protein, SEQ ID NO: 4499.	130	67
6862	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	114	53
6863	X92485	Plasmodium vivax	pval	105	63
6864	AF068294	Homo sapiens	HDCMB45P	206	61
6865	AF068294	Homo sapiens	HDCMB45P	128	46
6866	L00016	Homo sapiens	urf4	137	58
6867	X92485	Plasmodium vivax	pval	95	89
6868	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	77
6869	AF130089	Homo sapiens	PRO2550	162	67
6870	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	257	65
6871	X71972	Mus musculus	ribosomal protein S24	211	85
6872	M28016	Homo sapiens	cytochrome b	72	93
6873	M24069	Homo sapiens	DNA-binding protein A	1662	79
6874	AF130051	Homo sapiens	PRO0898	163	76
6875	AF006061	Homo sapiens	placental growth hormone isoform hGH-V3	263	90
6876	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	94	80
6877	AF130079	Homo sapiens	PRO2832	130	76
6878	S80905	Homo sapiens	Con1	148	38
6879	X55683	Lycopersicon esculentum	extensin (class I)	70	35
6880	U16359	Rattus norvegicus	nitric oxide synthase	106	94
6881	AK025047	Homo sapiens	unnamed protein product	167	50
6882	X92485	Plasmodium vivax	pval	110	63
6883	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	185	46
6884	AK024455	Homo sapiens	FLJ00047 protein	81	64
6885	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	113	47
6886	AF014008	Bos taurus	myocardial vascular inhibition factor	158	96
6887	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	183	83
6888	Y45382	Homo sapiens	Human secreted protein fragment	199	49



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded from gene 28.		
6889	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	140	67
6890	AF130051	Homo sapiens	PRO0898	135	65
6891	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	147	65
6892	X72963	Nicotiana tabacum	pAP8 product	80	44
6893	AF073957	Homo sapiens	CXC chemokine BRAK	399	82
6894	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	160	80
6895	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	70
6896	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	178	85
6897	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	142	62
6898	AF118082	Homo sapiens	PRO1902	144	53
6899	AF130051	Homo sapiens	PRO0898	187	72
6900	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	121	85
6901	AF130089	Homo sapiens	PRO2550	100	63
6902	Z29446	Hepatitis C virus	core region	60	36
6903	AF107406	Homo sapiens	GW128	71	63
6904	W03627	Homo sapiens	Human follicle stimulating hormone GPR N-terminal sequence.	173	64
6905	AF130089	Homo sapiens	PRO2550	88	65
6906	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	78	84
6907	U93569	Homo sapiens	p40	145	48
6908	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	186	50
6909	AF130089	Homo sapiens	PRO2550	244	77
6910	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	119	38
6911	AF130089	Homo sapiens	PRO2550	139	47
6912	G00228	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	146	60
6913	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	131	70
6914	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	106	74
6915	AF161361	Homo sapiens	HSPC098	79	66
6916	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	207	60
6917	AF130051	Homo sapiens	PRO0898	258	61
6918	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	108	65
6919	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	58
6920	G02635	Homo sapiens	Human secreted protein, SEQ ID NO: 6716.	168	80
6921	AF116661	Homo sapiens	PRO1438	71	48
6922	AF090940	Homo sapiens	PRO0644	72	85
6923	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	186	70
6924	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	89	55
6925	AF229067	Homo sapiens	PADI-H protein	122	72

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6926	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	105	37
6927	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	173	60
6928	X56603	Mus musculus	mouse 57-KD Calcium-binding protein (MCaBP)	103	52
6929	AF119851	Homo sapiens	PRO1722	148	76
6930	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	96	61
6931	AF077208	Homo sapiens	HSPC022	155	72
6932	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	111	62
6933	M22332	Homo sapiens	unknown protein	154	77
6934	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	146	60
6935	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	168	63
6936	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	124	50
6937	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	99	77
6938	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	111	68
6939	AF118082	Homo sapiens	PRO1902	120	54
6940	AF090942	Homo sapiens	PRO0657	149	72
6941	M22332	Homo sapiens	unknown protein	96	51
6942	AF130087	Homo sapiens	PRO2411	132	58
6943	M15530	Homo sapiens	B-cell growth factor	97	52
6944	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	87	52
6945	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	73	66
6946	Z10561_cd1	Homo sapiens	12-MAR-1998 DNA encoding G protein-coupled receptor protein designated SREB2.	330	96
6947	W53869	Homo sapiens	Gravin polypeptide fragment, residues 1526-1780.	170	89
6948	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	164	86
6949	AF118086	Homo sapiens	PRO1992	117	86
6950	AF090928	Homo sapiens	PRO0470	115	58
6951	AF130089	Homo sapiens	PRO2550	124	69
6952	Y38397	Homo sapiens	Human secreted protein encoded by gene No. 12.	94	64
6953	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	132	55
6954	X92485	Plasmodium vivax	pva1	108	64
6955	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	117	85
6956	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	93	53
6957	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	106	50
6958	AF130089	Homo sapiens	PRO2550	127	67
6959	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	119	49
6960	J02459	bacteriophage lambda	U (tail component;131)	492	92
6961	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	180	68

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7214.		
6962	Z66490	Salmo trutta	slow myotomal muscle tropomyosin	182	72
6963	AF130089	Homo sapiens	PRO2550	108	73
6964	W21733	Homo sapiens	NIP-1 encoded by clone 59.	131	69
6965	AF161356	Homo sapiens	HSPC093	58	48
6966	AB047934	Macaca fascicularis	hypothetical protein	146	58
6967	X92485	Plasmodium vivax	pva i	116	55
6968	AF118082	Homo sapiens	PRO1902	85	65
6969	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	176	63
6970	AF116712	Homo sapiens	PRO2738	101	56
6971	X96667	Homo sapiens	beta-galactoside alpha-2,3-sialyltransferase	172	97
6972	Y86574	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:491.	150	82
6973	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	176	58
6974	AF162149	Mycoplasma bovis	variable surface lipoprotein	143	40
6975	W17971	Homo sapiens	RAC protein kinase C-terminal binding protein C-terminal region.	135	81
6976	AF130089	Homo sapiens	PRO2550	345	78
6977	AF130089	Homo sapiens	PRO2550	195	63
6978	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	75
6979	M60510	Mus musculus	beta-D-galactosidase fusion protein	96	47
6980	AF118086	Homo sapiens	PRO1992	131	64
6981	AF130089	Homo sapiens	PRO2550	132	64
6982	L27428	Homo sapiens	reverse transcriptase	128	35
6983	L93566	Homo sapiens	p40	98	31
6984	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	138	78
6985	L27428	Homo sapiens	reverse transcriptase	133	67
6986	AF090895	Homo sapiens	PRO0117	139	62
6987	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	212	60
6988	Y36203	Homo sapiens	Human secreted protein #75.	189	73
6989	AF116712	Homo sapiens	PRO2738	87	42
6990	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	63
6991	AF090930	Homo sapiens	PRO0478	154	52
6992	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	102	76
6993	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	151	48
6994	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	113	47
6995	J02974	Acanthamoeba castellanii	myosin IB heavy chain	120	43
6996	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	151	69
6997	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	153	60
6998	Y12961	Homo sapiens	Amino acid sequence of a human secreted peptide.	114	66
6999	AF113685	Homo sapiens	PRO0974	88	58
7000	AF130089	Homo sapiens	PRO2550	146	58

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7001	U93565	Homo sapiens	putative p150	96	46
7002	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	146	57
7003	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	206	92
7004	AF130089	Homo sapiens	PRO2550	104	50
7005	AL137472	Homo sapiens	hypothetical protein	179	55
7006	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	379	98
7007	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	121	38
7008	AF119851	Homo sapiens	PRO1722	136	63
7009	AF218028	Homo sapiens	unknown	104	52
7010	AF130079	Homo sapiens	PRO2852	129	60
7011	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	110	54
7012	X03145	Homo sapiens	pot. ORF VI	130	65
7013	AF090944	Homo sapiens	PRO0663	171	75
7014	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	122	65
7015	M26460	Homo sapiens	retinoblastoma 1	113	37
7016	X92485	Plasmodium vivax	pval	112	56
7017	X92485	Plasmodium vivax	pval	144	57
7018	AF130079	Homo sapiens	PRO2852	224	74
7019	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	129	43
7020	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	58
7021	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	106	69
7022	AF090901	Homo sapiens	PRO0195	103	88
7023	AF116661	Homo sapiens	PRO1438	120	47
7024	AF002460	Arabidopsis thaliana	gene_id:F1D9.26-unknown protein	325	60
7025	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	126	63
7026	AF119900	Homo sapiens	PRO2822	111	70
7027	AF130051	Homo sapiens	PRO0898	133	44
7028	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	179	68
7029	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	72	60
7030	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	130	50
7031	J03941	Mus musculus	ferritin heavy chain	124	57
7032	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	157	59
7033	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	120	65
7034	Y36156	Homo sapiens	Human secreted protein #28.	164	48
7035	U80761	Homo sapiens	CTG26 alternate open reading frame	116	48
7036	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	130	52
7037	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	113	55
7038	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	78	68
7039	AF130089	Homo sapiens	PRO2550	121	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7040	AF119855	Homo sapiens	PRO1847	158	65
7041	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	116	62
7042	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	117	54
7043	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	123	80
7044	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	63
7045	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	86	44
7046	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	80	72
7047	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	100	57
7048	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	152	66
7049	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	94	72
7050	AF176323	Macropus eugenii	small nuclear ribonucleoprotein B'	103	41
7051	AF255446	Cryptocodium johnii	Dipl-associated protein C	127	38
7052	M64792	Rattus norvegicus	salivary proline-rich protein	149	42
7053	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	69
7054	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	109	54
7055	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	185	86
7056	U60269	Homo sapiens	putative envelope protein; orf similar to env of Type A and Type B retroviruses and to class II HERVs	125	65
7057	AF068294	Homo sapiens	HDCMB45P	264	73
7058	Y86248	Homo sapiens	Human secreted protein IICHIPF68, SEQ ID NO:163.	190	95
7059	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	140	62
7060	AF090894	Homo sapiens	PRO0113	185	62
7061	AF107406	Homo sapiens	GW128	66	80
7062	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	86	46
7063	AF119851	Homo sapiens	PRO1722	117	74
7064	X92485	Plasmodium vivax	pva1	123	66
7065	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	79	59
7066	L23545	Homo sapiens	putative	135	44
7067	AF119851	Homo sapiens	PRO1722	301	69
7068	AF130079	Homo sapiens	PRO2852	118	71
7069	AF119851	Homo sapiens	PRO1722	150	64
7070	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	138	48
7071	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	94	39
7072	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	145	62
7073	G00397	Homo sapiens	Human secreted protein, SEQ ID NO:	155	44

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4478.		
7074	AF130089	Homo sapiens	PRO2550	146	60
7075	U49974	Homo sapiens	mariner transposase	198	83
7076	AF236085	Homo sapiens	CYP4F11	427	79
7077	AF130089	Homo sapiens	PRO2550	159	52
7078	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	206	85
7079	D32202	Homo sapiens	alpha 1C adrenergic receptor isoform 2	152	71
7080	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	88	62
7081	AB046048	Macaca fascicularis	unnamed portein product	135	46
7082	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	142	75
7083	X53581	Rattus norvegicus	ORF4	119	64
7084	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	111	62
7085	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	64
7086	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	71	66
7087	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	81	54
7088	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	148	50
7089	U08021	Homo sapiens	nicotinamide N-methyltransferase	116	100
7090	U93569	Homo sapiens	p40	199	82
7091	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	124	56
7092	X92485	Plasmodium vivax	pval	125	60
7093	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	109	62
7094	AF118082	Homo sapiens	PRO1902	191	50
7095	X92485	Plasmodium vivax	pval	129	67
7096	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	80	66
7097	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	162	67
7098	AF116715	Homo sapiens	PRO2829	123	63
7099	L27428	Homo sapiens	reverse transcriptase	189	50
7100	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	84	48
7101	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	65
7102	D85030	Schizosaccharomyces pombe	ribosomal protein S33 homolog	139	85
7103	G03021	Homo sapiens	Human secreted protein, SEQ ID NO: 7102.	177	77
7104	U72543	Sus scrofa	ubiquitin-like/S30 ribosomal fusion protein	129	100
7105	AC007787	AA 187-502	NFI-X3=transcription factor	190	84
7106	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	110	38
7107	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	157	56
7108	Z69381	Saccharomyces cerevisiae	N1114	450	91

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7109	V49572_cd1	Homo sapiens	13-NOV-1996 Human stomach cancer clone HP10122 cDNA #1.	353	70
7110	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	99	45
7111	AF068294	Homo sapiens	HDCMB45P	132	55
7112	AB033020	Homo sapiens	KIAA1194 protein	850	100
7113	AB019692	Homo sapiens	protein kinase PKNbeta	792	87
7114	M12140	Homo sapiens	envelope protein	154	79
7115	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	88	62
7116	AF124491	Homo sapiens	ARF GTPase-activating protein GIT2	1216	100
7117	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	153	54
7118	AF130089	Homo sapiens	PRO2550	184	64
7119	AF130079	Homo sapiens	PRO2852	144	68
7120	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	112	51
7121	AF032384	Xenopus laevis	metalloprotease-disintegrin	304	76
7122	K01664	Drosophila melanogaster	Bkm-like protein	99	71
7123	AJ238706	Drosophila melanogaster	monocarboxylate transporter 1 homologue	161	38
7124	X92485	Plasmodium vivax	pva1	127	54
7125	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	80	65
7126	AF116712	Homo sapiens	PRO2738	118	53
7127	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	115	64
7128	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	90	62
7129	AF118090	Homo sapiens	PRO2044	280	80
7130	AF129085	Homo sapiens	carboxy terminus of Hsp70-interacting protein	593	91
7131	AF054840	Homo sapiens	tetraspan TM4SF; Tspan-3	513	83
7132	L27428	Homo sapiens	reverse transcriptase	156	51
7133	AK001647	Homo sapiens	unnamed protein product	2334	99
7134	AF130051	Homo sapiens	PRO0898	142	84
7135	X53581	Rattus norvegicus	ORF4	213	46
7136	G03045	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	101	86
7137	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	194	68
7138	U21634	Onychomys torridus	cytochrome c oxidase subunit III	111	84
7139	X60592	Homo sapiens	CDw40	201	95
7140	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	63
7141	M76979	Homo sapiens	pigment epithelial-differentiating factor	458	93
7142	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	142	54
7143	Y27677	Homo sapiens	Human secreted protein encoded by gene No. 111.	323	90
7144	AF116712	Homo sapiens	PRO2738	132	60
7145	AB024057	Homo sapiens	vascular Rab-GAP/TBC-containing protein	121	45
7146	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	144	65

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SEQ ID NO:	Accession No.	Species	Description	Smith Waterman Score	% Identity
7147	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete viron genome.	141	76
7148	R06400	Homo sapiens	Lambda gt10ch2 encoded C-terminal alpha amidating enzyme.	337	85
7149	S87759	Homo sapiens	protein phosphatase 2C alpha, PP2Calpha	427	78
7150	M12140	Homo sapiens	envelope protein	541	64
7151	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	106	85
7152	X55683	Lycopersicon esculentum	extensin (class I)	70	38
7153	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	194	61
7154	AF130089	Homo sapiens	PRO2550	89	60
7155	AF100742	Homo sapiens	M-phase phosphoprotein homolog	714	94
7156	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	143	78
7157	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete viron genome	174	79
7158	AL031230	Homo sapiens	dJ73M23.3 (KIAA0319)	214	45
7159	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	155	37
7160	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	46
7161	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	150	53
7162	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	107	55
7163	M13043	Mus musculus	alpha-1 (IV) collagen	80	42
7164	AB011004	Homo sapiens	UDP-N-acetylglucosamine pyrophosphorylase	257	90
7165	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSIW18.	111	47
7166	AF119851	Homo sapiens	PRO1722	279	61
7167	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	136	51
7168	W73327	Homo sapiens	Bipolar affective disorder associated gene fsh16 product.	287	63
7169	Y35946	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 195.	1231	99
7170	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	132	76
7171	U83303	Homo sapiens	line-1 reverse transcriptase	184	60
7172	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	141	64
7173	AF129507	Homo sapiens	transcription factor ICBP90	245	55
7174	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	131	56
7175	AF161356	Homo sapiens	HSPC093	107	55
7176	AF218028	Homo sapiens	unknown	116	55
7177	G02654	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.	117	52
7178	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	94	38
7179	AF130089	Homo sapiens	PRO2550	124	47
7180	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	109	66
7181	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	65
7182	Y36156	Homo sapiens	Human secreted protein #28.	127	62



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7183	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	121	75
7184	X92485	Plasmodium vivax	pva1	129	60
7185	AF130089	Homo sapiens	PRO2550	116	53
7186	AF130089	Homo sapiens	PRO2550	137	64
7187	X51760	Homo sapiens	zinc finger protein (583 AA)	236	56
7188	X92485	Plasmodium vivax	pva1	131	50
7189	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	152	57
7190	AF068294	Homo sapiens	HDCMB45P	163	50
7191	AF119855	Homo sapiens	PRO1847	55	50
7192	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	142	57
7193	M15530	Homo sapiens	B-cell growth factor	106	53
7194	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	121	41
7195	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	124	60
7196	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	94	68
7197	U60315	Mollusca contagiosum virus subtype 1	MC054L	116	36
7198	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	116	67
7199	M15530	Homo sapiens	B-cell growth factor	146	59
7200	AF090894	Homo sapiens	PRO0113	165	65
7201	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	160	57
7202	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	53
7203	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	92	65
7204	AF126163	Homo sapiens	HLA3 protein	131	78
7205	X92485	Plasmodium vivax	pva1	116	42
7206	AF090931	Homo sapiens	PRO0483	156	83
7207	Y36156	Homo sapiens	Human secreted protein #28.	127	49
7208	Y12961	Homo sapiens	Amino acid sequence of a human secreted peptide.	158	55
7209	Y36203	Homo sapiens	Human secreted protein #75.	124	56
7210	M69008	Homo sapiens	alpha-1 type XIII collagen	90	34
7211	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	71
7212	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	133	60
7213	AF130089	Homo sapiens	PRO2550	163	86
7214	AF130089	Homo sapiens	PRO2550	111	52
7215	AF118082	Homo sapiens	PRO1902	150	63
7216	Y53663	Homo sapiens	A human B-cell growth factor related protein (BGFRP).	83	66
7217	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	68
7218	AF220264	Homo sapiens	MOST-1	123	66
7219	AF229067	Homo sapiens	PAI-1 protein	121	52
7220	AF118086	Homo sapiens	PRO1992	130	61
7221	Y86248	Homo sapiens	Human secreted protein HCHPF68.	179	100

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SEQ ID NO:163.		
7222	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	78
7223	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	200	95
7224	L27428	Homo sapiens	reverse transcriptase	127	55
7225	AB008227	Adiantum capillus-veneris	Extensin	121	43
7226	D38112	Homo sapiens	cytochrome c oxidase subunit I	113	78
7227	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	153	96
7228	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	74
7229	M15530	Homo sapiens	B-cell growth factor	137	44
7230	AF004341	Homo sapiens	cytochrome c oxidase subunit III	140	87
7231	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	162	46
7232	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA 1a (AF078683)	123	90
7233	X15769	Mus musculus	UIRNA-associated 70-kDa protein	105	29
7234	M15530	Homo sapiens	B-cell growth factor	113	61
7235	AF194537	Homo sapiens	NAG13	249	65
7236	R20313	Homo sapiens	Gly(5) beta-globin mutant.	296	80
7237	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	123	50
7238	Y36156	Homo sapiens	Human secreted protein #28.	97	80
7239	D38112	Homo sapiens	NADH dehydrogenase subunit 3	395	81
7240	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	122	70
7241	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA 1a (AF078683)	123	90
7242	AF090942	Homo sapiens	PRO0657	118	47
7243	AF119851	Homo sapiens	PRO1722	112	62
7244	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	100	53
7245	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	144	66
7246	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	129	78
7248	X92485	Plasmodium vivax	pva1	108	58
7249	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	170	74
7250	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	153	70
7251	U01849	Trypanosoma brucei	ORF2	93	39
7252	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	113	54
7253	G03473	Homo sapiens	Human secreted protein, SEQ ID NO: 7554.	110	83
7254	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	167	66
7255	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	179	83
7256	AF130079	Homo sapiens	PRO2852	147	70
7257	AF118082	Homo sapiens	PRO1902	140	45
7258	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	137	55
7259	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	90	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7260	X92485	Plasmodium vivax	pva1	105	85
7261	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	162	76
7262	AF130089	Homo sapiens	PRO2550	98	43
7263	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	114	60
7264	AF116661	Homo sapiens	PRO1438	139	67
7265	AF104021	Bovine viral diarrhea virus-2	polyprotein	161	40
7266	AL160493	Leishmania major	probable (nhv-6) u1102, variant a DNA, complete virion genome	116	43
7267	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	112	62
7268	M15530	Homo sapiens	B-cell growth factor	154	60
7269	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	95	54
7270	AF118082	Homo sapiens	PRO1902	139	62
7271	S52010	Mus sp.	orf1 5' of EpoR	93	33
7272	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	114	50
7273	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	166	61
7274	AF130089	Homo sapiens	PRO2550	124	43
7275	X92485	Plasmodium vivax	pva1	147	44
7276	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	81	59
7277	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	146	67
7278	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	89	67
7279	AF130087	Homo sapiens	PRO2411	72	65
7280	Y40039	Homo sapiens	Peptide sequence derived from a human secreted protein.	130	69
7281	J03507	Homo sapiens	complement protein C7 precursor	357	81
7282	AF116661	Homo sapiens	PRO1438	117	48
7284	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	137	61
7285	AF116715	Homo sapiens	PRO2829	128	75
7286	AF130079	Homo sapiens	PRO2852	122	52
7287	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	120	50
7288	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	338	75
7289	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	114	72
7290	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	146	59
7291	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	156	58
7292	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	167	61
7293	X92485	Plasmodium vivax	pva1	122	71
7294	AF130089	Homo sapiens	PRO2550	87	62
7295	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	140	50
7296	X92485	Plasmodium	pva1	152	75

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
7297	AF090894	Homo sapiens	PRO0113	172	65
7298	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	121	61
7299	AL359782	Trypanosoma brucei	possible (hfv-6) u1102, variant a dna, complete virion genome.	114	66
7300	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	228	80
7301	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	111	73
7302	U43360	Peromyscus maniculatus	reverse transcriptase	119	46
7303	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	168	76
7304	U58658	Homo sapiens	unknown	102	48
7305	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	118	53
7306	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	116	63
7307	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	149	58
7308	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	112	52
7309	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	115	54
7310	M15530	Homo sapiens	B-cell growth factor	131	54
7311	AF118082	Homo sapiens	PRO1902	168	46
7312	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	412	92
7313	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	326	74
7314	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMQ32.	149	59
7315	AF289099	Maackia amurensis	ENOD2f	107	32
7316	U17009	Phytophthora infestans	SecY-independent transporter protein	135	41
7317	AF220264	Homo sapiens	MOST-1	133	72
7318	U49973	Homo sapiens	ORF2: function unknown	111	53
7319	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	274	80
7320	AB047600	Macaca fascicularis	hypothetical protein	79	56
7321	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	205	95
7322	AC005175	Homo sapiens	TA2R HUMAN, BETA ISOFORM; TXA2-R; PROSTANOID TP RECEPTOR	127	57
7323	R48296	Homo sapiens	Human PGF-2/NT-3.	89	93
7324	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	157	60
7325	AF119855	Homo sapiens	PRO1847	172	66
7326	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	141	50
7327	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	56
7328	Y40039	Homo sapiens	Peptide sequence derived from a human secreted protein.	98	56
7329	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	161	64
7330	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	111	72

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7331	AF126163	Homo sapiens	HHLA3 protein	98	47
7332	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	122	61
7333	AF130079	Homo sapiens	PRO2852	136	54
7334	AK023563	Homo sapiens	unnamed protein product	265	73
7335	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	113	61
7336	M15530	Homo sapiens	B-cell growth factor	136	75
7337	D38112	Homo sapiens	cytochrome c oxidase subunit 1	168	81
7338	D38112	Homo sapiens	cytochrome c oxidase subunit 3	339	80
7339	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	170	74
7340	D38112	Homo sapiens	NADH dehydrogenase subunit 3	400	82
7341	L00016	Homo sapiens	urf4	295	72
7342	D38112	Homo sapiens	NADH dehydrogenase subunit 3	350	86
7343	M36647	Homo sapiens	mitochondrial hinge protein precursor	286	82
7344	X15917	Paramecium aurelia	ND2 protein (AA 1-193) (unusual start codon)	132	34
7345	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	82
7346	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	89	69
7347	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	133	69
7348	D38112	Homo sapiens	NADH dehydrogenase subunit 3	169	71
7349	D38112	Homo sapiens	cytochrome c oxidase subunit 1	347	83
7350	V00662	Homo sapiens	cytochrome oxidase I	325	85
7351	D38112	Homo sapiens	NADH dehydrogenase subunit 3	406	80
7352	D38112	Homo sapiens	NADH dehydrogenase subunit 3	224	79
7353	D38112	Homo sapiens	NADH dehydrogenase subunit 1	270	86
7354	D38112	Homo sapiens	NADH dehydrogenase subunit 3	167	90
7355	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	120	87
7356	D38112	Homo sapiens	NADH dehydrogenase subunit 3	362	84
7357	D38112	Homo sapiens	NADH dehydrogenase subunit 3	188	72
7358	D38112	Homo sapiens	NADH dehydrogenase subunit 3	335	72
7359	U09500	Homo sapiens	cytochrome b	275	80
7360	D38112	Homo sapiens	NADH dehydrogenase subunit 3	209	73
7361	AF118078	Homo sapiens	PRO1848	95	58
7362	AB017116	Homo sapiens	AD 1	148	89
7363	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	146	42
7364	D38112	Homo sapiens	NADH dehydrogenase subunit 1	203	82
7365	D38112	Homo sapiens	NADH dehydrogenase subunit 1	206	84
7366	D38112	Homo sapiens	NADH dehydrogenase subunit 3	408	82
7367	D38112	Homo sapiens	NADH dehydrogenase subunit 3	456	86
7368	D38112	Homo sapiens	cytochrome c oxidase subunit 3	481	85
7369	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	150	53
7370	AB017116	Homo sapiens	AD 1	145	91
7371	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	173	85
7372	AF118082	Homo sapiens	PRO1902	122	54
7373	G00492	Homo sapiens	Human secreted protein, SEQ ID NO: 4573.	163	62
7374	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	53
7375	AF090894	Homo sapiens	PRO0113	128	64
7376	AK000241	Homo sapiens	unnamed protein product	131	67

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7377	AF119855	Homo sapiens	PRO1847	164	62
7379	AF016099	Mus musculus	endonuclease/reverse transcriptase	114	37
7380	U57362	Rattus norvegicus	collagen XII alpha 1	148	47
7381	D38112	Homo sapiens	ATPase subunit 6	423	76
7382	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	135	58
7383	AB040938	Homo sapiens	KIAA1505 protein	983	76
7384	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	48
7385	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	122	75
7386	U63295	Homo sapiens	seven in absentia homolog	260	85
7387	A0003499	Drosophila melanogaster	CG12706 gene product	103	32
7388	X03342	Homo sapiens	rpL32 (aa 1-135)	123	51
7389	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	129	58
7390	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	154	100
7391	AK026800	Homo sapiens	unnamed protein product	137	52
7392	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	117	73
7393	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	89	70
7394	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	161	80
7395	M15530	Homo sapiens	B-cell growth factor	98	57
7396	L10908	Mus musculus	Gcap1 gene product	105	51
7397	AF119851	Homo sapiens	PRO1722	127	55
7398	X99256	Hyllobates lar	cytochrome oxidase subunit III	319	73
7399	D38112	Homo sapiens	cytochrome c oxidase subunit 3	497	77
7400	D38112	Homo sapiens	cytochrome c oxidase subunit 3	399	80
7401	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	170	83
7402	D38112	Homo sapiens	NADH dehydrogenase subunit 3	183	91
7403	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	189	88
7404	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	115	40
7405	D83006	Saccharomyces cerevisiae	gene required for phosphorylation of oligosaccharides/ has high homology with YJR061w	171	38
7406	AF144636	Gallus gallus	osteoblast regulatory factor 3A	108	44
7407	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	70
7408	D38112	Homo sapiens	cytochrome c oxidase subunit 3	407	93
7409	AF004341	Homo sapiens	cytochrome c oxidase subunit III	140	87
7410	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	111	59
7411	AF004341	Homo sapiens	cytochrome c oxidase subunit III	138	82
7412	D38112	Homo sapiens	NADH dehydrogenase subunit 3	431	82
7413	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	127	56
7414	AB036396	Rana nigromaculata	cytochrome b	109	87
7415	AF090930	Homo sapiens	PRO0478	121	76
7416	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	171	96
7417	D38112	Homo sapiens	NADH dehydrogenase subunit 3	446	91

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7418	AB018440	Echinococcus multilocularis	NADH dehydrogenase subunit 2	112	33
7419	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	123	66
7420	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	116	50
7421	AF155232	Pisum sativum	extensin	128	37
7422	AF161356	Homo sapiens	HSPC093	89	48
7423	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 3	162	81
7424	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	171	79
7425	AF275953	synthetic construct	Cox8ND6gfp fusion protein	214	93
7426	D38112	Homo sapiens	cytochrome c oxidase subunit 1.	156	73
7427	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	130	59
7428	AK024455	Homo sapiens	FLJ00047 protein	82	66
7429	D38112	Homo sapiens	NADH dehydrogenase subunit 1	212	82
7430	S79410	Mus musculus	nuclear localization signal binding protein	124	48
7431	D38112	Homo sapiens	cytochrome c oxidase subunit 1	195	90
7432	D38112	Homo sapiens	cytochrome c oxidase subunit 1	217	84
7433	U87145	Toxoplasma gondii	ORF D	89	36
7434	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	213	72
7435	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	135	57
7436	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7838.	151	82
7437	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	190	88
7438	D38112	Homo sapiens	NADH dehydrogenase subunit 1	141	78
7439	AF250284	Amsacta moorei entomopoxvirus	AMV012	88	31
7440	AF004341	Homo sapiens	cytochrome c oxidase subunit III	149	85
7441	U43360	Peromyscus maniculatus	reverse transcriptase	114	52
7442	AF275807	Homo sapiens	PNAS-110	157	48
7443	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	126	56
7444	D38112	Homo sapiens	NADH dehydrogenase subunit 4	475	95
7445	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	146	71
7446	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	130	60
7447	X92485	Plasmodium vivax	pva1	153	45
7448	AF119851	Homo sapiens	PRO1722	96	55
7449	AF130079	Homo sapiens	PRO2852	153	73
7450	AF119851	Homo sapiens	PRO1722	238	52
7451	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	113	38
7452	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	147	57
7453	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	136	63
7454	R14163	Homo sapiens	Cellular DNA-binding protein RS1.	270	42
7455	X63526	Homo sapiens	homologue to elongation factor 1-	387	80

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gamma from A.salina		
7456	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	140	80
7457	AF119851	Homo sapiens	PRO1722	102	55
7458	G02756	Homo sapiens	Human secreted protein, SEQ ID NO: 6837.	83	55
7459	AF119851	Homo sapiens	PRO1722	132	64
7460	L10908	Mus musculus	Gcap1 gene product	106	64
7461	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	124	54
7462	X77816	Rattus norvegicus	PR-Vbeta1	142	51
7463	Y34068	Homo sapiens	Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).	96	35
7464	AB046048	Macaca fascicularis	unnamed portein product	302	62
7465	X92485	Plasmodium vivax	pva1	115	47
7466	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	116	65
7467	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	91	35
7468	AF161361	Homo sapiens	HSPC098	92	57
7469	AF216389	Homo sapiens	semaphorin Rs	288	88
7470	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	153	73
7471	AF130089	Homo sapiens	PRO2550	108	48
7472	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	159	58
7473	AF217536	Homo sapiens	truncated mevalonate kinase	115	71
7474	X61296	Rattus norvegicus	open reading frame 2	134	49
7475	U22376	Homo sapiens	alternatively spliced product using exon 13A	165	46
7476	AF119851	Homo sapiens	PRO1722	133	46
7477	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	127	69
7478	D38112	Homo sapiens	NADH dehydrogenase subunit 4	533	87
7479	S79410	Mus musculus	nuclear localization signal binding protein	122	59
7480	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	168	84
7481	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	181	80
7482	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	122	56
7483	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	132	37
7484	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	166	100
7485	D38112	Homo sapiens	cytochrome c oxidase subunit 1	277	72
7486	M29294	Rattus norvegicus	small nuclear ribonucleoparticle-associated protein	132	42
7487	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	140	50
7488	AF090901	Homo sapiens	PRO0195	101	62
7489	X97249	Homo sapiens	leucine-rich primary response protein	304	93
7490	D38112	Homo sapiens	NADH dehydrogenase subunit 3	447	84
7491	AK024455	Homo sapiens	FLJ00047 protein	122	63
7492	U87269	Homo sapiens	p120E4F transcription factor	244	66
7493	A31036	Nicotiana glauca	PRP2	87	31



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7494	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	206	97
7495	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	166	91
7496	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	66
7497	AK024455	Homo sapiens	FLJ00047 protein	67	61
7498	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	174	84
7499	X75438	Sus scrofa	homologue of proline/arginine rich antibacterial peptides	116	44
7500	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	166	89
7501	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	137	61
7502	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	213	60
7503	AB042770	Pteropus dasymallus	cytochrome c oxidase subunit 3	169	89
7504	AF126163	Homo sapiens	HHLA3 protein	110	62
7505	D38112	Homo sapiens	cytochrome c oxidase subunit 3	299	90
7506	D38112	Homo sapiens	cytochrome c oxidase subunit 3	194	88
7507	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	128	72
7508	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	86
7509	D38112	Homo sapiens	cytochrome c oxidase subunit 1	116	65
7510	L38908	Nicotiana tabacum	extensin	114	36
7512	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	273	73
7513	Y36156	Homo sapiens	Human secreted protein #28.	168	44
7514	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	171	96
7515	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	46
7516	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 3	170	84
7517	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	105	43
7518	D38112	Homo sapiens	NADH dehydrogenase subunit 3	350	82
7519	D38114	Gorilla gorilla	NADH dehydrogenase subunit 3 (ND3)	141	84
7520	U12690	Homo sapiens	cytochrome oxidase subunit II	410	85
7521	D38112	Homo sapiens	cytochrome c oxidase subunit I	112	71
7522	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	96	46
7523	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	142	57
7524	AF220264	Homo sapiens	MOST-1	86	62
7525	AF130089	Homo sapiens	PRO2550	109	35
7526	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	106	79
7527	U49973	Homo sapiens	ORF2: function unknown	105	68
7528	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	122	62
7529	X05831	Rattus norvegicus	fibronectin precursor	100	64
7530	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	175	60
7531	X92485	Plasmodium	pva I	120	59

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
7532	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 3	383	75
7533	D38112	Homo sapiens	NADH dehydrogenase subunit 3	321	67
7534	AL359782	Trypanosoma brucei	possible (hly-6) u1102, variant a dna, complete virion genome.	126	72
7535	AF119851	Homo sapiens	PRO1722	110	67
7536	D38112	Homo sapiens	cytochrome c oxidase subunit 3	531	81
7537	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	75
7538	X92485	Plasmodium vivax	pva1	141	48
7539	AF119900	Homo sapiens	PRO2822	86	42
7540	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	126	50
7541	M15530	Homo sapiens	B-cell growth factor	136	53
7542	X53581	Rattus norvegicus	ORF4	174	46
7543	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	138	74
7544	D38112	Homo sapiens	cytochrome c oxidase subunit 1	116	86
7545	M15530	Homo sapiens	B-cell growth factor	96	47
7546	X92485	Plasmodium vivax	pva1	149	58
7547	AF113685	Homo sapiens	PRO0974	110	48
7548	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	226	73
7549	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	316	73
7550	S79410	Mus musculus	nuclear localization signal binding protein	107	70
7551	AF130089	Homo sapiens	PRO2550	130	45
7552	R95913	Homo sapiens	Neural thread protein.	99	56
7553	U93569	Homo sapiens	putative p150	171	47
7554	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	111	75
7555	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	207	56
7556	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	59
7557	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	125	43
7558	Y86445	Homo sapiens	Human gene 42-encoded protein fragment, SEQ ID NO:360.	95	71
7559	X83413	Human herpesvirus 6	U88	108	32
7560	A18812	Brassica napus	extensin	125	38
7561	D38112	Homo sapiens	ATPase subunit 6	495	87
7562	AF130089	Homo sapiens	PRO2550	141	46
7563	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	106	61
7564	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	128	62
7565	U50191	Caenorhabditis elegans	C. elegans collagen dpy-10 gene (Levy, A.D., Yang, J. and Kramer, J.M. Mol. Biol. Cell 4, 803-17, 1993)	101	37
7566	Y00672	Pan troglodytes	reading frame protein 4	294	73
7567	A18812	Brassica napus	extensin	145	48
7568	D38112	Homo sapiens	cytochrome c oxidase subunit 3	241	69
7569	L00016	Homo sapiens	urf4	284	71
7570	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	115	50
7571	G00673	Homo sapiens	Human secreted protein, SEQ ID NO:	124	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4754.		
7572	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	126	65
7573	X92485	Plasmodium vivax	pva1	157	49
7574	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	151	54
7575	AF130089	Homo sapiens	PRO2550	348	70
7576	R95913	Homo sapiens	Neural thread protein.	113	45
7577	L26953	Homo sapiens	chromosomal protein	148	38
7578	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	116	46
7579	AB047948	Macaca fascicularis	hypothetical protein	173	67
7580	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	149	57
7581	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	95	51
7582	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	125	85
7583	AC004079	Homo sapiens	human HOXA3; 95% similarity to e307530 (PID:g188841)	127	100
7584	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	171	71
7585	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	80
7586	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	222	100
7587	D38112	Homo sapiens	cytochrome c oxidase subunit 1	194	71
7588	D38112	Homo sapiens	NADH dehydrogenase subunit 1	115	80
7589	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	77
7590	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	112	60
7591	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	133	72
7592	A49807	Neisseria meningitidis	IGA-LPHA3	93	33
7593	Z67990	Caenorhabditis elegans	contains similarity to Pfam domain: PF01484 (Nematode cuticle collagen N-terminal domain), Score=27.5, E-value=0.0001, N=1	102	42
7594	U43627	Arabidopsis thaliana	extensin	99	44
7595	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	74
7596	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	49
7597	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	190	92
7598	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	96
7599	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	95
7600	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	192	85
7601	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	91
7602	D38112	Homo sapiens	NADH dehydrogenase subunit 3	333	71

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7603	D38112	Homo sapiens	cytochrome c oxidase subunit 3	190	86
7604	U09500	Homo sapiens	cytochrome b	279	93
7605	Z14016	Nicotiana tabacum	pistil extensin like protein, partial CDS	84	40
7606	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	108	71
7607	G03636	Homo sapiens	Human secreted protein, SEQ ID NO: 7717.	55	52
7608	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	114	54
7609	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	97	62
7610	D38112	Homo sapiens	NADH dehydrogenase subunit 3	434	87
7611	Y21418	Homo sapiens	Human high mobility group protein HMGI-C mutant fragment 2.	97	46
7613	X92485	Plasmodium vivax	pval	106	58
7614	AC003058	Arabidopsis thaliana	unknown protein	191	88
7615	S74221	Homo sapiens	IK factor=cytokine down-regulating HLA class II	153	65
7616	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	148	74
7617	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	169	56
7618	L35013	Homo sapiens	spliceosomal protein	95	55
7619	V00662	Homo sapiens	URF 3 (NADH dehydrogenase subunit)	441	85
7620	AF116638	Homo sapiens	PRO1546	172	42
7621	K03202	Homo sapiens	salivary proline-rich protein precursor	146	46
7622	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	145	72
7623	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	144	67
7624	U41031	Caenorhabditis elegans	proline-rich	92	59
7625	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	130	55
7626	L19098	Choristoneura fumiferana	cytochrome oxidase I	102	66
7627	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	99	76
7628	AF126163	Homo sapiens	HHLA3 protein	117	67
7629	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	69	53
7630	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	83	55
7631	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	87	64
7632	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	120	48
7633	R95913	Homo sapiens	Neural thread protein.	126	61
7634	V00662	Homo sapiens	cytochrome oxidase I	396	85
7635	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	205	84
7636	D38112	Homo sapiens	NADH dehydrogenase subunit 3	464	85
7637	D38112	Homo sapiens	NADH dehydrogenase subunit 2	165	94
7638	AF118086	Homo sapiens	PRO1992	120	68
7639	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	84

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7640	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	95	39
7641	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	143	68
7642	D38112	Homo sapiens	NADH dehydrogenase subunit 3	192	91
7643	D38112	Homo sapiens	NADH dehydrogenase subunit 3	416	80
7644	AF004341	Homo sapiens	cytochrome c oxidase subunit III	133	84
7645	U93570	Homo sapiens	putative p150	206	42
7646	D38112	Homo sapiens	ATPase subunit 6	192	80
7647	AF090942	Homo sapiens	PRO0657	128	71
7648	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	134	73
7649	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	115	52
7650	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	130	61
7651	X71442	Rattus norvegicus	ORF 1; putative	105	52
7652	L07545	Leishmania tarentolae	A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression	111	32
7653	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	89	53
7654	G02473	Homo sapiens	Human secreted protein, SEQ ID NO: 6554.	291	49
7655	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	165	63
7656	D38112	Homo sapiens	NADH dehydrogenase subunit 3	470	88
7657	D38112	Homo sapiens	NADH dehydrogenase subunit 3	367	80
7658	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	108	95
7659	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	109	50
7660	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	77
7661	AP002460	Arabidopsis thaliana	gene_id:F1D9.26-unknown protein	121	40
7662	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	137	96
7663	AF217973	Homo sapiens	unknown	124	51
7664	X92485	Plasmodium vivax	pval	118	59
7665	AF118082	Homo sapiens	PRO1902	123	44
7666	AB014563	Homo sapiens	KIAA0663 protein	267	90
7667	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	114	49
7668	AF119855	Homo sapiens	PRO1847	152	72
7669	AK025116	Homo sapiens	unnamed protein product	127	65
7670	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	140	55
7671	R14847	Homo sapiens	Protein associated with biochemical pathway involving cAMP.	164	89
7672	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	93	68
7673	U37426	Homo sapiens	kinesin-like spindle protein HKSP	247	81
7674	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHI-O29.	125	75
7675	S67633	Homo sapiens	class I major histocompatibility antigen	103	59

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7676	AF126163	Homo sapiens	HHLA3 protein	146	72
7677	AC005192	Homo sapiens	similar to mouse interferon-related protein PC4; 96% identical to P19182 (PID:g135861)	143	87
7678	X07882	Homo sapiens	Po protein	126	39
7679	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	148	60
7680	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	177	37
7681	AF090930	Homo sapiens	PRO0478	80	58
7682	X35654	Homo sapiens	cytochrome C oxidase II subunit	115	65
7683	AB046048	Macaca fascicularis	unnamed protein product	145	67
7684	AF130079	Homo sapiens	PRO2852	117	60
7685	M13101	Rattus norvegicus	unknown protein	114	53
7686	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	134	74
7687	AF126163	Homo sapiens	HHLA3 protein	141	84
7688	Y36156	Homo sapiens	Human secreted protein #28.	120	61
7689	M37197	Homo sapiens	CCAAT-box-binding factor	104	95
7690	AL390114	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	97	54
7691	AF220264	Homo sapiens	MOST-1	117	76
7692	AF063866	Melanoplus sanguinipes entomopoxvirus	ORF MSV233 hypothetical protein	94	31
7693	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	98	40
7694	AF118082	Homo sapiens	PRO1902	115	55
7695	G00317	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	116	56
7696	Y15163	Mus musculus	putative splice variant containing region C	133	51
7697	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	132	52
7698	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	155	77
7699	M15530	Homo sapiens	B-cell growth factor	106	79
7700	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	108	70
7701	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	166	62
7702	AF090931	Homo sapiens	PRO0483	125	68
7703	G03432	Homo sapiens	Human secreted protein, SEQ ID NO: 7513.	114	79
7704	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	175	63
7705	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	141	35
7706	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	58
7707	X92485	Plasmodium vivax	pva1	126	42
7708	AK023563	Homo sapiens	unnamed protein product	217	72
7709	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	58
7710	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	124	56
7711	G03714	Homo sapiens	Human secreted protein, SEQ ID NO:	131	62

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7795.		
7712	D38112	Homo sapiens	NADH dehydrogenase subunit 1	116	72
7713	D38112	Homo sapiens	cytochrome c oxidase subunit 1	194	58
7714	X92485	Plasmodium vivax	pva1	123	68
7715	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	137	48
7716	AF119851	Homo sapiens	PRO1722	168	60
7717	U93570	Homo sapiens	putative p150	133	35
7718	AF116712	Homo sapiens	PRO2738	94	68
7719	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	107	55
7720	U49973	Homo sapiens	ORF2: function unknown	200	85
7721	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	234	73
7722	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	155	76
7723	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	140	65
7724	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	70	73
7725	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	94	55
7726	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	130	75
7727	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	94	78
7728	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	163	65
7729	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	111	63
7730	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	119	69
7731	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	113	84
7732	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	94	38
7733	U09500	Homo sapiens	cytochrome b	463	84
7734	D38112	Homo sapiens	cytochrome c oxidase subunit 3	334	92
7735	Y00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	399	92
7736	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	128	55
7737	AC003058	Arabidopsis thaliana	unknown protein	167	66
7738	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	86	70
7739	D86854	Catharanthus roseus	extensin	154	40
7740	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	122	57
7741	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	99	49
7742	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	117	35
7743	V00662	Homo sapiens	cytochrome oxidase I	568	89
7744	R63235	Homo sapiens	CNS neural thread protein HB4.	145	93
7745	R63235	Homo sapiens	CNS neural thread protein HB4.	154	100
7746	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	61

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7747	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	126	71
7748	D38112	Homo sapiens	cytochrome c oxidase subunit 3	327	92
7749	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	150	71
7750	AF130079	Homo sapiens	PRO2852	147	81
7751	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	104	49
7752	U43627	Arabidopsis thaliana	extensin	116	37
7753	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	71
7754	D38112	Homo sapiens	NADH dehydrogenase subunit 1	551	83
7755	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	88	56
7756	AF119851	Homo sapiens	PRO1722	97	56
7757	U80955	Caenorhabditis elegans	similar to RE repeat region of PIR-S27806 D. melanogaster homeotic protein BarH2 protein (dual bar protein)	89	100
7758	AC002045	Homo sapiens	Unknown protein product C1987SK-A-589H1_1 splice form 2	97	94
7759	Y02775	Homo sapiens	Human secreted protein encoded by gene 12 clone HFTCU19.	288	98
7760	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	94	80
7761	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	199	76
7762	AF090931	Homo sapiens	PRO0483	153	84
7763	X92485	Plasmodium vivax	pval	114	62
7764	AF090931	Homo sapiens	PRO0483	107	86
7765	G02752	Homo sapiens	Human secreted protein, SEQ ID NO: 6833.	103	43
7766	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	73
7767	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	148	72
7768	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	222	83
7769	Y40039	Homo sapiens	Peptide sequence derived from a human secreted protein.	68	72
7770	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	62
7771	U93569	Homo sapiens	p40	188	43
7772	A1049934	Homo sapiens	hypothetical protein	113	47
7773	AF090931	Homo sapiens	PRO0483	86	65
7774	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	137	92
7775	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	143	65
7776	AF126163	Homo sapiens	HHLA3 protein	141	71
7777	G00423	Homo sapiens	Human secreted protein, SEQ ID NO: 4504.	93	47
7778	AF090942	Homo sapiens	PRO0657	148	74
7779	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	194	83
7780	U14966	Homo sapiens	ribosomal protein L5	315	81



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7781	R59843	Homo sapiens	ApoE4Lx2 protease.	126	47
7782	AF119855	Homo sapiens	PRO1847	131	51
7783	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	79	53
7784	D38112	Homo sapiens	NADH dehydrogenase subunit 3	405	82
7785	G00331	Homo sapiens	Human secreted protein, SEQ ID NO: 4412.	64	42
7786	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	59
7787	AF118082	Homo sapiens	PRO1902	131	48
7788	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	88	64
7789	J03807	Strongylocentrotus purpuratus	histone H1-delta	111	43
7790	D38112	Homo sapiens	NADH dehydrogenase subunit 1	139	85
7791	Y00662	Homo sapiens	cytochrome oxidase I	522	80
7792	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	153	72
7793	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	84	53
7794	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	82	46
7795	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	76
7796	D38112	Homo sapiens	ATPase subunit 8	166	77
7797	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	48
7798	AF090931	Homo sapiens	PRO0483	132	75
7799	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	97	57
7800	D21261	Homo sapiens	similar to human 22kDa, SM22 mRNA (HUM22SM).	99	84
7801	X64707	Homo sapiens	BBC1	232	77
7802	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	104	33
7803	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	50
7804	Y36203	Homo sapiens	Human secreted protein #75.	142	56
7805	AF119851	Homo sapiens	PRO1722	88	46
7806	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	149	57
7807	X68600	Hordeum vulgare	pZE40	90	37
7808	AK025047	Homo sapiens	unnamed protein product	138	54
7809	AF130089	Homo sapiens	PRO2550	375	71
7810	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	124	65
7811	R59842	Homo sapiens	ApoE4L1 protease.	156	58
7812	AF016446	Caenorhabditis elegans	similar to C. elegans cuticulin precursor CUT-2 (SP:P34682)	95	42
7813	R96800	Homo sapiens	Human histocyte-secreted factor HSF.	154	65
7814	AK025047	Homo sapiens	unnamed protein product	165	71
7815	W34499	Homo sapiens	Obesity receptor C protein.	309	89
7816	AJ222673	Hepatitis C virus type 2c	core protein	95	42
7817	AB011483	Arabidopsis thaliana	contains similarity to root cap protein-gene id:MUF9.16	104	61
7818	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	154	74

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7819	X92485	Plasmodium vivax	pva1	112	61
7820	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	103	60
7821	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	174	65
7822	AF130089	Homo sapiens	PRO2550	107	67
7823	AF118086	Homo sapiens	PRO1992	143	73
7824	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	132	63
7825	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	142	59
7826	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	42
7827	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	128	65
7828	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	104	58
7829	AF132961	Homo sapiens	CGI-27 protein	154	49
7830	X70343	Nicotiana glauca	extensin	105	30
7831	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	100	62
7832	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	129	51
7833	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	99	46
7834	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	74	65
7835	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	163	55
7836	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	72	52
7837	AF090942	Homo sapiens	PRO0657	126	59
7838	Z33426	Human respiratory syncytial virus	glycoprotein	110	34
7839	D63480	Homo sapiens	The KIAA0146 gene product is novel.	158	89
7840	W48352	Homo sapiens	Human breast cancer related protein BCFLT1.	88	63
7841	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	156	60
7842	W90847	Homo sapiens	Human lymphocyte targeted peptide #15.	145	100
7843	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	127	66
7844	M28016	Homo sapiens	cytochrome b	214	78
7845	D38112	Homo sapiens	cytochrome c oxidase subunit 3	283	82
7846	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	94	73
7847	D38112	Homo sapiens	cytochrome b	525	83
7848	L27428	Homo sapiens	reverse transcriptase	210	67
7849	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	156	96
7850	X92485	Plasmodium vivax	pva1	121	54
7851	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	147	59
7852	D38112	Homo sapiens	NADH dehydrogenase subunit 2	191	93

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7853	W48808	Homo sapiens	Homo sapiens clone CG109_1 protein	72	69
7854	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	76
7855	U43627	Arabidopsis thaliana	extensin	124	35
7856	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	95
7857	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	95	57
7858	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	157	91
7859	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	108	45
7860	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	159	54
7861	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	155	63
7862	D38112	Homo sapiens	cytochrome c oxidase subunit 3	265	77
7863	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	145	56
7864	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	222	100
7865	D38112	Homo sapiens	cytochrome c oxidase subunit 1	409	87
7866	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	112	50
7867	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	169	74
7868	AL031004	Arabidopsis thaliana	RSZp22 splicing factor	127	35
7869	U83771	Accipiter superciliosus	cytochrome oxidase I	168	73
7870	U83771	Accipiter superciliosus	cytochrome oxidase I	186	81
7871	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	203	56
7872	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	130	71
7873	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	106	44
7874	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	138	69
7875	AF119855	Homo sapiens	PRO1847	174	70
7876	AF210651	Homo sapiens	NAG18	164	76
7877	Z93244	Homo sapiens	bK116F5.2 (PUTATIVE RhoGAP (CDC42 GTPase Activating Protein) LIKE protein)	111	45
7878	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	227	79
7879	AK024455	Homo sapiens	FLJ00047 protein	120	68
7880	Y36156	Homo sapiens	Human secreted protein #28.	85	68
7881	AF116661	Homo sapiens	PRO1438	138	61
7882	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	141	55
7883	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	111	63
7884	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	106	64
7885	AK022821	Homo sapiens	unnamed protein product	175	72
7886	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	59

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7887	L27428	Homo sapiens	reverse transcriptase	165	63
7888	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	139	61
7889	M15530	Homo sapiens	B-cell growth factor	132	74
7890	Y01181	Homo sapiens	Polypeptide fragment encoded by gene 12.	81	64
7891	AB046048	Macaca fascicularis	unnamed portein product	150	61
7892	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	154	73
7893	AF130089	Homo sapiens	PRO2550	224	61
7894	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	127	69
7895	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	142	62
7896	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	50
7897	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	108	68
7898	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	144	65
7899	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	105	83
7900	AF026689	Homo sapiens	prostate-specific transglutaminase	104	57
7901	X03717	Homo sapiens	pot. unidentified reading frame	105	46
7902	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	94	67
7903	X61046	Hydra sp.	mini-collagen	107	46
7904	AF124726	Homo sapiens	acinusL	111	44
7905	U77049	Ovis aries	bactinecin II	116	38
7906	AF118086	Homo sapiens	PRO1992	130	73
7907	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	121	48
7908	AL359782	Trypanosoma brucei	possible (hly-6) u1102, variant a dna, complete virion genome.	124	83
7909	AC004450	Arabidopsis thaliana	putative extensin	167	34
7910	AF130079	Homo sapiens	PRO2852	110	42
7911	AF090942	Homo sapiens	PRO0657	144	66
7912	AF090931	Homo sapiens	PRO0483	96	80
7913	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	128	46
7914	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	87	68
7915	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	105	75
7916	X92485	Plasmodium vivax	pvaI	102	67
7917	AF090942	Homo sapiens	PRO0657	126	76
7918	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	108	47
7919	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	156	63
7920	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	138	61
7921	L26251	Trypanosoma brucei	CR5	95	37
7922	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	176	73

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7923	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	174	61
7924	L27428	Homo sapiens	reverse transcriptase	121	33
7925	Y36156	Homo sapiens	Human secreted protein #28.	137	67
7926	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	119	73
7927	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	138	65
7928	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	138	60
7929	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	166	61
7930	AF004341	Homo sapiens	cytochrome c oxidase subunit III	144	87
7931	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	176	53
7932	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	179	60
7933	Y00662	Homo sapiens	URF 3 (NADH dehydrogenase subunit)	279	92
7934	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	132	63
7935	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	101	64
7936	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	159	55
7937	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	320	80
7938	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	159	71
7939	AF144054	Homo sapiens	apoptosis related protein APR-4	127	65
7940	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	314	73
7941	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	121	57
7942	AB040936	Homo sapiens	KIAA1503 protein	149	71
7943	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	107	83
7944	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	74	60
7945	Y13141	Bromheadia finlaysoniana	extensin	68	35
7946	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	126	50
7947	AP000735	Arabidopsis thaliana	extensin protein-like	214	40
7948	AF161356	Homo sapiens	HSPC093	134	75
7949	AF090942	Homo sapiens	PRO0657	110	48
7950	AJ249395	Globodera pallida	cytochrome b	117	36
7951	AF116661	Homo sapiens	PRO1438	135	49
7952	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	92
7953	M15530	Homo sapiens	B-cell growth factor	143	65
7954	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	137	68
7955	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	130	62
7956	AF130089	Homo sapiens	PRO2550	153	62
7957	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	99	48
7958	AF161356	Homo sapiens	HSPC093	154	56

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7959	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	131	57
7960	X92485	Plasmodium vivax	pva1	107	53
7961	AF210651	Homo sapiens	NAG18	113	77
7962	AF130051	Homo sapiens	PRO0898	84	71
7963	R59842	Homo sapiens	ApoE4L1 protease.	116	68
7964	AF090931	Homo sapiens	PRO0483	129	56
7965	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	151	51
7966	R95913	Homo sapiens	Neural thread protein.	110	40
7967	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	180	50
7968	AF090894	Homo sapiens	PRO0113	104	58
7969	Y21040	Homo sapiens	Human glial fibrillary acidic protein GFAP mutant fragment 49.	285	100
7970	AK001452	Homo sapiens	unnamed protein product	346	56
7971	Y00672	Pan troglodytes	reading frame protein 4	134	90
7972	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	48
7973	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	104	84
7974	AF116661	Homo sapiens	PRO1438	140	62
7975	AF119882	Homo sapiens	PRO2492	112	48
7976	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	80	65
7977	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	124	89
7978	M11901	Rattus norvegicus	proline-rich salivary protein	125	36
7979	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	149	68
7980	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	289	84
7981	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	59
7982	X77816	Rattus norvegicus	PR-Vbeta1	109	69
7983	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	149	73
7984	R96800	Homo sapiens	Human histocyte-secreted factor HSF.	128	72
7985	R59842	Homo sapiens	ApoE4L1 protease.	130	82
7986	AF090895	Homo sapiens	PRO0117	83	58
7987	X07881	Homo sapiens	proline-rich protein G1	131	41
7988	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	123	53
7989	AF090894	Homo sapiens	PRO0113	104	61
7990	Z93244	Homo sapiens	bK116F5.2 (PUTATIVE RhoGAP (CDC42 GTPase Activating Protein) LIKE protein)	100	61
7991	AK024455	Homo sapiens	FLJ00047 protein	131	56
7992	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	136	61
7993	AF210651	Homo sapiens	NAG18	133	61
7994	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	92	42
7995	D38112	Homo sapiens	cytochrome c oxidase subunit I	171	82
7996	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	54

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7997	AF090928	Homo sapiens	PRO0470	86	76
7998	AJ251579	Arabidopsis thaliana	cef protein	113	37
7999	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	119	60
8000	R95913	Homo sapiens	Neural thread protein.	105	70
8001	AF229067	Homo sapiens	PADI-H protein	118	61
8002	W83609	Homo sapiens	Secreted protein encoded by gene 76 clone HKIXL73.	83	65
8003	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	85	61
8004	S79410	Mus musculus	nuclear localization signal binding protein	123	43
8005	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	93	68
8006	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	64
8007	AF016099	Mus musculus	endonuclease/reverse transcriptase	147	38
8008	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	72
8009	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	71
8010	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	92	54
8011	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	152	59
8012	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	123	66
8013	AF161356	Homo sapiens	HSPC093	185	64
8014	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	107	54
8015	G00413	Homo sapiens	Human secreted protein, SEQ ID NO: 4494.	71	65
8016	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	139	66
8017	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	94	77
8018	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	108	46
8019	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	178	61
8020	G03639	Homo sapiens	Human secreted protein, SEQ ID NO: 7720.	85	65
8021	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	108	51
8022	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	202	77
8023	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	195	68
8024	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	158	53
8025	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	133	58
8026	X92485	Plasmodium vivax	pva1	128	56
8027	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	135	61
8028	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	105	66
8029	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	126	59

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8030	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	117	40
8031	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	126	72
8032	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	125	41
8033	Y40039	Homo sapiens	Peptide sequence derived from a human secreted protein.	113	69
8034	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	102	66
8035	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	221	95
8036	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	106	36
8037	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	113	55
8038	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	108	64
8039	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	110	68
8040	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	169	86
8041	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	170	56
8042	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	95	58
8043	AK024455	Homo sapiens	FLJ00047 protein	152	68
8044	AF220264	Homo sapiens	MOST-1	83	68
8045	AK024455	Homo sapiens	FLJ00047 protein	131	55
8046	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	181	78
8047	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	147	61
8048	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	102	43
8049	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	59
8050	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	154	56
8051	D00570	Mus musculus	open reading frame (196 AA)	127	59
8052	AF040964	Homo sapiens	unknown protein IT1	143	50
8053	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	83
8054	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	108	70
8055	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	134	62
8056	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	65
8057	AF090895	Homo sapiens	PRO0117	110	77
8058	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	90
8059	AF118082	Homo sapiens	PRO1902	117	50
8060	AK022217	Homo sapiens	unnamed protein product	145	53
8061	AF130089	Homo sapiens	PRO2550	160	76
8062	AF119851	Homo sapiens	PRO1722	177	54
8063	D38112	Homo sapiens	NADH dehydrogenase subunit 3	362	73
8064	D38112	Homo sapiens	NADH dehydrogenase subunit 3	426	85
8065	D38112	Homo sapiens	NADH dehydrogenase subunit 3	344	90
8066	AF068294	Homo sapiens	HDCMB45P	146	60
8067	V00662	Homo sapiens	URF 3 (NADH dehydrogenase subunit)	461	87
8068	D38112	Homo sapiens	NADH dehydrogenase subunit 4	504	90



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8069	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	97	40
8070	R59842	Homo sapiens	ApoE4L1 protease.	147	47
8071	AF119851	Homo sapiens	PRO1722	139	59
8072	X92485	Plasmodium vivax	pval	183	45
8073	AF116712	Homo sapiens	PRO2738	95	52
8074	AF213465	Homo sapiens	dual oxidase	184	80
8075	AF090895	Homo sapiens	PRO0117	153	57
8076	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	162	73
8077	T85403_cd1	Homo sapiens	19-APR-1993 Human cadherin-11 coding sequence.	284	98
8078	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	99	63
8079	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	162	73
8080	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	142	52
8081	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	130	37
8082	X05285	Drosophila melanogaster	fibrillarin	100	34
8083	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	142	65
8084	G02216	Homo sapiens	Human secreted protein, SEQ ID NO: 6297.	380	82
8085	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	64
8086	X92485	Plasmodium vivax	pval	138	64
8087	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	82
8088	D38112	Homo sapiens	NADH dehydrogenase subunit 5	180	79
8089	U27143	Homo sapiens	protein kinase C inhibitor-1	119	41
8090	AF119851	Homo sapiens	PRO1722	85	47
8091	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	112	73
8092	S79410	Mus musculus	nuclear localization signal binding protein	133	64
8093	AF119854	Homo sapiens	PRO1843	522	100
8094	X92485	Plasmodium vivax	pval	115	82
8095	D38112	Homo sapiens	NADH dehydrogenase subunit 1	598	86
8096	AF097473	Mus musculus	ORF1	109	46
8097	AF097473	Mus musculus	ORF1	109	46
8098	Y17833	Human endogenous retrovirus K	pol protein	281	73
8099	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	156	69
8100	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	126	42
8101	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	126	65
8102	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	145	70
8103	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	163	71

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8104	AF130089	Homo sapiens	PRO2550	130	42
8105	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	116	57
8106	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	132	61
8107	AF090942	Homo sapiens	PRO0657	123	41
8108	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	134	38
8109	AL160371	Leishmania major	probable (hly-6) u1102, variant a DNA, complete virion genome	101	77
8110	D38112	Homo sapiens	cytochrome c oxidase subunit 1	340	90
8111	AF130089	Homo sapiens	PRO2550	123	86
8112	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	122	90
8113	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	182	47
8114	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	101	77
8115	G00452	Homo sapiens	Human secreted protein, SEQ ID NO: 4533.	72	50
8116	D38112	Homo sapiens	NADH dehydrogenase subunit 3	459	88
8117	L17318	Rattus norvegicus	proline-rich proteoglycan	110	45
8118	S79410	Mus musculus	nuclear localization signal binding protein	125	62
8119	G03639	Homo sapiens	Human secreted protein, SEQ ID NO: 7720.	106	78
8120	D38112	Homo sapiens	NADH dehydrogenase subunit 1	106	84
8121	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	110	45
8122	D86854	Catharanthus roseus	extensin	142	35
8123	X92485	Plasmodium vivax	pva1	144	53
8124	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	138	59
8125	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	67
8126	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	145	62
8127	X07881	Homo sapiens	proline-rich protein G1	142	37
8128	X70343	Nicotiana glauca	extensin	102	29
8129	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	113	48
8130	AF090895	Homo sapiens	PRO0117	150	71
8131	D00570	Mus musculus	open reading frame (251 AA)	130	41
8132	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	106	61
8133	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	128	61
8134	AF130079	Homo sapiens	PRO2852	181	77
8135	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	109	58
8136	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	98	64
8137	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	112	43
8138	AF119900	Homo sapiens	PRO2822	113	57
8139	D38112	Homo sapiens	NADH dehydrogenase subunit 3	427	86

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8140	AF004341	Homo sapiens	cytochrome c oxidase subunit III	155	88
8141	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	163	58
8142	D70836	Homo sapiens	Zinc-finger protein	156	47
8143	AC002291	Arabidopsis thaliana	extensin	153	37
8144	X55683	Lycopersicon esculentum	extensin (class I)	85	34
8145	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	100	76
8146	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	108	63
8147	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	110	79
8148	M22332	Homo sapiens	unknown protein	156	40
8149	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	92	76
8150	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	131	66
8151	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	441	76
8152	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	155	67
8153	AF130089	Homo sapiens	PRO2550	129	42
8154	AF130089	Homo sapiens	PRO2550	173	50
8155	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	64
8156	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	171	82
8157	L27428	Homo sapiens	reverse transcriptase	181	50
8158	U11271	Homo sapiens	thromboxane A2 receptor	138	73
8159	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	145	53
8160	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	139	58
8161	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	155	59
8162	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	64
8163	AF161361	Homo sapiens	HSPC098	89	66
8164	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	117	58
8165	AF130089	Homo sapiens	PRO2550	121	63
8166	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	148	85
8167	X92485	Plasmodium vivax	pva1	97	56
8168	X92485	Plasmodium vivax	pva1	115	57
8169	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	124	61
8170	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	60
8171	X92485	Plasmodium vivax	pva1	105	44
8172	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	75	64
8173	S79410	Mus musculus	nuclear localization signal binding protein	106	65
8174	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	108	44

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8175	Y36203	Homo sapiens	Human secreted protein #75.	150	51
8176	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	114	41
8177	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	135	68
8178	AF090928	Homo sapiens	PRO0470	119	72
8179	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	141	75
8180	AF220264	Homo sapiens	MOST-1	94	61
8181	AF119851	Homo sapiens	PRO1722	143	73
8182	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	134	64
8183	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	143	59
8184	X92485	Plasmodium vivax	pval	127	72
8185	X92485	Plasmodium vivax	pval	130	65
8186	AF119851	Homo sapiens	PRO1722	285	64
8187	AF090942	Homo sapiens	PRO0657	137	38
8188	AF090931	Homo sapiens	PRO0483	154	66
8189	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	148	43
8190	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	268	79
8191	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	110	43
8192	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	129	78
8193	AF113685	Homo sapiens	PRO0974	86	52
8194	Y36203	Homo sapiens	Human secreted protein #75.	132	61
8195	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	225	77
8196	S80119	Rattus sp.	reverse transcriptase homolog	105	40
8197	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	124	39
8198	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	121	60
8199	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	91	68
8200	Y36203	Homo sapiens	Human secreted protein #75.	131	56
8201	Y36203	Homo sapiens	Human secreted protein #75.	136	44
8202	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	166	48
8203	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	50
8204	Y36203	Homo sapiens	Human secreted protein #75.	127	58
8205	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	139	61
8206	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	190	92
8207	AF090931	Homo sapiens	PRO0483	160	87
8208	AF126163	Homo sapiens	IIHLA3 protein	107	67
8209	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	93	41
8210	Y36156	Homo sapiens	Human secreted protein #28.	100	62
8211	AF161356	Homo sapiens	HSPC093	73	60
8212	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	107	34
8213	AB046048	Macaca	unnamed protein product	146	61

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		fascicularis			
8214	AF130079	Homo sapiens	PRO2852	121	59
8215	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	109	50
8216	AF090930	Homo sapiens	PRO0478	153	79
8217	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	105	60
8218	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	135	56
8219	M11901	Rattus norvegicus	proline-rich salivary protein	102	42
8220	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	95	32
8221	X52235	Homo sapiens	ORFII	174	39
8222	AF130089	Homo sapiens	PRO2550	159	67
8223	AF068294	Homo sapiens	HDCMB45P	161	58
8224	M62387	Oryctolagus cuniculus	ubiquitin conjugating-protein	219	90
8225	AF113685	Homo sapiens	PRO0974	136	65
8226	D38112	Homo sapiens	NADH dehydrogenase subunit 3	430	85
8227	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	115	58
8228	Y36156	Homo sapiens	Human secreted protein #28.	117	50
8229	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	130	44
8230	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	145	50
8231	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	105	46
8232	S62928	Homo sapiens	PRB1M protein precursor	113	37
8233	AB047600	Macaca fascicularis	hypothetical protein	142	62
8234	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	104	48
8235	U12695	Pan paniscus	cytochrome oxidase subunit II	259	84
8236	K01664	Drosophila melanogaster	Bkm-like protein	116	61
8237	AF116661	Homo sapiens	PRO1438	135	56
8238	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	107	53
8239	U93572	Homo sapiens	p40	168	49
8240	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	100	72
8241	Z70292	Homo sapiens	chemokine CC-1	231	83
8242	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	119	82
8243	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	97	83
8244	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	114	78
8245	G00358	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	81	65
8246	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	74	60
8247	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	115	58
8248	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	127	58
8249	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	107	84
8250	AF118082	Homo sapiens	PRO1902	136	50

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8251	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	196	59
8252	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	106	81
8253	AFI30089	Homo sapiens	PRO2550	143	53
8254	AK024455	Homo sapiens	FLJ00047 protein	151	68
8255	AK022821	Homo sapiens	unnamed protein product	140	68
8256	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	143	53
8257	M24509	Mus musculus	ferritin heavy chain	347	69
8258	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	142	57
8259	U93570	Homo sapiens	p40	254	57
8260	AF218028	Homo sapiens	unknown	129	71
8261	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	77	68
8262	D38112	Homo sapiens	cytochrome c oxidase subunit 3	604	90
8263	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	132	60
8264	AL139298	Streptomyces coelicolor A3(2)	putative membrane protein	92	34
8265	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	138	70
8266	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	100	64
8267	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	113	38
8268	X92485	Plasmodium vivax	pva1	102	63
8269	X61048	Hydra sp.	mini-collagen	110	46
8270	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	88	82
8271	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	121	75
8272	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	107	48
8273	AF090944	Homo sapiens	PRO0663	122	42
8274	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	81	85
8275	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	140	54
8276	AFI30089	Homo sapiens	PRO2550	275	56
8277	L27428	Homo sapiens	reverse transcriptase	105	27
8278	S79410	Mus musculus	nuclear localization signal binding protein	112	54
8279	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	159	73
8280	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	109	71
8281	AFI04921	Homo sapiens	succinyl-CoA synthetase alpha subunit	188	42
8282	Y86248	Homo sapiens	Human secreted protein HCHIPF68, SEQ ID NO:163.	117	39
8283	X55683	Lycopersicon esculentum	extensin (class I)	96	36
8284	AF225910	Mus musculus	DAZ-associated protein 1	117	33
8285	AFI30089	Homo sapiens	PRO2550	347	75
8286	AB046100	Macaca fascicularis	unnamed protein product	140	45
8287	X55684	Lycopersicon	extensin (class I)	67	45

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		esculentum			
8288	AF029670	Homo sapiens	Rad51C truncated protein	186	69
8289	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	149	50
8290	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	119	67
8291	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	152	50
8292	D89999	Gallus gallus	muscle derived protein	1134	66
8293	L11566	Homo sapiens	ribosomal protein L18	335	69
8294	W61170	Homo sapiens	Partial polypeptide sequence from CP140 partial cDNA.	441	95
8295	S62077	Homo sapiens	HP1Hs alpha=25 kda chromosomal autoantigen	175	94
8296	AF119882	Homo sapiens	PRO2492	125	48
8297	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	54
8298	AK025116	Homo sapiens	unnamed protein product	259	82
8300	X92485	Plasmodium vivax	pva1	162	47
8301	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	137	76
8302	AF092176	Homo sapiens	MHC class II antigen	280	84
8303	AF118082	Homo sapiens	PRO1902	174	52
8304	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	105	50
8305	AK023563	Homo sapiens	unnamed protein product	244	60
8306	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	136	66
8307	U15647	Mus musculus	reverse transcriptase	107	38
8308	R96800	Homo sapiens	Human histocyte-secreted factor HSF.	110	40
8309	AB005540	Rattus rattus	PCTAIRE2	166	59
8310	M37679	Mus musculus	Ig heavy chain precursor	95	64
8311	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	137	82
8312	W29643	Homo sapiens	Human secreted protein CW383.1.	312	100
8313	AF113685	Homo sapiens	PRO0974	116	39
8314	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	128	69
8315	Z28407	Homo sapiens	ribosomal protein L8	497	78
8316	AE003536	Drosophila melanogaster	CG6451 gene product	237	51
8317	M19419	Mus musculus	proline-rich salivary protein	115	39
8318	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	92	53
8319	Y29862	Homo sapiens	Human secreted protein clone du515.21.	399	81
8320	Z34278	Homo sapiens	mucin	103	25
8321	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	142	91
8322	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	82	62
8323	Z46791	Caenorhabditis elegans	contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=67.1, E-value=1.2e-16, N=3; PF01484 (Nematode cuticle collagen N-terminal domain), Score=82.0, E-value=3.9e-21, N=1	122	37
8324	AF021232	Homo sapiens	TRAIL-R4-A	113	100

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8325	AB046085	Macaca fascicularis	unnamed protein product	292	75
8326	AF113944	Muntiacus muntjak	prion protein	96	39
8327	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	125	63
8328	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	123	62
8329	AJ005897	Homo sapiens	JM5	275	73
8330	AF119900	Homo sapiens	PRO2822	138	76
8331	AF163573	Homo sapiens	CARL	359	84
8332	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	103	37
8333	AF026246	Homo sapiens	HERV-E integrase	354	78
8334	J03756	Homo sapiens	hGH-V2	362	82
8335	AB001517	Homo sapiens	KNP-I alpha protein	126	76
8336	X97490	Mus musculus	PNG protein	469	98
8337	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	74
8338	V18354_cd1	Homo sapiens	17-NOV-1992 Human R20 seven transmembrane (7TM) receptor genomic DNA.	379	92
8339	V18354_cd1	Homo sapiens	17-NOV-1992 Human R20 seven transmembrane (7TM) receptor genomic DNA.	402	93
8340	Z11502	Homo sapiens	intestine-specific annexin	385	89
8341	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8155.	110	54
8342	AC003113	Arabidopsis thaliana	F24O1.6	68	50
8343	X12517	Homo sapiens	C protein (AA 1-159)	321	82
8344	D86549	Homo sapiens	p97 homologous protein	279	96
8345	Y73384	Homo sapiens	HTRM clone Z284580 protein sequence.	1513	100
8346	AP001745	Homo sapiens	human cDNA DKFZp586F0422, Accession No. AL050173	118	40
8347	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	121	49
8348	AF091090	Homo sapiens	unknown	125	44
8349	AF106542	Homo sapiens	pregnancy-specific beta-1 glycoprotein 1	145	100
8350	AF090942	Homo sapiens	PRO0657	252	65
8351	L23116	Homo sapiens	galactocerebrosidase	185	85
8352	AJ243803	Streptomyces coelicolor A3(2)	hypothetical protein	97	36
8353	Y11339	Homo sapiens	GalNAc alpha-2,6-sialyltransferase I	306	100
8354	U09477	Homo sapiens	p53-binding protein	388	100
8355	L27584	Homo sapiens	Ca channel B3 subunit	197	100
8356	AF071569	Homo sapiens	multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform	574	100
8357	W54282	Homo sapiens	Protein sequence of the di-alpha hemoglobin gene contained in pSS1.	321	81
8358	Y12916	Homo sapiens	Amino acid sequence of a human secreted peptide.	759	100
8359	AF038961	Homo sapiens	SL15 protein	166	100
8360	W75093	Homo sapiens	Human secreted protein encoded by gene 37 clone HFVGS85.	328	90
8361	R95326	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 2DD).	386	97



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8362	AF026954	Bos taurus	pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDPt	269	88
8363	X07855	Homo sapiens	G-Protein	289	98
8364	AL110247	Homo sapiens	hypothetical protein	265	97
8365	AB046774	Homo sapiens	KIAA1554 protein	3619	99
8366	M10050	Homo sapiens	fatty acid binding protein	97	100
8367	M20882	Homo sapiens	pregnancy-specific beta-glycoprotein c	1097	99
8368	AB051901	Homo sapiens	VDUP1	662	98
8369	U72678	Mus musculus	EF-9	176	65
8370	AL117237	Homo sapiens	hypothetical protein	478	60
8371	M10617	Homo sapiens	L-FABP	104	84
8372	AJ249980	Homo sapiens	hypothetical protein	1527	97
8373	AF003136	Caenorhabditis elegans	contains weak similarity to an AMP-binding motif	242	55
8374	X91638	Gallus gallus	BIRM protein	225	90
8375	W75093	Homo sapiens	Human secreted protein encoded by gene 37 clone HFVGS85.	369	100
8376	Z36714	Homo sapiens	cyclin F	519	95
8377	X86401	Homo sapiens	L-arginine: glycine amidotransferase	200	97
8378	M12413	Homo sapiens	apolipoprotein B100	1278	99
8379	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	159	66
8380	AF151860	Homo sapiens	CGI-102 protein	202	77
8381	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	255	92
8382	AF017807	Homo sapiens	Arp2/3 complex 16kDa subunit	418	87
8383	U28727	Homo sapiens	pregnancy-associated plasma protein-A preproform	196	97
8384	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	128	85
8385	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	203	69
8386	AF090931	Homo sapiens	PRO0483	145	77
8387	S63758	Mus sp.	metallothionein-I gene transcription activator	324	98
8388	W89030	Homo sapiens	Polypeptide fragment encoded by gene 165.	174	66
8389	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	93	70
8390	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	157	46
8391	V29245_cd1	Homo sapiens	15-NOV-1996 Nucleotide sequence of the human selenium-binding protein.	421	82
8392	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	184	77
8393	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	99	77
8394	AK023563	Homo sapiens	unnamed protein product	285	75
8395	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	161	75
8396	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	121	61
8397	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	108	70
8398	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	57
8399	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	108	63
8400	W88607	Homo sapiens	Secreted protein encoded by gene 74 clone HHSEG23.	146	55

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8401	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	90	69
8402	AF119851	Homo sapiens	PRO1722	133	65
8403	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	67	76
8404	L06498	Homo sapiens	ribosomal protein S20	170	94
8405	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	58
8406	AF118086	Homo sapiens	PRO1992	142	80
8407	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	153	81
8408	AF090919	Homo sapiens	PRO0327	96	74
8409	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	127	62
8410	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	100
8411	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	103	75
8412	AF116715	Homo sapiens	PRO2829	158	76
8413	AF229067	Homo sapiens	PADI-H protein	137	56
8414	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	131	77
8415	AF068294	Homo sapiens	HDGMB45P	132	54
8416	W34499	Homo sapiens	Obesity receptor C protein.	251	77
8417	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	272	57
8418	S79410	Mus musculus	nuclear localization signal binding protein	113	54
8419	AK025047	Homo sapiens	unnamed protein product	128	58
8420	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	130	46
8421	AL132841	Caenorhabditis elegans	Y15E3A.3	135	56
8422	AF130051	Homo sapiens	PRO0898	164	72
8423	G00092	Homo sapiens	Human secreted protein, SEQ ID NO: 4173.	161	96
8424	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	100
8425	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	134	75
8426	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	91	48
8427	AF194641	Homo sapiens	immunoglobulin lambda light chain variable region	174	69
8428	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	146	68
8429	M64322	Homo sapiens	protein tyrosine phosphatase	201	100
8430	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	135	55
8431	AF090931	Homo sapiens	PRO0483	158	87
8432	J04495	Macaca mulatta	alpha-globin	150	100
8433	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	150	78
8434	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	137	48
8435	AJ272324	Homo sapiens	adaptor molecule-1	333	100
8436	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	91	48
8437	M18085	Homo sapiens	glycoprotein IIb	154	100

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8438	X92485	Plasmodium vivax	pva1	138	64
8439	G03136	Homo sapiens	Human secreted protein, SEQ ID NO: 7217.	126	56
8440	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	105	72
8441	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein thala.	122	55
8442	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	139	69
8443	Y36203	Homo sapiens	Human secreted protein #75.	103	70
8444	AB034633	Mus musculus	deubiquitinating enzyme	129	100
8445	U01849	Trypanosoma brucei	ORF2	95	41
8446	J05497	Rattus norvegicus	snRNP-associated polypeptide N	115	37
8447	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	137	50
8448	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	222	100
8449	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	94
8450	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	63
8451	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	91
8452	W78226	Homo sapiens	Fragment of human secreted protein encoded by gene 1.	804	97
8453	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	109	100
8454	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	138	88
8455	AF099505	Homo sapiens	colon carcinoma related protein	100	63
8456	AF217511	Homo sapiens	uncharacterized bone marrow protein BM034	130	96
8457	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	70
8458	L17007	Didelphis marsupialis	protamine 1	101	80
8459	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	145	62
8460	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	121	75
8461	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	110	81
8462	AF016371	Homo sapiens	U-snRNP-associated cyclophilin	108	70
8463	Y19767	Homo sapiens	SEQ ID NO 485 from WO922243.	80	93
8464	AF130089	Homo sapiens	PRO2530	190	65
8465	AF197913	Helicoverpa armigera nuclear polyhedrosis virus	basic DNA-binding protein BDBP	159	55
8466	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	183	70
8467	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	97	60
8468	AF118082	Homo sapiens	PRO1902	72	42
8469	AF217449	Schistosoma mekongi	NADH dehydrogenase subunit 6	107	40
8470	G03258	Homo sapiens	Human secreted protein, SEQ ID NO:	88	75

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7339.		
8471	AF090931	Homo sapiens	PRO0483	161	79
8472	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	127	56
8473	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	50
8474	AF022789	Homo sapiens	ubiquitin hydrolyzing enzyme I	140	100
8475	X03145	Homo sapiens	pot. ORF VI	349	81
8476	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	65
8477	R59842	Homo sapiens	ApoE4LI protease.	115	69
8478	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	112	56
8479	K01664	Drosophila melanogaster	Bkm-like protein	140	44
8480	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	95	70
8481	AF090931	Homo sapiens	PRO0483	111	67
8482	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	122	92
8483	M59297	Homo sapiens	ORF 3	102	39
8484	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	148	72
8485	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	136	65
8486	AF032906	Homo sapiens	cathepsin Z precursor; CTSZ	299	100
8487	X15917	Paramecium aurelia	ND2 protein (AA 1-193) (unusual start codon)	94	35
8488	U93574	Homo sapiens	putative p150	109	35
8489	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	142	72
8490	X92485	Plasmodium vivax	pval	120	85
8491	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	109	42
8492	M15530	Homo sapiens	B-cell growth factor	126	64
8493	AF090895	Homo sapiens	PRO0117	123	60
8494	G02403	Homo sapiens	Human secreted protein, SEQ ID NO: 6484.	166	100
8495	AF116661	Homo sapiens	PRO1438	126	63
8496	AF130089	Homo sapiens	PRO2550	298	70
8497	AF090895	Homo sapiens	PRO0117	113	75
8498	AF090930	Homo sapiens	PRO0478	142	68
8499	AF126163	Homo sapiens	HLA3 protein	159	72
8500	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	109	75
8501	S79410	Mus musculus	nuclear localization signal binding protein	98	48
8502	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	132	63
8503	AF119851	Homo sapiens	PRO1722	107	53
8504	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	158	67
8505	AF090931	Homo sapiens	PRO0483	128	50
8506	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	126	56
8507	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	154	82
8508	X92485	Plasmodium	pval	83	70



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6953.		
8544	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	117	85
8545	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	110	95
8546	AF119851	Homo sapiens	PRO1722	146	80
8547	U49973	Homo sapiens	ORF2: function unknown	105	86
8548	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	71
8549	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	152	53
8550	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	80	40
8551	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	140	74
8552	V00672	Pan troglodytes	reading frame protein 4	142	92
8553	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	164	63
8554	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	148	71
8555	AB046100	Macaca fascicularis	unnamed protein product	144	58
8556	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	322	73
8557	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	140	62
8558	U30888	Homo sapiens	tRNA-Guanine Transglycosylase	276	86
8559	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	114	71
8560	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	108	72
8561	G03136	Homo sapiens	Human secreted protein, SEQ ID NO: 7217.	110	57
8562	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	140	83
8563	W34499	Homo sapiens	Obesity receptor C protein.	188	92
8564	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	124	56
8565	L07946	Volvox carteri	histone H1-I	108	38
8566	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	132	77
8567	M13941	Human herpesvirus 4	nuclear antigen 1	100	43
8568	Y36156	Homo sapiens	Human secreted protein #28.	136	67
8569	X70343	Nicotiana sylvestris	extensin	92	34
8570	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	381	87
8571	V00672	Pan troglodytes	reading frame protein 4	146	93
8572	D38116	Pan paniscus	ATPase subunit 6	116	96
8573	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	132	52
8574	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	217	100
8575	M58009	Pan troglodytes	cytochrome c oxidase subunit II	271	84
8576	D38112	Homo sapiens	ATPase subunit 6	117	96
8577	D38112	Homo sapiens	ATPase subunit 6	180	93
8578	D38112	Homo sapiens	NADH dehydrogenase subunit 1	179	91
8579	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	88

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8580	M15530	Homo sapiens	B-cell growth factor	109	71
8581	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	77
8582	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	109	47
8583	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	71
8584	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	241	97
8585	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	185	80
8586	M28016	Homo sapiens	cytochrome b	129	92
8587	M58009	Pan troglodytes	cytochrome c oxidase subunit II	153	96
8588	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	90
8589	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	109	51
8590	L00016	Homo sapiens	urfa	176	94
8591	AF150105	Homo sapiens	small zinc finger-like protein	523	100
8592	U15306	Homo sapiens	NFX1	123	95
8594	R44519	Homo sapiens	Adult: human alpha-globin V1078.	222	78
8595	Y03000	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	128	70
8596	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	151	90
8597	X67688	Homo sapiens	transketolase	123	84
8598	L00016	Homo sapiens	urfa	130	85
8599	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	109	54
8600	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	89
8601	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	151	54
8602	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	115	43
8603	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	95
8604	S79980	Bos taurus	ribosomal protein L37	109	84
8605	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	127	48
8606	D38112	Homo sapiens	ATPase subunit 6	202	100
8607	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	42
8608	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	127	58
8609	AF229067	Homo sapiens	PADI-H protein	112	78
8610	AF130089	Homo sapiens	PRO2550	125	86
8611	J03071	Homo sapiens	chorionic somatomammotropin CS-5	710	97
8612	AL390114	Leishmania major	extremely cysteine/valine rich protein	104	41
8613	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	84
8614	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	70
8615	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	91
8616	M28016	Homo sapiens	cytochrome b	148	93
8617	AF118082	Homo sapiens	PRO1902	94	66
8618	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	182	82
8619	X02585	Xenopus laevis	unidentified open reading frame 1 (166	170	72

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			aa)		
8620	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	125	57
8621	AC004450	Arabidopsis thaliana	putative extensin	140	48
8622	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	79
8623	AF130089	Homo sapiens	PRO2550	150	78
8624	L00016	Homo sapiens	ur14	280	92
8625	AF130051	Homo sapiens	PRO0898	161	76
8626	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	123	49
8627	L00016	Homo sapiens	ur14	201	95
8628	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	169	82
8629	AF119851	Homo sapiens	PRO1722	171	65
8630	X55654	Homo sapiens	cytochrome C oxidase II subunit	120	92
8631	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	56
8632	X55654	Homo sapiens	cytochrome C oxidase II subunit	107	95
8633	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	132	86
8634	AJ224997	Rattus norvegicus	huntingtin	73	59
8635	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	80
8636	M19061	Ateles geoffroyi	delta-globin	100	40
8637	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	102	65
8638	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	104	50
8639	AF116715	Homo sapiens	PRO2829	158	76
8640	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	142	62
8641	Y09010	Mus musculus	Ser/Thr kinase	193	95
8642	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	227	79
8643	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	116	95
8644	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	88
8645	V46311_cd1	Homo sapiens	12-JAN-1998 Human secreted protein cDNA from clone D157.	197	100
8646	Y17379	Homo sapiens	NADH:ubiquinone oxidoreductase 51-kD subunit	240	97
8647	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	142	68
8648	AJ388520	Canis familiaris	Ribosomal protein	134	100
8649	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	136	56
8650	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	116	80
8651	S79410	Mus musculus	nuclear localization signal binding protein	99	36
8652	G00492	Homo sapiens	Human secreted protein, SEQ ID NO: 4573.	136	64
8653	AF229067	Homo sapiens	PADI-H protein	134	69
8654	AF090942	Homo sapiens	PRO0657	103	42
8655	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	84



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8656	U37359	Homo sapiens	MRE111 homologue hMre11	238	97
8657	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	113	60
8658	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	124	83
8659	AF161356	Homo sapiens	HSPC093	149	64
8660	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	121	44
8661	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	107	37
8662	U19098	Lycopersicon chilense	proline-rich protein	72	48
8663	AF118082	Homo sapiens	PRO1902	95	75
8664	AF130089	Homo sapiens	PRO2550	307	79
8665	AL390114	Leishmania major	extremely cysteine/valine rich protein	115	40
8666	X55683	Lycopersicon esculentum	extensin (class I)	102	32
8667	AK026841	Homo sapiens	unnamed protein product	276	100
8668	AL109963	Homo sapiens	dJ1183J2.1 (FSH primary response (LRPR1, rat) homolog 1)	597	100
8669	Y01181	Homo sapiens	Polypeptide fragment encoded by gene 12.	123	58
8670	W48352	Homo sapiens	Human breast cancer related protein BCFLT1.	103	65
8671	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	121	61
8672	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	82
8673	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	211	93
8674	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	126	61
8675	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	114	66
8676	X55691	Lycopersicon esculentum	glycine-rich protein	85	38
8677	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	188	80
8678	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	183	75
8679	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	71
8680	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	96	82
8681	U80761	Homo sapiens	CTG26 alternate open reading frame	136	88
8682	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	137	93
8683	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	107	45
8684	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	90
8685	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	127	55
8686	W64486	Homo sapiens	Human DR3 protein.	139	100
8687	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	134	33
8688	K03202	Homo sapiens	salivary proline-rich protein precursor	119	35
8689	U36448	Homo sapiens	Ca2+-dependent activator protein for	107	91

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			secretion		
8690	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	80	43
8691	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	147	74
8692	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	126	95
8693	AF130089	Homo sapiens	PRO2550	126	35
8694	M58009	Pan troglodytes	cytochrome c oxidase subunit II	233	97
8695	M11902	Mus musculus	proline-rich salivary protein	98	35
8696	W34499	Homo sapiens	Obesity receptor C protein.	263	83
8697	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	181	73
8698	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	48
8699	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	88
8700	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	51
8701	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	73
8702	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	133	62
8703	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	92
8704	D38112	Homo sapiens	ATPase subunit 6	117	96
8705	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	97	58
8706	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	115	79
8707	AF118086	Homo sapiens	PRO1992	167	81
8708	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	114	51
8709	L10908	Mus musculus	Gcap1 gene product	179	38
8710	S79410	Mus musculus	nuclear localization signal binding protein	135	69
8711	AF130089	Homo sapiens	PRO2550	399	78
8712	X55654	Homo sapiens	cytochrome C oxidase II subunit	107	95
8713	AF118082	Homo sapiens	PRO1902	123	58
8714	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	173	81
8715	V35554_cdl	Homo sapiens	21-NOV-1996 Human tumour antigen protein (clone 3) encoding cDNA.	258	83
8716	AF130089	Homo sapiens	PRO2550	143	51
8717	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	92	52
8718	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	147	71
8719	AF153208	Homo sapiens	GC-rich sequence DNA-binding factor candidate	115	70
8720	AF090931	Homo sapiens	PRO0483	145	87
8721	X92485	Plasmodium vivax	pva1	125	79
8722	U72543	Sus scrofa	ubiquitin-like/S30 ribosomal fusion protein	201	97
8723	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	223	85
8724	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	121	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8725	AF130051	Homo sapiens	PRO0898	102	72
8726	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	185	78
8727	R24750	Homo sapiens	hGH variant #38 - 174S 176Y 10F 14S 18F 21L 167S 171D 175T 179T.	116	82
8728	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	92	72
8729	X53375	Helianthus annuus	anther-specific protein SF18	114	39
8730	S74221	Homo sapiens	IK factor—cytokine down-regulating HLA class II	159	42
8731	AC003058	Arabidopsis thaliana	unknown protein	166	89
8732	AB027508	Homo sapiens	hVPS11	194	50
8733	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	144	93
8734	AF266479	Homo sapiens	rectachrome 1	116	74
8735	AL132841	Caenorhabditis elegans	Y15E3A.3	125	60
8736	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	152	65
8737	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	79	56
8738	U93565	Homo sapiens	putative p150	190	52
8739	AF026689	Homo sapiens	prostate-specific transglutaminase	117	57
8740	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	109	70
8741	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	165	61
8742	M58009	Pan troglodytes	cytochrome c oxidase subunit II	213	97
8743	M17887	Homo sapiens	acidic ribosomal phosphoprotein (P2)	106	74
8744	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	116	49
8745	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	134	68
8746	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	135	71
8747	M76546	Helianthus annuus	hydroxyproline-rich protein	94	40
8748	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	173	76
8749	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	67
8750	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	272	57
8751	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	131	71
8752	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	123	37
8753	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	180	55
8754	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	105	44
8755	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	78
8756	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	284	87
8757	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	150	89

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8758	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	103	40
8759	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	120	61
8760	AF132984	Homo sapiens	nuclear pore complex interacting protein NP1P	196	94
8761	AF130079	Homo sapiens	PRO2852	125	65
8762	AF155232	Pisum sativum	extensin	177	42
8763	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	95
8764	X75438	Sus scrofa	homologue of proline/arginine rich antibacterial peptides	96	38
8765	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	157	96
8766	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	137	75
8767	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	207	95
8768	AL161543	Arabidopsis thaliana	extensin like protein	100	38
8769	K03202	Homo sapiens	salivary proline-rich protein precursor	110	47
8770	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	178	78
8771	D83407	Homo sapiens	a thyroid hormone responsive gene in human skin fibroblasts	133	100
8772	V00662	Homo sapiens	URF A6L (NADH dehydrogenase subunit)	172	73
8773	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	107	66
8774	AL390114	Leishmania major	extremely cysteine/valine rich protein	117	100
8775	AF090931	Homo sapiens	PRO0483	175	88
8776	S79410	Mus musculus	nuclear localization signal binding protein	125	58
8777	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	126	73
8778	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	154	70
8779	AL359782	Trypanosoma brucei	possible (hfv-6) u1102, variant a dna, complete virion genome.	149	50
8780	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	170	91
8781	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	103	65
8782	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	184	70
8783	AC003058	Arabidopsis thaliana	unknown protein	169	97
8784	U55376	Caenorhabditis elegans	F16H11.2 gene product	141	90
8785	U55376	Caenorhabditis elegans	F16H11.2 gene product	150	100
8786	AL132841	Caenorhabditis elegans	Y15E3A.3	127	96
8787	AF266479	Homo sapiens	rectachrome 1	148	61
8788	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	106	95
8789	AL132841	Caenorhabditis elegans	Y15E3A.3	162	96
8790	AC006693	Caenorhabditis	Hypothetical protein W02H5.e	180	94

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		<i>elegans</i>			
8791	U28971	<i>Caenorhabditis elegans</i>	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	159	80
8792	AF150105	<i>Homo sapiens</i>	small zinc finger-like protein	505	98
8793	AL390935	<i>Leishmania major</i>	probable pro0195	85	31
8794	Y19767	<i>Homo sapiens</i>	SEQ ID NO 485 from WO9922243.	115	55
8795	AF118082	<i>Homo sapiens</i>	PRO1902	123	75
8796	D38112	<i>Homo sapiens</i>	ATPase subunit 6	438	82
8797	AF118086	<i>Homo sapiens</i>	PRO1992	156	81
8798	Y53037	<i>Homo sapiens</i>	Human secreted protein clone dx219 13 protein sequence SEQ ID NO:80.	196	100
8799	X92485	<i>Plasmodium vivax</i>	pval	132	63
8800	G02532	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 6613.	170	65
8801	G00397	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 4478.	123	58
8802	AF116909	<i>Homo sapiens</i>	unknown	116	63
8803	X92485	<i>Plasmodium vivax</i>	pval	127	82
8804	G03438	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7519.	140	67
8805	Z95114	<i>Homo sapiens</i>	bK212A2.2 (apolipoprotein L 2)	294	100
8806	AF143369	<i>Mus musculus</i>	msg1-related protein 2	348	83
8807	G00500	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 4581.	110	76
8808	AP000616	<i>Oryza sativa</i>	similar to RING-H2 finger protein RHA1a (AF078683)	129	91
8809	AF230279	<i>Caenorhabditis elegans</i>	SWB-like protein; PSA-1	126	37
8810	D38112	<i>Homo sapiens</i>	NADH dehydrogenase subunit 4L	168	82
8811	Y86248	<i>Homo sapiens</i>	Human secreted protein HCHPF68, SEQ ID NO:163.	122	54
8812	D38112	<i>Homo sapiens</i>	ATPase subunit 6	207	100
8813	W99376	<i>Homo sapiens</i>	Human fibroblast growth factor 2 24 kD isoform N-terminus.	93	41
8814	G03043	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7124.	157	57
8815	X54978	<i>Bos taurus</i>	17,000 dalton myosin light chain	133	96
8816	M58459	<i>Homo sapiens</i>	ribosomal protein S4Y isoform	260	100
8817	D38112	<i>Homo sapiens</i>	NADH dehydrogenase subunit 1	256	90
8818	U23947	<i>Mycoplasma pulmonis</i>	VsaD1	132	31
8819	G03172	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7253.	140	69
8820	L00016	<i>Homo sapiens</i>	urf4	205	90
8821	X55683	<i>Lycopersicon esculentum</i>	extensin (class I)	111	43
8822	AL160493	<i>Leishmania major</i>	probable (hiv-6) u1102, variant a DNA, complete virion genome	94	43
8823	X66285	<i>Mus musculus</i>	HCI ORF	94	53
8824	AF061340	<i>Artibeus jamaicensis</i>	F1 ATPase subunit 6	97	90
8825	M18093	<i>Phaseolus vulgaris</i>	hydroxyproline-rich glycoprotein	123	36
8826	AF119855	<i>Homo sapiens</i>	PRO1847	113	52

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8827	M28016	Homo sapiens	cytochrome b	140	93
8828	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	56
8829	AK024455	Homo sapiens	FLJ00047 protein	145	59
8830	D38112	Homo sapiens	ATPase subunit 6	194	95
8831	D38112	Homo sapiens	ATPase subunit 6	184	90
8832	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	60
8833	AF130079	Homo sapiens	PRO2852	115	88
8834	AB003784	Drosophila simulans	Histone H3	135	100
8835	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	173	82
8836	X70343	Nicotiana glauca	extensin	112	37
8837	L17318	Rattus norvegicus	proline-rich proteoglycan	142	38
8838	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	148	74
8839	W34625	Homo sapiens	Human C3 protein mutant FT-3.	277	100
8840	AF116638	Homo sapiens	PRO1546	78	41
8841	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	138	61
8842	AF130087	Homo sapiens	PRO2411	131	67
8843	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	150	72
8844	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	155	60
8845	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	108	66
8846	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	68
8847	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	146	70
8848	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	68
8849	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	273	79
8850	K02120	Bovine leukemia virus	gag	201	54
8851	AF229067	Homo sapiens	PADI-H protein	162	57
8852	AF090931	Homo sapiens	PRO0483	125	82
8853	R14584	Homo sapiens	TGF beta 1 binding protein encoded by clone BPA 13.	189	100
8854	U52197	Mus musculus	poly(A) polymerase III	183	85
8855	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	193	72
8856	G00549	Homo sapiens	Human secreted protein, SEQ ID NO: 4630.	104	66
8857	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	93	64
8858	Q55625_cdl	Homo sapiens	22-JUN-1992 Human beta globin 5'-UTR-CDS-3'-UTR.	412	98
8859	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	152	67
8860	G02828	Homo sapiens	Human secreted protein, SEQ ID NO: 6909.	112	72
8861	AF130079	Homo sapiens	PRO2852	160	64
8862	G00407	Homo sapiens	Human secreted protein, SEQ ID NO:	101	61

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4488.		
8863	X64707	Homo sapiens	BBC1	216	100
8864	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	127	65
8865	G00092	Homo sapiens	Human secreted protein, SEQ ID NO: 4173.	210	100
8866	AL137351	Homo sapiens	hypothetical protein	327	100
8867	AF090942	Homo sapiens	PRO0657	105	38
8868	AK023050	Homo sapiens	unnamed protein product	137	60
8869	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	101	65
8870	AF216751	Homo sapiens	CDA14	282	96
8871	AL133262	Homo sapiens	dJ319D22.1 (CDC5-like protein)	158	90
8872	V32779_cd1	Homo sapiens	11-MAR-1997 Novel human F0 ATP synthase subunit encoding DNA sequence.	267	81
8873	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	118	58
8874	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	89	43
8875	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	154	63
8876	AK001873	Homo sapiens	unnamed protein product	373	100
8877	X52138	Homo sapiens	L7a protein	259	82
8878	X52138	Homo sapiens	L7a protein	273	87
8879	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	147	57
8880	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	128	57
8881	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	159	71
8882	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	153	67
8883	AF130089	Homo sapiens	PRO2550	134	79
8884	U36898	Rattus norvegicus	pheromone receptor VN6	143	53
8885	S79410	Mus musculus	nuclear localization signal binding protein	143	64
8886	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	138	92
8887	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	124	72
8888	R48296	Homo sapiens	Human PGF-2/NT-3.	118	66
8889	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	81	77
8890	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	120	50
8891	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	121	77
8892	X53375	Helianthus annuus	anther-specific protein SF18	109	64
8893	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	119	54
8894	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	136	68
8895	AF090894	Homo sapiens	PRO0113	114	60
8896	AF161356	Homo sapiens	HSPC093	148	51
8897	AF116638	Homo sapiens	PRO1546	91	45
8898	U22231	Felis catus	ribosomal protein S3a	201	100

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8899	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	114	75
8900	AF090894	Homo sapiens	PRO0113	114	61
8901	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	63
8902	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	126	95
8903	R90288	Homo sapiens	Modified pigment epithelium-derived factor (rPEDF).	258	88
8904	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	86
8905	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	66
8906	X70343	Nicotiana glauca	extensin	122	37
8907	G02586	Homo sapiens	Human secreted protein, SEQ ID NO: 6467.	162	70
8908	AF130089	Homo sapiens	PRO2550	125	85
8909	AF220264	Homo sapiens	MOST-1	113	47
8910	Y25769	Homo sapiens	Human secreted protein encoded from gene 59.	119	77
8911	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	77	52
8912	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	162	83
8913	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	104	77
8914	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	138	64
8915	AF090944	Homo sapiens	PRO0663	73	58
8916	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	151	76
8917	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	84	47
8918	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	64
8919	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	254	82
8920	AJ245416	Homo sapiens	G7b protein	360	86
8921	D90228	Homo sapiens	mitochondrial acetoacetyl-CoA thiolase precursor	190	100
8922	AF229067	Homo sapiens	PADI-H protein	157	65
8923	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	132	65
8924	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	62	68
8925	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	116	63
8926	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	65
8927	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	59
8928	AF287892	Homo sapiens	sialic acid binding immunoglobulin-like lectin 8 long splice variant	994	76
8929	AF030131	Mus musculus	Plenty of SH3s; POSH	181	77
8930	J02459	bacteriophage lambda	E (capsid component;341)	814	98
8931	U13866	unidentified cloning vector	non-functional lacZ alpha peptide	112	59



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8932	U67540	Methanococcus jannaschii	conserved hypothetical protein	98	56
8933	Z74472	Caenorhabditis elegans	<p>predicted using Genefinder—contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=84.3, E-value=8.1e-22, N=2; PF01484 (Nematode cuticle collagen N-terminal domain), Score=34.2, E-value=9.9e-07, N=1—cDNA EST yk100d10.3 comes from this gene; cDNA EST EMBL-D65979 comes from this gene—cDNA EST yk100d4.3 comes from this gene; cDNA EST yk123g7.3 comes from this gene—cDNA EST yk58e6.3 comes from this gene; cDNA EST yk67a5.3 comes from this gene—cDNA EST EMBL-T01590 comes from this gene; cDNA EST yk60c11.3 comes from this gene—cDNA EST yk89c10.3 comes from this gene; cDNA EST yk85g9.3 comes from this gene—cDNA EST yk83e2.5 comes from this gene; cDNA EST yk75f2.3 comes from this gene—cDNA EST CEESK90F comes from this gene; cDNA EST yk79f5.5 comes from this gene—cDNA EST yk64b12.3 comes from this gene; cDNA EST yk64h9.3 comes from this gene—cDNA EST yk74d1.3 comes from this gene; cDNA EST yk75e4.3 comes from this gene—cDNA EST yk83e2.3 comes from this gene; cDNA EST yk91c12.3 comes from this gene—cDNA EST yk98f2.3 comes from this gene; cDNA EST yk60h4.5 comes from this gene—cDNA EST yk60c11.5 comes from this gene; cDNA EST yk64h9.5 comes from this gene—cDNA EST yk64a9.5 comes from this gene; cDNA EST yk64b12.5 comes from this gene—cDNA EST yk67a5.5 comes from this gene; cDNA EST yk74d1.5 comes from this gene—cDNA EST yk75e4.5 comes from this gene; cDNA EST yk75f2.5 comes from this gene—cDNA EST yk79e6.5 comes from this gene; cDNA EST yk80d2.5 comes from this gene—cDNA EST yk85g9.5 comes from this gene; cDNA EST yk89c10.5 comes from this gene—cDNA EST yk89e4.5 comes from this gene; cDNA EST yk90e11.5 comes from this gene—cDNA EST yk91c12.5 comes from this gene; cDNA EST yk96e2.5 comes from this gene—cDNA EST yk98c2.5 comes from this gene; cDNA EST yk98f2.5 comes from this gene—cDNA EST yk98h11.5 comes</p>	101	38

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			from this gene; cDNA EST yk107e7.5 comes from this gene-cDNA EST yk313g9.3 comes from this gene; cDNA EST yk313g9.5 comes from this gene-cDNA EST yk312g1.3 comes from this gene; cDNA EST yk312g1.5 comes from this gene-cDNA EST yk293c4.3 comes from this gene; cDNA EST yk293c4.5 comes from this gene		
8934	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	63
8935	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	48
8936	X03741	Homo sapiens	myosin heavy chain (635 AA)	1343	99
8937	M29295	Rattus norvegicus	small nuclear ribonucleoparticle-associated protein	106	52
8938	D00097	Homo sapiens	serum amyloid P component	188	100
8939	W34499	Homo sapiens	Obesity receptor C protein.	255	83
8940	L00016	Homo sapiens	urf4	293	83
8941	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	164	94
8942	AB007148	Homo sapiens	ribosomal protein S3a	153	73
8943	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	213	95
8944	M10119	Homo sapiens	ferritin light subunit	129	100
8945	M74718	Homo sapiens	SEF2-1A protein	118	84
8946	AL355178	Homo sapiens	dJ947L8.1.6 (novel CUB and Sushi (SCR repeat) domain protein)	366	51
8947	Y56033	Homo sapiens	Polyproline-rich domain from dynamin.	70	51
8948	X06547	Homo sapiens	glutathione S-transferase (GST-P1) (AA 1 - 210)	172	97
8949	AF119851	Homo sapiens	PRO1722	154	78
8950	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	123	88
8951	X54802	Homo sapiens	cytochrome-c oxidase subunit IV	116	95
8952	AJ011580	bacteriophage PS34	gp23	338	98
8953	Y59441	Homo sapiens	Human delta3 fragment #5.	271	96
8954	J02459	bacteriophage lambda	B (capsid component;533)	807	99
8955	AL132841	Caenorhabditis elegans	Y15E3A.3	172	94
8956	W34499	Homo sapiens	Obesity receptor C protein.	166	89
8957	X92485	Plasmodium vivax	pva1	135	71
8958	AB010340	Mus musculus	mszf81	122	60
8959	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	103	51
8960	X14898	Cricetus sp.	ORF (AA 1-286) (1 is 2nd base in codon)	108	54
8961	AF090931	Homo sapiens	PRO0483	119	82
8962	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	130	72
8963	AF170724	Homo sapiens	cell cycle checkpoint protein CHFR	1364	99
8964	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	151	43
8965	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	250	74

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8966	Y87233	Homo sapiens	Human signal peptide containing protein HSPP-10 SEQ ID NO:10.	445	100
8967	AF127085	Mus musculus	semaphorin cytoplasmic domain-associated protein 3B	112	80
8968	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	109	46
8969	AF090894	Homo sapiens	PRO0113	153	61
8970	Y19730	Homo sapiens	SEQ ID NO 448 from WO9922243.	158	49
8971	U38544	Mus musculus	alpha-1 type I collagen	102	52
8972	X92485	Plasmodium vivax	pval	113	50
8973	AF241228	Xenopus laevis	Friend of GATA	143	100
8974	AF090930	Homo sapiens	PRO0478	79	41
8975	AF238374	Homo sapiens	mutant fibroblast growth factor receptor 3; FGFR3	115	50
8976	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	99	43
8977	AB001838	Homo sapiens	recoverin	179	80
8978	AF118082	Homo sapiens	PRO1902	73	70
8979	AF116715	Homo sapiens	PRO2829	102	76
8980	AF090942	Homo sapiens	PRO0657	132	61
8981	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	158	65
8982	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	108	84
8983	A00127	Homo sapiens	melanoma associated antigen P97	366	94
8984	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	158	88
8985	Y59778	Homo sapiens	Human normal ovarian tissue derived protein 55.	71	61
8986	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	42
8987	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	98	50
8988	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	80	51
8989	Y24025	Homo sapiens	Amino acid sequence of the human MMSC1 protein.	160	100
8990	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	130	67
8991	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	165	82
8992	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein thal.a.	111	62
8993	M28016	Homo sapiens	cytochrome b	130	100
8994	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	133	90
8995	D58112	Homo sapiens	NADH dehydrogenase subunit 4L	298	89
8996	Y16430	Mus musculus	ribosomal protein L35a	101	65
8997	Y45318	Homo sapiens	Human secreted protein fragment encoded from gene 18.	96	76
8998	AL049659	Arabidopsis thaliana	putative protein	126	42
8999	AE003500	Drosophila melanogaster	CG12379 gene product	285	67
9000	R37991	Homo sapiens	Sequence of a new cytokine which inhibits induction by gamma interferon of expression of Class II histocompatibility antigens.	124	48

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9001	AF090930	Homo sapiens	PRO0478	193	89
9002	AF000381	Arabidopsis thaliana	gb AAF57656.1-gene_id:K17E12.13-similar to unknown protein	193	29
9003	M17885	Homo sapiens	acidic ribosomal phosphoprotein (P0)	364	66
9004	D63424	Homo sapiens	glycogen synthase kinase 3alpha	126	81
9005	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	75
9006	AL117637	Homo sapiens	hypothetical protein	257	92
9007	AE001381	Plasmodium falciparum	hypothetical protein	141	26
9008	W34499	Homo sapiens	Obesity receptor C protein.	152	86
9009	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	199	80
9010	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	202	94
9011	AF090931	Homo sapiens	PRO0483	135	68
9012	M11717	Homo sapiens	heat shock protein	696	100
9013	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	123	75
9014	R59842	Homo sapiens	ApoE4L1 protease.	86	85
9015	AL160371	Leishmania major	probable (hhv-6) u1 I02, variant a DNA, complete virion genome	96	65
9016	AF229067	Homo sapiens	PADI-H protein	119	54
9017	AF090944	Homo sapiens	PRO0663	138	54
9018	AL160371	Leishmania major	probable (hhv-6) u1 I02, variant a DNA, complete virion genome	103	50
9019	X92485	Plasmodium vivax	pval	101	73
9020	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	82	72
9021	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	116	66
9022	AF229067	Homo sapiens	PADI-H protein	127	45
9023	M33112	Homo sapiens	amyloid-beta protein	105	67
9024	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	79	68
9025	AF161361	Homo sapiens	HSPC098	130	55
9026	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	169	72
9027	AF130051	Homo sapiens	PRO0898	138	77
9028	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	132	49
9029	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	117	58
9030	AC002310	Homo sapiens	Unknown gene product	155	85
9031	X92485	Plasmodium vivax	pval	112	42
9032	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	130	52
9033	G00487	Homo sapiens	Human secreted protein, SEQ ID NO: 4568.	123	69
9034	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	138	61
9035	AL390114	Leishmania major	extremely cysteine/valine rich protein	111	66
9036	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	173	59
9037	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	100	54
9038	AF220264	Homo sapiens	MOS1-1	96	80

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9039	AF130051	Homo sapiens	PRO0898	119	68
9040	AF116715	Homo sapiens	PRO2829	121	63
9041	L76200	Homo sapiens	guanylate kinase	193	83
9042	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	125	55
9043	AF152513	Homo sapiens	protocadherin gamma A6 short form protein	334	100
9044	AF130079	Homo sapiens	PRO2852	125	33
9045	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	128	64
9046	AF090942	Homo sapiens	PRO0657	126	65
9047	AF284223	Homo sapiens	terra-like protein	228	100
9048	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	68
9049	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	132	92
9050	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	123	75
9051	AL034344	Homo sapiens	dj118B18.1 (forkhead box C1)	323	100
9052	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	106	62
9053	AF225910	Mus musculus	DAZ-associated protein 1	100	45
9054	AF130087	Homo sapiens	PRO2411	147	70
9055	W80400	Homo sapiens	A secreted protein encoded by clone dd71.2.	858	97
9056	X70343	Nicotiana sylvestris	extensin	113	33
9057	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	57
9058	R95913	Homo sapiens	Neural thread protein.	142	38
9059	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	131	56
9060	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	131	50
9061	X70343	Nicotiana sylvestris	extensin	103	42
9062	AJ271872	Nicotiana sylvestris	extensin	129	33
9063	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	151	73
9064	AF266164	Rattus norvegicus	densin-180 variant D	144	96
9065	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	135	68
9066	M28016	Homo sapiens	cytochrome b	178	87
9067	M28016	Homo sapiens	cytochrome b	193	95
9068	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	148	60
9069	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	111	100
9070	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	141	72
9071	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	147	64
9072	AL390114	Leishmania major	extremely cysteine/valine rich protein	109	69
9073	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	171	85
9074	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	88	88
9075	Y14482	Homo sapiens	Fragment of human secreted protein	137	62

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded by gene 17.		
9076	L38941	Homo sapiens	ribosomal protein L34	139	88
9077	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	164	86
9078	X55684	Lycopersicon esculentum	extensin (class I)	72	35
9079	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	82
9080	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	229	59
9081	AF130089	Homo sapiens	PRO2550	118	71
9082	X92485	Plasmodium vivax	pva1	125	71
9083	AF216650	Homo sapiens	MTAP	154	73
9084	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	124	78
9085	J02459	bacteriophage lambda	F (capsid component;341)	191	73
9086	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	138	61
9087	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	130	75
9088	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	144	61
9089	AK024455	Homo sapiens	FLJ00047 protein	145	82
9090	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	181	60
9091	AF090895	Homo sapiens	PRO0117	87	66
9092	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	211	86
9093	AF130079	Homo sapiens	PRO2852	157	74
9094	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	180	82
9095	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	97	42
9096	X65551	Homo sapiens	antigen of the monoclonal antibody Ki-67	106	65
9097	W34499	Homo sapiens	Obesity receptor C protein.	231	80
9098	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	127	63
9099	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	129	78
9100	AF229067	Homo sapiens	PADI-H protein	162	59
9101	G00673	Homo sapiens	Human secreted protein, SEQ ID NO: 4754.	157	65
9102	Y60010	Homo sapiens	Human endometrium tumour EST encoded protein 70.	69	63
9103	R95913	Homo sapiens	Neural thread protein.	124	72
9104	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	104	68
9105	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	156	88
9106	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	170	57
9107	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	163	89
9108	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	123	41
9109	L41944	Homo sapiens	interferon receptor	162	66

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9110	AK000496	Homo sapiens	unnamed protein product	138	78
9111	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	81	62
9112	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	142	52
9113	M26361	Mus musculus	L1NE/fg H-chain fusion protein	105	50
9114	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	119	56
9115	AF119900	Homo sapiens	PRO2822	140	58
9116	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	158	60
9117	L00016	Homo sapiens	ur15	171	97
9118	AC006276	Homo sapiens	R28379_3	138	100
9119	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	131	72
9120	AF119855	Homo sapiens	PRO1847	155	81
9121	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	105	84
9122	Y87103	Homo sapiens	Human secreted protein sequence SEQ ID NO:142.	115	78
9123	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	134	53
9124	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	103	40
9125	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	96	63
9126	AF130089	Homo sapiens	PRO2550	125	78
9127	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	98	56
9128	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	107	75
9129	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	131	49
9130	AK024455	Homo sapiens	FLJ00047 protein	130	78
9131	W88435	Homo sapiens	Disease associated protein kinase DAPK-4.	336	100
9132	U63332	Homo sapiens	super cysteine rich protein; SCRP	144	59
9133	Y94922	Homo sapiens	Human secreted protein clone pv6_1 protein sequence SEQ ID NO:50.	154	90
9134	AF317425	Homo sapiens	GAC-1	182	70
9135	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	174	54
9136	AF116715	Homo sapiens	PRO2829	116	71
9137	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	122	65
9138	AF130089	Homo sapiens	PRO2550	140	62
9139	AF161221	Homo sapiens	kallikrein-like protein 6	204	90
9140	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	110	48
9141	U27486	Pseudorabies virus	EP0	84	44
9142	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	150	96
9143	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	220	80
9144	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	163	84
9145	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	180	77
9146	U52077	Homo sapiens	mariner transposase	365	78
9147	W88627	Homo sapiens	Secreted protein encoded by gene 94	143	67

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HPMBQ32.		
9148	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	100	81
9149	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	118	66
9150	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	54
9151	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	101	70
9152	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	66
9153	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	160	72
9154	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	106	63
9155	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	95	80
9156	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	133	67
9157	G03924	Homo sapiens	Human secreted protein, SEQ ID NO: 8005.	265	80
9158	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	131	72
9159	AF130089	Homo sapiens	PRO2550	180	61
9160	AF116715	Homo sapiens	PRO2829	184	82
9161	K01664	Drosophila melanogaster	Bkm-like protein	200	69
9162	D88146	Homo sapiens	UDP-galactose transporter 2	101	100
9163	AF107406	Homo sapiens	GW128	155	60
9164	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	97	51
9165	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	60
9166	AF210651	Homo sapiens	NAG18	83	65
9167	V00672	Pan troglodytes	reading frame protein 4	119	95
9168	Y01155	Homo sapiens	Secreted protein encoded by gene 4 clone HIBCW32.	225	74
9169	AF161356	Homo sapiens	HSPC093	100	75
9170	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	174	66
9171	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	115	86
9172	AF119855	Homo sapiens	PRO1847	178	59
9173	AF130087	Homo sapiens	PRO2411	129	48
9174	AF130079	Homo sapiens	PRO2852	149	59
9175	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	101	90
9176	AF090894	Homo sapiens	PRO0113	118	65
9177	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	105	46
9178	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	100	52
9179	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	70
9180	AF116715	Homo sapiens	PRO2829	127	64
9181	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	144	71
9182	AF229067	Homo sapiens	PADI-H protein	164	64
9183	G02532	Homo sapiens	Human secreted protein, SEQ ID NO:	134	80



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6613.		
9184	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	106	64
9185	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	132	57
9186	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	113	65
9187	AF090931	Homo sapiens	PRO0483	117	68
9188	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	136	67
9189	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	130	47
9190	D38112	Homo sapiens	cytochrome c oxidase subunit I	269	85
9191	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	150	40
9192	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	153	73
9193	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	62
9194	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	103	31
9195	X77816	Rattus norvegicus	PR-Vbeta1	98	47
9196	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	107	48
9197	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	111	68
9198	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	164	83
9199	J02459	bacteriophage lambda	E (capsid component;341)	235	85
9200	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	117	65
9201	X67640	Homo sapiens	HS24/P52	222	75
9202	X67640	Homo sapiens	HS24/P52	231	81
9203	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	128	66
9204	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	107	74
9206	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	186	66
9207	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	136	56
9208	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	160	67
9209	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	68
9210	AF116715	Homo sapiens	PRO2829	123	81
9211	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	70
9212	AF118086	Homo sapiens	PRO1992	84	57
9213	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	115	62
9214	J02459	bacteriophage lambda	E (capsid component;341)	247	92
9215	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	74	76
9216	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	134	74

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9217	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	137	53
9218	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	130	44
9219	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	68
9220	L41944	Homo sapiens	interferon receptor	141	50
9221	AF130079	Homo sapiens	PRO2852	170	70
9222	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	100	85
9223	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	142	56
9224	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	104	63
9225	U80761	Homo sapiens	CTG26 alternate open reading frame	92	84
9226	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	157	65
9227	AK027208	Homo sapiens	unnamed protein product	138	68
9228	B25722	Homo sapiens	Human secreted protein sequence encoded by gene 9 SEQ ID NO:111.	125	87
9229	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	127	88
9230	AK025047	Homo sapiens	unnamed protein product	179	64
9231	AF090894	Homo sapiens	PRO0113	195	57
9232	AB046048	Macaca fascicularis	unnamed portein product	176	54
9233	AB008227	Adiantum capillus-veneris	Extensin	93	34
9234	AF130089	Homo sapiens	PRO2550	98	73
9235	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	135	52
9236	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	162	62
9237	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	126	59
9238	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	126	52
9239	AE003499	Drosophila melanogaster	CG12706 gene product	166	37
9240	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	161	64
9241	X92485	Plasmodium vivax	pva1	112	61
9242	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	69	42
9243	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	140	80
9244	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	187	92
9245	M22332	Homo sapiens	unknown protein	117	40
9246	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	109	66
9247	AL136173	Homo sapiens	dJ914B9.1 (novel protein (HSPC162) similar to Rattus norvegicus bithoraxoid-like protein)	305	76
9248	AF116661	Homo sapiens	PRO1438	141	53
9249	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	144	76

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9250	J02459	bacteriophage lambda	E (capsid component;341)	245	89
9251	J02459	bacteriophage lambda	E (capsid component;341)	245	92
9252	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene I21.	128	63
9253	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	124	72
9254	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	90
9255	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	132	65
9256	X52164	Mus musculus	Q300 protein (AA 1-77)	106	62
9257	AF217374	Acanthaster planci	cytochrome oxidase subunit I	259	98
9258	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	64
9259	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	107	54
9260	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	66
9261	M28016	Homo sapiens	cytochrome b	148	93
9262	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	68
9263	R55749	Homo sapiens	Extracellular domain of human high affinity IFN-gamma receptor.	116	83
9264	K02403	Homo sapiens	complement component C4a	9025	99
9265	X92485	Plasmodium vivax	pval	161	55
9266	AK024455	Homo sapiens	FLJ00047 protein	98	83
9267	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	103	51
9268	AF130089	Homo sapiens	PRO2550	124	77
9269	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	94	54
9270	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	96	81
9271	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	132	53
9272	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	155	72
9273	AF229067	Homo sapiens	PADI-H protein	127	54
9274	Y36203	Homo sapiens	Human secreted protein #75.	154	77
9275	X92485	Plasmodium vivax	pval	157	72
9276	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	132	60
9277	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	156	84
9278	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	138	84
9279	Y20772	Homo sapiens	Human neurofilament-M mutant protein fragment 54.	112	70
9280	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	146	59
9281	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	103	63
9282	K01664	Drosophila melanogaster	Bkm-like protein	89	60
9283	X92485	Plasmodium	pval	124	79

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
9284	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	95	75
9285	AF130087	Homo sapiens	PRO2411	138	78
9286	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	140	54
9287	AF004340	Homo sapiens	ATPase 6/8	98	100
9288	S79410	Mus musculus	nuclear localization signal binding protein	102	68
9289	J02459	bacteriophage lambda	I (tail component;223)	457	97
9290	AC003058	Arabidopsis thaliana	unknown protein	177	84
9291	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	107	87
9292	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	311	91
9293	S79410	Mus musculus	nuclear localization signal binding protein	139	61
9294	R28916	Homo sapiens	Type III procollagen (prior art).	117	33
9295	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	126	77
9296	AF130089	Homo sapiens	PRO2550	137	52
9297	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	93	79
9298	U22376	Homo sapiens	alternatively spliced product using exon 13A	239	77
9299	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	134	69
9300	AL390114	Leishmania major	extremely cysteine/valine rich protein	105	24
9301	D90282	Homo sapiens	carbamyl phosphate synthetase I (EC 6.3.4.16)	276	96
9302	J02459	bacteriophage lambda	E (capsid component;341)	231	93
9303	M15077	Photinus pyralis	Luciferase	557	100
9304	L00016	Homo sapiens	urf4	303	93
9305	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	141	69
9306	L46721	Homo sapiens	mucin	204	80
9307	S79410	Mus musculus	nuclear localization signal binding protein	110	84
9308	J02459	bacteriophage lambda	E (capsid component;341)	218	93
9309	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	78	66
9310	AF130075	Homo sapiens	PRO2532	92	69
9311	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	97	51
9312	J02459	bacteriophage lambda	E (capsid component;341)	201	79
9313	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	133	95
9314	AK024455	Homo sapiens	FLJ00047 protein	128	68
9315	D38112	Homo sapiens	ATPase subunit 6	223	81
9316	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	113	85
9317	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	117	88
9318	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	257	72

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9319	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	101	61
9320	AK001116	Homo sapiens	unnamed protein product	96	40
9321	G02535	Homo sapiens	Human secreted protein, SEQ ID NO: 6616.	174	60
9322	AF037081	Pan troglodytes	ribonuclease k6 precursor	109	100
9323	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	149	63
9324	AF153056	Fasciola hepatica	tegumental antigen	60	44
9325	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	200	69
9326	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	80	57
9327	AF118086	Homo sapiens	PRO1992	139	60
9328	G02560	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	110	73
9329	AF107406	Homo sapiens	GW128	142	56
9330	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	75
9331	X92485	Plasmodium vivax	pval	121	56
9332	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	179	52
9333	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	67
9334	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	108	46
9335	M22332	Homo sapiens	unknown protein	158	60
9336	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	95	46
9337	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	160	76
9338	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	150	68
9339	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	169	59
9340	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	154	64
9341	AK024455	Homo sapiens	FLJ00047 protein	117	79
9342	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	191	76
9343	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	133	82
9344	AF032457	Homo sapiens	BimEL	123	100
9345	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	117	46
9346	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	153	75
9347	X53020	Plasmodium falciparum	erythrocyte membrane-associated antigen	68	75
9348	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	120	70
9349	AF130089	Homo sapiens	PRO2550	116	69
9350	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	165	72
9351	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	94	82
9352	AL080242	Homo sapiens	bA554C12.1 (RBX1 or ROC1 (ring-box or ring finger protein 1))	184	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9353	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	125	64
9354	X71442	Rattus norvegicus	ORF 1; putative	96	40
9355	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	98	46
9356	AF090931	Homo sapiens	PRO0483	148	76
9357	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	144	56
9358	AC005175	Homo sapiens	TA2R_HUMAN, BETA ISOFORM; TXA2-R; PROSTANOID 1P RECEPTOR	153	63
9359	AF116715	Homo sapiens	PRO2829	125	66
9360	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	143	72
9361	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	178	75
9362	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSAWA27.	90	57
9363	G03536	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	86	76
9364	AF229067	Homo sapiens	PADI-H protein	116	51
9365	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	248	64
9366	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	104	76
9367	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	95	76
9368	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	105	74
9369	R86406	Homo sapiens	Human matrix metalloprotease MMP1a.	108	83
9370	AF181977	Hepatitis GB virus C	E2 protein	95	38
9371	AF090931	Homo sapiens	PRO0483	151	62
9372	AF090894	Homo sapiens	PRO0113	133	57
9373	AK002154	Homo sapiens	unnamed protein product	226	55
9374	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	140	71
9375	U77494	Homo sapiens	RANBP8	166	100
9376	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	155	52
9377	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	126	63
9378	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	151	78
9379	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	97	68
9380	AL160493	Leishmania major	probable (hlyv-6) u1102, variant a DNA, complete virion genome	117	62
9381	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	104	47
9382	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	57
9384	AB047936	Macaca fascicularis	hypothetical protein	95	41
9385	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	57	64
9386	U04810	Homo sapiens	tastin	151	100
9387	U79260	Homo sapiens	unknown	97	79

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9388	U18339	Variola virus	D4L	103	65
9389	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	134	75
9390	AL390935	Leishmania major	possible dopap	99	88
9391	AB015633	Homo sapiens	type II membrane protein	108	100
9392	AF113685	Homo sapiens	PRO0974	98	62
9393	AF064819	Homo sapiens	serine protease DESC1	227	69
9394	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	219	68
9395	G01400	Homo sapiens	Human secreted protein, SEQ ID NO: 5481.	104	100
9396	AK024455	Homo sapiens	FLJ00047 protein	153	68
9397	AF033260	porcine endogenous type C retrovirus	reverse transcriptase	155	53
9398	X12517	Homo sapiens	C protein (AA 1-159)	147	55
9399	AB029948	Homo sapiens	mitochondrial seryl-tRNA synthetase	1203	100
9400	Y87075	Homo sapiens	Human secreted protein sequence SEQ ID NO: 114.	234	93
9401	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	150	58
9402	M15530	Homo sapiens	B-cell growth factor	113	74
9403	X56932	Homo sapiens	23 kD highly basic protein	114	85
9404	AC018748	Arabidopsis thaliana	Contains similarity to P11 protein from Drosophila melanogaster gb X59691.	75	65
9405	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	114	88
9406	AF220264	Homo sapiens	MOST-1	124	70
9407	AF119851	Homo sapiens	PRO1722	157	65
9408	X92485	Plasmodium vivax	pval	163	78
9409	X92485	Plasmodium vivax	pval	165	77
9410	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	97	55
9411	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	104	64
9412	AF130089	Homo sapiens	PRO2550	147	55
9413	AF130089	Homo sapiens	PRO2550	175	65
9414	L14848	Homo sapiens	MHC class I-related protein	225	97
9415	R95913	Homo sapiens	Neural thread protein.	107	74
9416	AB001684	Chlorella vulgaris	ORF49b	68	53
9417	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	111	50
9418	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	107	73
9419	AL050285	Homo sapiens	hypothetical protein	194	100
9420	AF090944	Homo sapiens	PRO0663	132	59
9421	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	153	61
9422	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	140	70
9423	M20030	Homo sapiens	small proline rich protein	62	41
9424	AF116718	Homo sapiens	PRO2900	396	100
9425	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	102	35
9426	X61047	Hydra sp.	mini-collagen	92	45

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9427	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	105	71
9428	L10908	Mus musculus	Gcap1 gene product	107	44
9429	Y19767	Homo sapiens	SEQ ID NO 485 from WO922243.	79	87
9430	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	123	61
9431	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	111	80
9432	X12580	Medicago sativa	put. nodulin (soybean N-75 homolog.)	87	33
9433	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	106	48
9434	AC003028	Arabidopsis thaliana	30S ribosomal protein S31	79	42
9435	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	106	75
9436	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	207	75
9437	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	163	85
9438	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	84	57
9439	AF118086	Homo sapiens	PRO1992	145	75
9440	AF229067	Homo sapiens	PADI-H protein	140	64
9441	M36913	Zea mays	cell wall protein (put.); putative	107	38
9442	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	161	59
9443	AF229067	Homo sapiens	PADI-H protein	147	85
9444	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	171	79
9445	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	155	57
9446	X92485	Plasmodium vivax	pva1	97	55
9447	AF119851	Homo sapiens	PRO1722	123	55
9448	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	88
9449	AL391688	Homo sapiens	bA524D16A.2.1 (novel protein similar to mouse granuphilin-a)	258	97
9450	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	91
9451	X92485	Plasmodium vivax	pva1	123	88
9452	X83000	Myocastor coypus	lipase related protein 2	168	43
9453	M35603	Mus musculus	Hox-3.1 protein	447	78
9454	M35520	Canis familiaris	GTP-binding protein (rab5)	271	98
9455	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	362	86
9456	A13595	synthetic construct	immunosuppressive protein PP15	111	100
9457	X67788	Rattus norvegicus	ezrin, p81	185	97
9458	U28068	Mus musculus	neurogenic differentiation factor	132	89
9459	AF155140	Homo sapiens	gonadotropin-regulated testicular RNA helicase; GRTH	556	88
9460	AF155140	Homo sapiens	gonadotropin-regulated testicular RNA helicase; GRTH	379	94
9461	AF169689	Homo sapiens	protocadherin alpha 10 alternate isoform	208	95
9462	U73193	Homo sapiens	inward rectifier potassium channel	236	96



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			Kir1.2		
9463	U83278	Bos taurus	neural specific protein CRMP-2	157	61
9464	W48352	Homo sapiens	Human breast cancer related protein BCFL1.	74	57
9465	AL031673	Homo sapiens	dJ694B14.3 (PUTATIVE novel haloacid dehalogenase-like hydrolase family protein similar to (archaea) bacterial proteins)	444	100
9466	X67247	Homo sapiens	ribosomal protein S8	519	90
9467	S79410	Mus musculus	nuclear localization signal binding protein	115	51
9468	U80761	Homo sapiens	CTG26 alternate open reading frame	95	84
9469	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	145	71
9470	AF130056	Homo sapiens	PRO1367	98	76
9471	X71354	Homo sapiens	vesicular monoamine transporter	102	95
9472	U66372	Bos taurus	ribosomal protein S29	120	95
9473	D32002	Homo sapiens	nuclear cap binding protein	583	96
9474	W34282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSS1.	469	91
9475	V49572_cd1	Homo sapiens	I3-NOV-1996 Human stomach cancer clone HP10122 cDNA #1.	562	100
9476	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	247	88
9477	AB043820	Homo sapiens	platelet glycoprotein VI-2	95	47
9478	AB020236	Homo sapiens	ribosomal protein L27A	437	86
9479	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	149	52
9480	AF205633	Homo sapiens	ninjurin2	364	100
9481	D14886	Homo sapiens	TIFA-37	196	100
9482	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	166	76
9483	AF178842	Homo sapiens	Rhesus blood group-associated glycoprotein	128	75
9484	AF134895	Homo sapiens	glyoxylate reductase	838	95
9485	AC004832	Homo sapiens	similar to 45 kDa secretory protein ; similar to CAA10644.1 (PID:g4164418)	562	98
9486	Z35761	Homo sapiens	TEL/ABL	230	71
9487	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	149	72
9488	AL032631	Caenorhabditis elegans	predicted using Genefinder	159	31
9489	AJ271079	Oenothera clata subsp. hookeri	Ycf2 protein	113	36
9490	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	135	40
9491	Y53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16.	124	61
9492	Y21091	Homo sapiens	Human p53 cellular tumour antigen mutant protein fragment 28.	85	41
9493	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	153	76
9494	AF119851	Homo sapiens	PRO1722	94	54
9495	R04932	Homo sapiens	Interferon-gamma receptor segment from clone 39 responsible for binding the target.	142	100
9496	U40952	Caenorhabditis elegans	C03B1.10 gene product	103	75
9497	M63838	Homo sapiens	interferon-gamma induced protein	128	92

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9498	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	147	44
9499	AF108831	Homo sapiens	KcCl cotransporter 3	244	77
9500	R07037	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	154	68
9501	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	139	63
9502	AE003499	Drosophila melanogaster	CG12706 gene product	180	36
9503	X02344	Homo sapiens	beta-tubulin	363	94
9504	D78014	Homo sapiens	dihydropyrimidinase related protein-3	189	84
9505	U59446	Brassica napus	myrosinase-binding protein related protein	116	40
9506	AB010437	Rattus rattus	cadherin-8	239	50
9507	AF229067	Homo sapiens	PADI-H protein	178	74
9508	AJ224819	Homo sapiens	tumor suppressor	291	85
9509	AF017275	Mus musculus	growth factor independence-1B	242	40
9510	AF177203	Homo sapiens	cerebral cell adhesion molecule	388	52
9511	A7007160	Homo sapiens	similar to Homo sapiens CGI-57 protein mRNA with GenBank Accession Number AF151815.1	1533	99
9512	AL160371	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	104	66
9513	X52164	Mus musculus	Q300 protein (AA 1-77)	92	59
9514	X80035	Oryctolagus cuniculus	cysteine rich hair keratin associated protein	96	40
9515	D86491	Xenopus laevis	Nfr1	1777	76
9516	Y70761	Homo sapiens	Human beta-amyloid peptide (BAP) binding protein, BBP3.	168	80
9517	AK024500	Homo sapiens	FLJ00109 protein	1714	100
9518	AF008220	Bacillus subtilis	YtaG	104	41
9519	AF099977	Mus musculus	schlafen4	163	35
9520	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	162	72
9521	AL035068	Homo sapiens	dJ116G19.1 (novel protein)	102	76
9522	B24527	Homo sapiens	Human secreted protein sequence encoded by gene 15 SEQ ID NO:153.	729	90
9523	AF129756	Homo sapiens	MSH5	182	100
9524	AJ238706	Drosophila melanogaster	monocarboxylate transporter 1 homologue	126	32
9525	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	250	97
9526	D86604	Mus musculus	Bach2	200	92
9527	AB032918	Hyllobates moloch	dopamine receptor D4	91	36
9528	AB007830	Homo sapiens	CSR2	995	99
9529	AC004472	Homo sapiens	P1.11659_4	449	98
9530	AF273047	Homo sapiens	CTCL tumor antigen se20-7	104	29
9531	AF130079	Homo sapiens	PRO2852	153	67
9532	X07881	Homo sapiens	proline-rich protein G1	105	43
9533	AK001845	Homo sapiens	unnamed protein product	1368	63
9534	S79410	Mus musculus	nuclear localization signal binding protein	94	41
9535	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	185	86
9536	X99583	Homo sapiens	CHL1 protein	635	98
9537	AL022170	Homo sapiens	dJ501N12.1	111	37
9538	X66179	Xenopus laevis	p70 S6 kinase	120	75

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9539	U68380	Gallus gallus	csdp	289	98
9540	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	97	90
9541	AB013918	Homo sapiens	CAD	369	78
9542	U29380	Caenorhabditis elegans	similar to adenylate cyclase	501	42
9543	AF020312	Mus musculus	proline-rich protein 9-1	95	51
9544	G03435	Homo sapiens	Human secreted protein, SEQ ID NO: 7516.	142	96
9545	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	142	66
9546	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	110	47
9547	AB044546	Homo sapiens	mitogen-activated protein kinase Kinase kinase	407	60
9548	U52111	Homo sapiens	Ca2+/Calmodulin-dependent protein kinase I	660	100
9549	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	129	68
9550	Y87852	Homo sapiens	Human FGF-5 protein fragment.	146	100
9551	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	109	50
9552	D45131	Homo sapiens	basigin	311	66
9553	A14656		synthetic protein antigen	450	89
9554	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	133	52
9555	X73458	Homo sapiens	protein kinase	568	85
9556	AJ131890	Homo sapiens	DNA polymerase lambda	1549	100
9557	S56555	Homo sapiens	paraoxonase/arylesterase	224	85
9558	M22332	Homo sapiens	unknown protein	90	38
9559	B24598	Homo sapiens	Human secreted protein sequence encoded by gene 47 SEQ ID NO:224.	66	44
9560	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	95	51
9561	Y08061	Homo sapiens	Human c-myc protein fragment.	77	76
9562	X55687	Lycopersicon esculentum	extensin (class II)	69	60
9563	AC002333	Arabidopsis thaliana	putative SF16 protein {Helianthus annuus}	111	31
9564	AF118082	Homo sapiens	PRO1502	106	61
9565	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	85	52
9566	U10323	Homo sapiens	NF45 protein	480	82
9567	AF100757	Homo sapiens	COP9 complex subunit 4	686	90
9568	AL035608	Homo sapiens	dJ479J7.2 (transmembrane 4 superfamily member 6)	293	90
9569	G00413	Homo sapiens	Human secreted protein, SEQ ID NO: 4494.	118	63
9570	U47856	Araneus diadematus	fibroin-4	98	44
9571	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	83	54
9572	AJ006239	Homo sapiens	dihydropteridine reductase	461	84
9573	G00821	Homo sapiens	Human secreted protein, SEQ ID NO: 4902.	248	75
9574	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	90	36
9575	V00488	Homo sapiens	alpha globin	508	84
9576	AF116719	Homo sapiens	PRO2987	483	91

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9577	L77967	Ovis aries	small proline-rich protein with paired repeat	62	38
9578	D38112	Homo sapiens	NADH dehydrogenase subunit 4	474	92
9579	P90387	Homo sapiens (Human)	N-terminal of human serum albumin polypeptide.	274	67
9580	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	271	88
9581	U15779	Homo sapiens	p70	101	57
9582	M19419	Mus musculus	proline-rich salivary protein	102	36
9583	L22030	Glycine max	hydroxyproline-rich glycoprotein	114	40
9584	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	105	32
9585	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	141	61
9586	U93569	Homo sapiens	putative p150	232	51
9587	AF144054	Homo sapiens	apoptosis related protein APR-4	120	52
9588	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	128	58
9589	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	90	61
9590	L27428	Homo sapiens	reverse transcriptase	120	46
9591	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	85	62
9592	AJ133489	Canis familiaris	albumin	204	60
9593	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	294	68
9594	M15386	Homo sapiens	gamma-globin	316	77
9595	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	134	68
9596	AF116719	Homo sapiens	PRO2987	309	89
9597	AF116719	Homo sapiens	PRO2987	485	94
9598	AF068294	Homo sapiens	HDCMB45P	131	34
9599	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	152	70
9600	AF118082	Homo sapiens	PRO1902	151	59
9601	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	186	68
9602	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	176	65
9603	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	261	80
9604	AF194537	Homo sapiens	NAG13	154	61
9605	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	96	67
9606	K02576	Homo sapiens	salivary proline-rich protein 1	100	33
9607	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	134	48
9608	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	129	67
9609	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	101	32
9610	AF118080	Homo sapiens	PRO1880	237	100
9611	AF119851	Homo sapiens	PRO1722	138	81
9612	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	178	55
9613	AF090930	Homo sapiens	PRO0478	88	71
9614	AF068294	Homo sapiens	HDCMB45P	121	49
9615	G01657	Homo sapiens	Human secreted protein, SEQ ID NO: 118	118	79

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			5738.		
9616	AF090931	Homo sapiens	PRO0483	143	63
9617	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	92	44
9618	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	121	56
9619	AB046061	Macaca fascicularis	unnamed protein product	93	44
9620	Y87116	Homo sapiens	Human secreted protein sequence SEQ ID NO:155.	122	71
9621	AF113685	Homo sapiens	PRO0974	136	65
9622	AF097178	Equus caballus	glyceraldehyde-3-phosphate dehydrogenase	119	75
9623	U83303	Homo sapiens	line-1 reverse transcriptase	134	62
9624	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	112	53
9625	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	123	77
9626	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	164	73
9627	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	236	71
9628	AF130079	Homo sapiens	PRO2852	138	50
9629	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	130	60
9630	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	167	61
9631	G03102	Homo sapiens	Human secreted protein, SEQ ID NO: 7183.	87	50
9632	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	128	41
9633	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	134	81
9634	AF118082	Homo sapiens	PRO1902	114	57
9635	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	133	54
9636	L07543	Leishmania tarentolae	MURF4	85	42
9637	U49973	Homo sapiens	ORF2: function unknown	163	44
9638	AF090895	Homo sapiens	PRO0117	77	41
9639	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	108	71
9640	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	90	46
9641	AF118078	Homo sapiens	PRO1848	114	66
9642	AK024455	Homo sapiens	FLJ00047 protein	131	79
9643	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	130	62
9644	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	141	42
9645	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	69	62
9646	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	69	35
9647	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	478	90
9648	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	155	50
9649	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	104	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6619.		
9650	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	173	38
9651	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	118	36
9652	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	162	64
9653	D00570	Mus musculus	open reading frame (196 AA)	182	51
9654	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	138	54
9655	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone H1DAD22.	105	74
9656	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	82	70
9657	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	79	39
9658	M24732	Homo sapiens	Jarmin-like protein	76	31
9659	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	161	73
9660	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hcm) gene product.	149	48
9661	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	135	62
9662	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	126	71
9663	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	141	63
9664	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	153	66
9665	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	142	93
9666	AF113685	Homo sapiens	PRO0974	112	73
9667	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	133	62
9668	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	102	47
9669	B12310	Homo sapiens	Human secreted protein encoded by gene 10 clone HDPGP94.	80	41
9670	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	106	58
9671	AF090942	Homo sapiens	PRO0657	118	66
9672	AF161356	Homo sapiens	HSPC093	94	63
9673	AF090930	Homo sapiens	PRO0478	167	64
9674	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	98	50
9675	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	87	70
9676	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	119	60
9677	X13412	Rattus rattus	flk protein	614	69
9678	AJ006770	Cicer arietinum	extensin	163	48
9679	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	120	67
9680	G00494	Homo sapiens	Human secreted protein, SEQ ID NO: 4575.	106	58
9681	U63542	Homo sapiens	FAP protein	120	68
9682	M15530	Homo sapiens	B-cell growth factor	146	76
9683	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	180	62
9684	AF321379	Callicebus moloch	gamma2-globin	108	86

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9685	L27428	Homo sapiens	reverse transcriptase	122	39
9686	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	77	51
9687	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	104	58
9688	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	123	58
9689	X81713	Homo sapiens	smallest subunit of TFIIA	210	91
9690	AF193330	Human respiratory syncytial virus	G protein	100	25
9691	AF150100	Homo sapiens	small zinc finger-like protein	205	83
9692	AF068294	Homo sapiens	HDCMB45P	122	54
9693	AF189307	Homo sapiens	unknown	96	50
9694	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	165	50
9695	AF130089	Homo sapiens	PRO2550	198	68
9696	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	170	80
9697	AK024455	Homo sapiens	FLJ00047 protein	137	63
9698	M24732	Homo sapiens	lamin-like protein	92	42
9699	AF116715	Homo sapiens	PRO2829	119	75
9700	AF130089	Homo sapiens	PRO2550	234	57
9701	V00662	Homo sapiens	ATPase 6	255	77
9702	L10908	Mus musculus	Gcap1 gene product	93	35
9703	AF130089	Homo sapiens	PRO2550	208	78
9704	AF194537	Homo sapiens	NAG13	89	51
9705	U79260	Homo sapiens	unknown	98	77
9706	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	78	43
9707	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	70	92
9708	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	136	60
9709	AF194537	Homo sapiens	NAG13	99	48
9710	AF130089	Homo sapiens	PRO2550	87	58
9711	X03145	Homo sapiens	pot. ORF III	135	41
9712	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	97	35
9713	AF116695	Homo sapiens	PRO2221	185	50
9714	AF130051	Homo sapiens	PRO0898	108	68
9715	AF130089	Homo sapiens	PRO2550	143	50
9716	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	124	49
9717	L27428	Homo sapiens	reverse transcriptase	133	50
9718	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	88	43
9719	L27428	Homo sapiens	reverse transcriptase	127	56
9720	M74009	Theropithecus gelada	cytochrome c oxidase subunit II	283	67
9721	M10546	Homo sapiens	cytochrome oxidase I	292	84
9722	AF130051	Homo sapiens	PRO0898	96	57
9723	U93564	Homo sapiens	putative p150	144	49
9724	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	373	76
9725	AK000496	Homo sapiens	unnamed protein product	155	55
9726	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	94	62

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9727	AF130089	Homo sapiens	PRO2550	154	40
9728	AF130089	Homo sapiens	PRO2550	127	61
9729	M19419	Mus musculus	proline-rich salivary protein	98	39
9730	D90053	Sus scrofa	destin	119	43
9731	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	138	50
9732	AF090942	Homo sapiens	PRO0657	72	45
9733	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	110	44
9734	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	94
9735	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	150	85
9736	L27428	Homo sapiens	reverse transcriptase	217	33
9737	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	89	65
9738	AF007064	Saccharomyces cerevisiae	basic protein	108	31
9739	B01372	Homo sapiens	Neuron-associated protein.	128	60
9740	G03140	Homo sapiens	Human secreted protein, SEQ ID NO: 7221.	109	50
9741	AF194537	Homo sapiens	NAG13	123	54
9742	Y69166	Homo sapiens	A mature human N-acetylglucosaminyl transferase protein.	101	77
9743	X92485	Plasmodium vivax	pval	106	41
9744	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	122	76
9745	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	128	50
9746	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	87	64
9747	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	163	69
9748	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	124	74
9749	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	97	66
9750	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	156	71
9751	G03925	Homo sapiens	Human secreted protein, SEQ ID NO: 8006.	157	71
9752	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	97	51
9753	X92485	Plasmodium vivax	pval	91	39
9754	Y07786	Vibrio cholerae	Rfc-like protein	92	32
9755	AF068294	Homo sapiens	HDCMB45P	125	63
9756	L27428	Homo sapiens	reverse transcriptase	91	34
9757	AK024455	Homo sapiens	FLJ00047 protein	143	59
9758	S79410	Mus musculus	nuclear localization signal binding protein	103	41
9759	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	96	67
9760	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	179	58
9761	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	154	65
9762	G03807	Homo sapiens	Human secreted protein, SEQ ID NO:	91	78



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7888.		
9763	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	119	60
9764	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	111	85
9765	R13556	Homo sapiens	Protein encoded downstream of hbc_M oncoprotein.	116	36
9766	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	165	74
9767	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	162	74
9768	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	117	52
9769	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	92	50
9770	AF130089	Homo sapiens	PRO2550	104	31
9771	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	154	62
9772	U52077	Homo sapiens	mariner transposase	194	56
9773	Y87297	Homo sapiens	Human signal peptide containing protein HSPP-74 SEQ ID NO:74.	345	100
9774	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	73	36
9775	M11901	Rattus norvegicus	proline-rich salivary protein	96	32
9776	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	124	53
9777	L27428	Homo sapiens	reverse transcriptase	251	53
9778	K02576	Homo sapiens	salivary proline-rich protein 1	141	40
9779	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	111	58
9780	AJ224997	Rattus norvegicus	huntingtin	64	64
9781	AF283769	Homo sapiens	similar to GenBank Accession Number AC021163	119	53
9782	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	81	50
9783	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	68
9784	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	85	65
9785	AF144054	Homo sapiens	apoptosis related protein APR-4	83	53
9786	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	75	41
9787	M64792	Rattus norvegicus	salivary proline-rich protein	122	45
9788	D90053	Sus scrofa	destrin	146	43
9789	A18812	Brassica napus	extensin	104	34
9790	AF130089	Homo sapiens	PRO2550	102	66
9791	AF130089	Homo sapiens	PRO2550	326	70
9792	D38112	Homo sapiens	cytochrome c oxidase subunit I	495	79
9793	M10546	Homo sapiens	cytochrome oxidase I	343	75
9794	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	106	58
9795	X92485	Plasmodium vivax	pval	108	48
9796	M15530	Homo sapiens	B-cell growth factor	119	70
9797	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	148	65
9798	X61046	Hydra sp.	mini-collagen	101	55

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9799	U93571	Homo sapiens	p40	82	36
9800	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	170	52
9801	X92485	Plasmodium vivax	pval	113	45
9802	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	63	44
9803	D38112	Homo sapiens	cytochrome c oxidase subunit 3	583	89
9804	G01736	Homo sapiens	Human secreted protein, SEQ ID NO: 5817.	150	47
9805	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	132	71
9806	X92485	Plasmodium vivax	pval	106	53
9807	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	163	67
9808	AF119851	Homo sapiens	PRO1722	341	68
9809	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	77	57
9810	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	72
9811	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	65
9812	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	118	37
9813	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	121	72
9814	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	72	92
9815	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	71	71
9816	AF118082	Homo sapiens	PRO1902	93	45
9817	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	207	59
9818	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	99	46
9819	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	130	69
9820	L10908	Mus musculus	Gcap1 gene product	99	37
9821	A00469	Homo sapiens	growth hormone	254	81
9822	U79260	Homo sapiens	unknown	85	39
9823	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	125	62
9824	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	103	74
9825	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	126	51
9826	U49973	Homo sapiens	ORF1, MER37; putative transposase similar to pogo element	148	44
9827	Y24789	Homo sapiens	Human secreted protein bf377.1.	265	100
9828	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	72	60
9829	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	118	45
9830	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	104	51
9831	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	118	74
9832	AF151866	Homo sapiens	CGI-108 protein	115	31
9833	U93563	Homo sapiens	putative p150	127	61

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9834	AE003859	Xylella fastidiosa	hypothetical protein	97	30
9835	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	138	65
9836	B01372	Homo sapiens	Neuron-associated protein.	150	88
9837	G03115	Homo sapiens	Human secreted protein, SEQ ID NO: 7196.	115	57
9838	AF068294	Homo sapiens	HDCMB45P	90	65
9839	S77772	Homo sapiens	aspartylglucosaminidase, AGA {C-terminal, alternatively spliced} (EC 3.5.1.26)	71	66
9840	AF090942	Homo sapiens	PRO0657	115	76
9841	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	75	54
9842	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	156	67
9843	AF130089	Homo sapiens	PRO2550	216	75
9844	M15530	Homo sapiens	B-cell growth factor	113	67
9845	U93567	Homo sapiens	p40	248	75
9846	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	151	55
9847	AK024455	Homo sapiens	FLJ00047 protein	151	64
9848	AF118082	Homo sapiens	PRO1902	58	81
9849	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	129	65
9850	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	329	77
9851	AF090944	Homo sapiens	PRO0663	122	80
9852	X71442	Rattus norvegicus	ORF 1; putative	109	48
9853	AF130089	Homo sapiens	PRO2550	126	60
9854	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	98	62
9855	U93563	Homo sapiens	putative p150	136	48
9856	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	276	74
9857	AF017777	Drosophila melanogaster	la costa	99	43
9858	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	99	37
9859	K02576	Homo sapiens	salivary proline-rich protein 1	106	37
9860	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	138	71
9861	AF116909	Homo sapiens	unknown	103	43
9862	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	113	38
9863	Y21811	Homo sapiens	CPF polypeptide 36PRO.	131	58
9864	U93567	Homo sapiens	p40	252	70
9865	AF090895	Homo sapiens	PRO0117	164	60
9866	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	109	47
9867	AF090930	Homo sapiens	PRO0478	106	84
9868	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	167	84
9869	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	83	60
9870	AF119900	Homo sapiens	PRO2822	134	48
9871	AF116715	Homo sapiens	PRO2829	111	81
9872	U52077	Homo sapiens	mariner transposase	332	76

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9873	Y69166	Homo sapiens	A mature human N-acetylglucosaminyl transferase protein.	95	85
9874	U93570	Homo sapiens	putative p150	243	44
9875	L27428	Homo sapiens	reverse transcriptase	127	54
9876	S80119	Rattus sp.	reverse transcriptase homolog	163	43
9877	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	113	64
9878	AF187823	Zea mays	transposase DOPA	132	38
9879	W40353	Homo sapiens	Human unspecified protein from US5702907.	101	41
9880	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	133	43
9881	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	101	59
9882	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	148	52
9883	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	57	65
9884	X92485	Plasmodium vivax	pval	129	43
9885	M64792	Rattus norvegicus	salivary proline-rich protein	98	37
9886	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	89	59
9887	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	155	54
9888	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	121	40
9889	D38112	Homo sapiens	NADH dehydrogenase subunit 2	346	68
9890	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	133	38
9891	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	143	66
9892	X53581	Rattus norvegicus	ORF7	81	56
9893	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	109	53
9894	AE003859	Xylella fastidiosa	hypothetical protein	99	27
9895	U83303	Homo sapiens	line-1 reverse transcriptase	157	58
9896	L26953	Homo sapiens	chromosomal protein	107	68
9897	AL390114	Leishmania major	probable (hlyv-6) u1102, variant a DNA, complete virion genome	95	51
9898	U93569	Homo sapiens	putative p150	106	52
9899	U15647	Mus musculus	reverse transcriptase	118	47
9900	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	118	70
9901	U93563	Homo sapiens	putative p150	116	39
9902	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	153	81
9903	X03145	Homo sapiens	pot. ORF V	148	54
9904	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	84	65
9905	AF066073	Dictyostelium discoideum	SP85; Psb	113	52
9906	AF090895	Homo sapiens	PRO0117	125	58
9907	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	102	57
9908	M24732	Homo sapiens	lamin-like protein	95	35

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9909	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	96	55
9910	AF118080	Homo sapiens	PRO1880	120	66
9911	AF116719	Homo sapiens	PRO2987	216	72
9912	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	150	75
9913	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	129	76
9914	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	72	58
9915	G00233	Homo sapiens	Human secreted protein, SEQ ID NO: 4314.	103	71
9916	S79410	Mus musculus	nuclear localization signal binding protein	114	75
9917	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	75	83
9918	AF116712	Homo sapiens	PRO2738	106	69
9919	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	90	77
9920	AF068294	Homo sapiens	HDCMB45P	296	59
9921	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	58	54
9922	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	143	69
9923	U38979	Homo sapiens	hPMSR3	135	46
9924	AB002317	Homo sapiens	KIAA0319	294	75
9925	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	169	42
9926	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	153	59
9927	G00214	Homo sapiens	Human secreted protein, SEQ ID NO: 4295.	261	97
9928	Y14483	Homo sapiens	Fragment of human secreted protein encoded by gene 18.	863	76
9929	AF130051	Homo sapiens	PRO0898	128	60
9930	AF130089	Homo sapiens	PRO2550	123	41
9931	AF064597	Homo sapiens	LINE-1 like protein	101	48
9932	AF027144	Homo sapiens	zinc finger protein	76	42
9933	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	120	44
9934	U93569	Homo sapiens	putative p150	105	68
9935	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	133	51
9936	Y73344	Homo sapiens	HTRM clone 0258181 protein sequence.	145	46
9937	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	123	77
9938	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	40
9939	D63643	Homo sapiens	clathrin coat assembly protein-like	232	69
9940	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	75	65
9941	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	176	71
9942	X04588	Homo sapiens	cytoskeletal tropomyosin (AA 1-248)	379	81
9943	G03683	Homo sapiens	Human secreted protein, SEQ ID NO: 7764.	58	52
9944	AF130114	Homo sapiens	PRO2459	117	67
9945	U49973	Homo sapiens	ORF1; MER37; putative transposase	297	64

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			similar to pogo element		
9946	D00570	Mus musculus	open reading frame (251 AA)	214	63
9947	X03717	Homo sapiens	pot. unidentified reading frame	76	35
9948	C00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	127	64
9949	J02621	Homo sapiens	high mobility group protein 14	90	50
9950	AF090931	Homo sapiens	PRO0483	114	75
9951	AF164612	Homo sapiens	Gag protein	132	63
9952	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	112	65
9953	Y08061	Homo sapiens	Human c-myb protein fragment.	118	59
9954	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	138	74
9955	G00974	Homo sapiens	Human secreted protein, SEQ ID NO: 5055.	94	38
9956	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	124	61
9957	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	177	51
9958	X92485	Plasmodium vivax	pva1	137	44
9959	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ52.	142	53
9960	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	174	68
9961	S79410	Mus musculus	nuclear localization signal binding protein	123	38
9962	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	124	56
9963	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	80	57
9964	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	136	82
9965	Y27908	Homo sapiens	Human secreted protein encoded by gene No. 119.	92	53
9966	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	76	40
9967	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	136	38
9968	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	101	67
9969	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	90	83
9970	Y36156	Homo sapiens	Human secreted protein #28.	170	68
9971	U79260	Homo sapiens	unknown	142	67
9972	L27428	Homo sapiens	reverse transcriptase	108	63
9973	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	119	60
9974	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	78	85
9975	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	79	39
9976	AF090944	Homo sapiens	PRO0663	109	73
9977	AF116715	Homo sapiens	PRO2829	120	56
9978	U93563	Homo sapiens	putative p150	132	57
9979	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	97	80
9980	U42580	Paramecium bursaria	A658R	70	40

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		Chlorella virus 1			
9981	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	87	61
9982	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	135	70
9983	X61047	Hydra sp.	mini-collagen	90	36
9984	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	98	40
9985	Y41552	Homo sapiens	Fragment of human secreted protein encoded by gene 80.	90	42
9986	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	132	52
9987	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	115	41
9988	AF042832	Homo sapiens	forkhead-related transcription factor FREAC-9	89	36
9989	X03717	Homo sapiens	pot. unidentified reading frame	105	67
9990	AL390935	Leishmania major	possible dopap	118	74
9991	AF201949	Homo sapiens	60S ribosomal protein L30 isolog	109	58
9992	AF130114	Homo sapiens	PRO2459	115	68
9993	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	83
9994	AF068294	Homo sapiens	HDCMB45P	196	43
9995	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	117	54
9996	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	74	53
9997	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	132	55
9998	AF102771	Homo sapiens	cardiac-specific ras association (RalGDS/AF-6) domain family 1 protein isoform 1D	148	100
9999	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	213	88
10000	D38112	Homo sapiens	ATPase subunit 6	279	69
10001	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	97	39
10002	AK000496	Homo sapiens	unnamed protein product	154	74
10003	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	125	74
10004	B07702	Homo sapiens	Protein encoded by the endogenetic fragment of HERV-W.	143	56
10005	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	97	65
10006	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	154	72
10007	AF021231	Mus musculus	acetylcholinesterase-associated collagen	109	41
10008	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	69	78
10009	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	170	78
10010	AF130051	Homo sapiens	PRO0898	134	67
10011	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	100	44
10012	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	95	78
10013	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	90	52
10014	AF130052	Homo sapiens	PRO0956	104	50

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10015	X92485	Plasmodium vivax	pval	119	46
10016	AF130089	Homo sapiens	PRO2550	171	56
10017	AF130089	Homo sapiens	PRO2550	172	58
10018	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	146	38
10019	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	109	54
10020	G02584	Homo sapiens	Human secreted protein, SEQ ID NO: 6665.	109	43
10021	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	70	51
10022	AF090942	Homo sapiens	PRO0657	113	67
10023	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	77	33
10024	X55681	Lycopersicon esculentum	extensin (class I)	95	35
10025	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	93	61
10026	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	153	42
10027	Y73377	Homo sapiens	HTRM clone 1645941 protein sequence.	1180	84
10028	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	108	59
10029	G00366	Homo sapiens	Human secreted protein, SEQ ID NO: 4447.	112	65
10030	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	163	82
10031	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncprotein.	131	66
10032	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	74	48
10033	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	104	85
10034	G03093	Homo sapiens	Human secreted protein, SEQ ID NO: 7174.	192	60
10035	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	153	55
10036	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	128	76
10037	AF118086	Homo sapiens	PRO1992	148	68
10038	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	125	47
10039	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	137	65
10040	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	139	45
10041	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	128	75
10042	U83303	Homo sapiens	hnc-1 reverse transcriptase	100	33
10043	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	102	64
10044	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	135	71
10045	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	148	46
10046	X92485	Plasmodium vivax	pval	98	58



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10047	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	102	87
10048	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	63	84
10049	U09202	Homo sapiens	ornithine decarboxylase antizyme	202	67
10050	X92485	Plasmodium vivax	pval	77	34
10051	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	87	40
10052	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	114	57
10053	AC005396	Arabidopsis thaliana	putative proline-rich protein	100	33
10054	G03600	Homo sapiens	Human secreted protein, SEQ ID NO: 7681.	91	94
10055	X73434	Ovis aries	KAP5.4 keratin protein	76	45
10056	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	82	62
10057	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	115	66
10058	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	116	55
10059	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	130	73
10060	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	100	42
10061	L27428	Homo sapiens	reverse transcriptase	107	43
10062	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	92	47
10063	G03112	Homo sapiens	Human secreted protein, SEQ ID NO: 7193.	93	46
10064	AF220264	Homo sapiens	MOST-1	135	48
10065	AF130114	Homo sapiens	PRO2459	87	68
10066	D86853	Catharanthus roseus	extensin	115	35
10067	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	79	71
10068	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	102	54
10069	U16359	Rattus norvegicus	nitric oxide synthase	93	77
10070	AJ235597	Mus musculus	reverse transcriptase	65	36
10071	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	94	67
10072	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	114	51
10073	AK024455	Homo sapiens	FLJ00047 protein	146	66
10074	X92485	Plasmodium vivax	pval	121	36
10075	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	130	64
10076	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	73	43
10077	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	165	75
10078	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	106	72
10079	AF130050	Homo sapiens	PRO0872	102	63
10080	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	130	44

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			8153.		
10081	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	285	78
10082	AF068294	Homo sapiens	HDCMB45P	144	68
10083	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	98	48
10084	X92485	Plasmodium vivax	pva1	108	53
10085	AF118082	Homo sapiens	PRO1902	117	57
10086	AF090942	Homo sapiens	PRO0657	88	53
10087	AF118086	Homo sapiens	PRO1992	172	71
10088	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	119	68
10089	K02576	Homo sapiens	salivary proline-rich protein 1	117	34
10090	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	154	77
10091	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	138	56
10092	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	90	56
10093	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	134	66
10094	M15530	Homo sapiens	B-cell growth factor	116	64
10095	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	124	65
10096	M15530	Homo sapiens	B-cell growth factor	87	68
10097	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	84	79
10098	G00359	Homo sapiens	Human secreted protein, SEQ ID NO: 4450.	150	66
10099	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	157	70
10100	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	103	60
10101	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	114	70
10102	AL359782	Trypanosoma brucei	possible (hlv-6) u1102, variant a dna, complete virion genome.	130	53
10103	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	156	52
10104	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	87	60
10105	L27428	Homo sapiens	reverse transcriptase	220	38
10106	W90834	Homo sapiens	Human lymphocyte targeted peptide #2.	91	43
10107	AF161356	Homo sapiens	HSPC093	227	61
10108	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	123	64
10109	AF130089	Homo sapiens	PRO2550	126	77
10110	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	118	60
10111	M63274	Plasmodium falciparum	malaria antigen	81	54
10112	AF090944	Homo sapiens	PRO0663	133	70
10113	L27428	Homo sapiens	reverse transcriptase	91	32
10114	Y17221	Homo sapiens	Human secreted protein (clone fk317-3).	112	64
10115	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	85	44

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10116	L27428	Homo sapiens	reverse transcriptase	112	44
10117	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	115	61
10118	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	79	34
10119	AF194537	Homo sapiens	NAG13	295	51
10120	D00570	Mus musculus	open reading frame (196 AA)	97	40
10121	X77816	Rattus norvegicus	PR-Vbeta1	122	47
10122	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	148	55
10123	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	92	66
10124	AF090942	Homo sapiens	PRO0657	127	78
10125	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	145	68
10126	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	113	49
10127	U93563	Homo sapiens	putative p150	94	35
10128	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	146	79
10129	AF130089	Homo sapiens	PRO2550	208	75
10130	M15530	Homo sapiens	B-cell growth factor	102	73
10131	X55685	Lycopersicon esculentum	extensin (class I)	122	30
10132	L27428	Homo sapiens	reverse transcriptase	197	40
10133	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	99	73
10134	AF194537	Homo sapiens	NAG13	220	48
10135	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	116	75
10136	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	117	61
10137	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	223	59
10138	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	178	75
10139	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	170	52
10140	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	133	64
10141	AF072164	Homo sapiens	HFSE-1	80	60
10142	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	103	74
10143	M15530	Homo sapiens	B-cell growth factor	91	40
10144	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	103	61
10145	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	162	65
10146	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	128	53
10147	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	112	61
10148	X71975	Drosophila melanogaster	put. homologue to S.cerevisiae GARI gene	118	39
10149	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	123	49
10150	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	163	81

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10151	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	106	83
10152	AL390114	Leishmania major	extremely cysteine/valine rich protein	117	52
10153	AF113685	Homo sapiens	PRO0974	133	62
10154	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	129	67
10155	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	89	50
10156	K02576	Homo sapiens	salivary proline-rich protein 1	131	41
10157	AB011099	Homo sapiens	KIAA0527 protein	94	35
10158	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	78	72
10159	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	139	71
10160	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	161	68
10161	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	162	88
10162	M15530	Homo sapiens	B-cell growth factor	137	63
10163	AF090895	Homo sapiens	PRO0117	93	67
10164	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	60
10165	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	126	52
10166	AF118082	Homo sapiens	PRO1902	111	55
10167	AF090895	Homo sapiens	PRO0117	112	75
10168	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	135	69
10169	AF090942	Homo sapiens	PRO0657	149	67
10170	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	145	68
10171	AL160371	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	85	51
10172	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	136	62
10173	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	158	63
10174	AF090942	Homo sapiens	PRO0657	75	44
10175	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	97	47
10176	Y01154	Homo sapiens	Protein sequence Seq Id 54 from WO9901020.	108	75
10177	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	168	80
10178	M22332	Homo sapiens	unknown protein	131	62
10179	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	160	60
10180	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	65	68
10181	AF119900	Homo sapiens	PRO2822	132	72
10182	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	114	56
10183	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	124	59
10184	AF210651	Homo sapiens	NAG18	150	65
10185	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	109	46
10186	X71442	Rattus	ORF 1; putative	91	47

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		norvegicus			
10187	AK024455	Homo sapiens	FLJ00047 protein	122	54
10188	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	82	72
10189	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	78	61
10190	AF220264	Homo sapiens	MOST-1	165	81
10191	Y91617	Homo sapiens	Human secreted protein sequence encoded by gene 19 SEQ ID NO:290.	54	44
10192	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	119	80
10193	X92485	Plasmodium vivax	pva1	128	57
10194	X61296	Rattus norvegicus	open reading frame 2	79	72
10195	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	116	62
10196	AF130089	Homo sapiens	PRO2550	144	62
10197	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	124	56
10198	AF090942	Homo sapiens	PRO0657	133	76
10199	S79304	Rattus sp.	cytochrome oxidase subunit I; COX I	280	66
10200	S61070	Homo sapiens	reverse transcriptase homolog-pol {retroviral element}	188	49
10201	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	51
10202	AF068294	Homo sapiens	HDCMB45P	174	65
10203	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	174	50
10204	U93572	Homo sapiens	putative p150	77	40
10205	L27428	Homo sapiens	reverse transcriptase	133	50
10206	J02621	Homo sapiens	high mobility group protein 14	94	57
10207	AF130079	Homo sapiens	PRO2852	144	73
10208	R95913	Homo sapiens	Neural thread protein.	134	51
10209	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	154	76
10210	AB046048	Macaca fascicularis	unnamed portein product	162	60
10211	AF090931	Homo sapiens	PRO0483	128	79
10212	AF130051	Homo sapiens	PRO0898	144	76
10213	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	95	54
10214	AF130089	Homo sapiens	PRO2550	158	70
10215	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	96	55
10216	M15894	Homo sapiens	chorionic somatomammotropin precursor	116	63
10217	AK024372	Homo sapiens	unnamed protein product	85	56
10218	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	118	69
10219	M37679	Mus musculus	Ig heavy chain precursor	64	83
10220	G03806	Homo sapiens	Human secreted protein, SEQ ID NO: 7887.	91	69
10221	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	127	47
10222	Y36505	Homo sapiens	Fragment of human secreted protein encoded by gene 29.	102	48
10223	AF090940	Homo sapiens	PRO0644	105	76
10224	U49974	Homo sapiens	mariner transposase	155	76
10225	K02576	Homo sapiens	salivary proline-rich protein 1	154	42

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10226	AF293639	Homo sapiens	dioxin receptor repressor	819	98
10227	L27428	Homo sapiens	reverse transcriptase	137	44
10228	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	106	70
10229	U93566	Homo sapiens	p40	206	80
10230	Y08061	Homo sapiens	Human c-myc protein fragment.	114	66
10231	AF118082	Homo sapiens	PRO1902	76	52
10232	AF118086	Homo sapiens	PRO1992	99	75
10233	X53375	Helianthus annuus	anther-specific protein SF18	95	64
10234	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	156	72
10235	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	100	35
10236	L27428	Homo sapiens	reverse transcriptase	244	50
10237	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	93	70
10238	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	142	72
10239	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	149	80
10240	S52010	Mus sp.	1st Met is at position 21	98	42
10241	AL110147	Homo sapiens	hypothetical protein	125	35
10242	X98485	Plasmodium vivax	putative	85	51
10243	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	70	65
10244	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO: 103.	125	49
10245	U49973	Homo sapiens	ORF2: function unknown	150	81
10246	K02576	Homo sapiens	salivary proline-rich protein 1	113	56
10247	AF130089	Homo sapiens	PRO2550	139	73
10248	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	160	59
10249	U93565	Homo sapiens	putative p150	109	43
10250	AF130089	Homo sapiens	PRO2550	104	54
10251	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	78	36
10252	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	110	58
10253	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	123	54
10254	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	95	57
10255	X03145	Homo sapiens	pot. ORF V	76	63
10256	Y01405	Homo sapiens	Secreted protein encoded by gene 23 clone HDPBA48.	116	65
10257	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	113	68
10258	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	138	68
10259	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	135	60
10260	G02528	Homo sapiens	Human secreted protein, SEQ ID NO: 6609.	95	59
10261	M86246	Homo sapiens	EHS-2	96	62
10262	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	180	66
10263	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 102	102	62

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7871.		
10264	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	313	84
10265	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	144	56
10266	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	150	61
10267	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	408	89
10268	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	74	26
10269	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	133	52
10270	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	105	61
10271	X61048	Hydra sp.	mini-collagen	121	40
10272	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	150	66
10273	L24521	Homo sapiens	transformation-related protein	134	51
10274	G03806	Homo sapiens	Human secreted protein, SEQ ID NO: 7887.	96	47
10275	U59446	Brassica napus	myrosinase-binding protein related protein	115	39
10276	G01480	Homo sapiens	Human secreted protein, SEQ ID NO: 5561.	482	98
10277	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	143	81
10278	U93564	Homo sapiens	putative p150	130	46
10279	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	123	44
10280	AF090944	Homo sapiens	PRO0663	156	73
10281	AF130079	Homo sapiens	PRO2852	146	75
10282	X89401	Homo sapiens	ribosomal protein L21	108	48
10283	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	65	66
10284	Y25821	Homo sapiens	Human secreted protein fragment encoded from gene 41.	1602	98
10285	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	308	43
10286	AF090931	Homo sapiens	PRO0483	131	74
10287	Y48480	Homo sapiens	Human breast tumour-associated protein 25.	203	90
10288	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	116	44
10289	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	160	64
10290	X67863	Mus musculus	T2	147	37
10291	AF229067	Homo sapiens	PADI-H protein	123	43
10292	AF078844	Homo sapiens	hqp0376 protein	125	59
10293	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	123	37
10294	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	103	64
10295	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	162	70
10296	Y00662	Homo sapiens	ATPase 6	268	88
10297	AB007861	Homo sapiens	KIAA0401	424	92
10298	M24732	Homo sapiens	lamin-like protein	183	40
10299	D90053	Sus scrofa	destrin	123	48
10300	X61047	Hydra sp.	mini-collagen	86	43

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10301	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	180	50
10302	AF118078	Homo sapiens	PRO1848	157	63
10303	X55681	Lycopersicon esculentum	extensin (class I)	87	36
10304	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	105	62
10305	X70944	Homo sapiens	PTB-associated splicing factor	84	32
10306	AF068294	Homo sapiens	HDCMB45P	220	42
10307	S79410	Mus musculus	nuclear localization signal binding protein	96	41
10308	AJ005559	Mus musculus	SPR2A protein	64	42
10309	AL353995	Arabidopsis thaliana	AtAGP4	98	38
10310	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	213	92
10311	M15386	Homo sapiens	gamma-globin	614	88
10312	V00488	Homo sapiens	alpha globin	574	90
10313	AL049730	Arabidopsis thaliana	pEARL1 1-like protein	117	38
10314	AL356299	Homo sapiens	bK3216D2.1.1 (S-adenosylhomocysteine hydrolase (SAHH), isoform 1)	256	70
10315	AF194537	Homo sapiens	NAG13	113	63
10316	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	99	62
10317	AF090931	Homo sapiens	PRO0483	86	68
10318	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	102	77
10319	L29219	Homo sapiens	clik1; putative	341	100
10320	V00488	Homo sapiens	alpha globin	314	89
10321	AJ223953	Homo sapiens	hPTTG	354	89
10322	X79389	Homo sapiens	glutathione transferase T1	78	75
10323	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	101	66
10324	AF116715	Homo sapiens	PRO2829	128	73
10325	AF116619	Homo sapiens	PRO1051	125	77
10326	Y14318	Homo sapiens	peroxisomal ABC-transporter	249	100
10327	U73844	Homo sapiens	ESE-1a	185	90
10328	AB051901	Homo sapiens	VDUP1	132	83
10329	AL163300	Homo sapiens	human ubiquitin conjugating enzyme G2 EC 6.3.2.19.	720	100
10330	AF117237	Homo sapiens	prefoldin subunit 2	729	100
10331	D42054	Homo sapiens	KIAA0092 gene product is distantly related to smooth muscle myosin.	352	84
10332	AF038965	Homo sapiens	26S proteasome ATPase subunit	431	100
10333	Y94960	Homo sapiens	Human secreted protein clone m1117_1 protein sequence SEQ ID NO:126.	399	96
10334	X60376	Brassica napus	proline-rich protein	114	31
10335	M34427	Homo sapiens	T-plastin	343	91
10336	V00488	Homo sapiens	alpha globin	445	88
10337	M15386	Homo sapiens	gamma-globin	402	85
10338	X61123	Homo sapiens	BTGI	367	90
10339	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	278	87
10340	A03992	synthetic construct	growth hormone	145	61
10341	G00437	Homo sapiens	Human secreted protein, SEQ ID NO:	126	57



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4518.		
10342	U02680	Homo sapiens	protein tyrosine kinase	140	92
10343	AF180681	Homo sapiens	guanine nucleotide exchange factor	1425	88
10344	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	123	69
10345	V00488	Homo sapiens	alpha globin	318	93
10346	M17885	Homo sapiens	acidic ribosomal phosphoprotein (P0)	329	98
10347	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	100	66
10348	U29953	Homo sapiens	pigment epithelium-derived factor	359	74
10349	G01790	Homo sapiens	Human secreted protein, SEQ ID NO: 5871.	85	66
10350	V00488	Homo sapiens	alpha globin	361	90
10351	U93567	Homo sapiens	p40	203	84
10352	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	253	85
10353	AF194537	Homo sapiens	NAG13	196	41
10354	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	297	81
10355	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	144	65
10356	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	94	54
10357	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	153	68
10358	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	136	53
10359	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	95	77
10360	X61296	Rattus norvegicus	open reading frame 2	87	40
10361	L24521	Homo sapiens	transformation-related protein	103	32
10362	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	101	55
10363	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	89	80
10364	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	101	58
10365	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	322	85
10366	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	59
10367	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	125	53
10368	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	120	59
10369	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	60	83
10370	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	169	81
10371	X62677	Cryptolagus cuniculus	retrovirus related reverse transcriptase	80	75
10372	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	60	83
10373	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	89	77
10375	AF130089	Homo sapiens	PRO2550	139	78
10376	G03793	Homo sapiens	Human secreted protein, SEQ ID NO:	146	62

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7874.		
10377	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	96	51
10378	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	132	58
10379	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	117	71
10380	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	125	54
10381	U93569	Homo sapiens	putative p150	160	60
10382	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	140	77
10383	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	83	71
10384	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	137	63
10385	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	67	50
10386	X62691	Homo sapiens	ribosomal protein homologous to yeast S24	117	58
10387	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	141	45
10388	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	153	70
10389	U93570	Homo sapiens	putative p150	112	58
10390	AF090942	Homo sapiens	PRO0657	126	68
10391	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	123	64
10392	AF130089	Homo sapiens	PRO2550	144	71
10393	U40739	Homo sapiens	cyclin C	464	86
10394	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	151	75
10395	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	137	55
10396	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	165	66
10397	AF090930	Homo sapiens	PRO0478	133	80
10398	AK024455	Homo sapiens	FLJ00047 protein	153	62
10399	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	142	69
10400	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	73	51
10401	AB030033	Dictyostelium discoideum	AmiB	82	33
10402	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	113	63
10403	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	148	77
10404	AK024455	Homo sapiens	FLJ00047 protein	138	71
10405	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	128	59
10406	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	143	76
10407	AF090942	Homo sapiens	PRO0657	105	64
10408	SS8722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEIL8c}	93	54
10409	J02621	Homo sapiens	high mobility group protein 14	140	64
10410	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	87	46
10411	G03798	Homo sapiens	Human secreted protein, SEQ ID NO:	79	56

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7879.		
10412	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	79	66
10413	AF130079	Homo sapiens	PRO2852	184	90
10414	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	237	77
10415	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	122	64
10416	AF016099	Mus musculus	endonuclease/reverse transcriptase	89	78
10417	S80864	Homo sapiens	cytochrome c-like polypeptide	184	52
10418	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	131	75
10419	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	160	90
10420	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	131	59
10421	AF090942	Homo sapiens	PRO0657	154	57
10423	L78669	Homo sapiens	CoxII/D-loop DNA fusion protein	106	90
10424	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	105	75
10425	AL359782	Trypanosoma brucei	probable similar to ring-f2 finger protein rha1a.	130	64
10426	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	122	64
10427	AF068294	Homo sapiens	HDCMB45P	256	56
10428	AF194537	Homo sapiens	NAG13	182	54
10429	AF090931	Homo sapiens	PRO0483	108	79
10430	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	93	68
10431	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10432	X67920	Homo sapiens	tryptophanyl-tRNA synthetase	138	84
10433	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	294	78
10434	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10435	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	125	75
10436	S79410	Mus musculus	nuclear localization signal binding protein	117	72
10437	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	120	67
10438	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	140	69
10439	AF130089	Homo sapiens	PRO2550	106	80
10440	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	331	83
10441	W94294	Homo sapiens	Human phosphatidylinositol transfer protein gamma.	143	96
10442	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	121	87
10443	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10444	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	141	67
10445	U93567	Homo sapiens	p40	262	69
10446	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	112	92
10447	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1	120	83

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			protein		
10448	G02597	Homo sapiens	Human secreted protein, SEQ ID NO: 6678.	104	68
10449	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	115	80
10450	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	117	80
10451	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	104	80
10452	AF130089	Homo sapiens	PRO2550	315	68
10453	G02530	Homo sapiens	Human secreted protein, SEQ ID NO: 6611.	110	71
10454	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	86	34
10455	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	113	85
10456	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	180	83
10457	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	119	96
10458	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	133	58
10459	Y41710	Homo sapiens	Human PRO618 protein sequence.	894	71
10460	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	84	71
10461	K02401	Homo sapiens	chorionic somatomammotropin	471	88
10462	G02113	Homo sapiens	Human secreted protein, SEQ ID NO: 6194.	241	73
10463	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	93	68
10464	U15647	Mus musculus	reverse transcriptase	110	47
10465	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	97	57
10466	G02754	Homo sapiens	Human secreted protein, SEQ ID NO: 6835.	145	93
10467	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	137	57
10468	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	62	55
10469	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	93	86
10470	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEL8c}	119	63
10471	AF068294	Homo sapiens	HDCMB45P	117	43
10472	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	335	72
10473	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	121	62
10474	X79238	Homo sapiens	ribosomal protein L30	126	58
10475	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10476	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	106	61
10477	AC006693	Caenorhabditis elegans	Hypothetical protein W02H5.e	119	41
10478	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	87	66
10479	AF130079	Homo sapiens	PRO2852	97	54
10480	AK024455	Homo sapiens	FLJ00047 protein	135	69

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10481	K02401	Homo sapiens	chorionic somatomammotropin	463	80
10482	G00398	Homo sapiens	Human secreted protein, SEQ ID NO: 4479.	69	83
10483	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	132	61
10484	R13556	Homo sapiens	Protein encoded downstream of hhe_M oncogene.	119	80
10485	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	90	54
10486	U79260	Homo sapiens	unknown	105	90
10487	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	243	53
10488	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	90	78
10489	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	120	64
10490	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	123	60
10491	Y48576	Homo sapiens	Human breast tumour-associated protein 37.	471	84
10492	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	176	77
10493	S79410	Mus musculus	nuclear localization signal binding protein	135	64
10494	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	123	44
10495	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	86	46
10496	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	145	40
10497	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	111	50
10498	SS8722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	96	73
10499	AL132841	Caenorhabditis elegans	Y15E3A.3	142	96
10500	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	120	49
10501	AF220264	Homo sapiens	MOST-1	93	83
10502	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	116	57
10503	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	100	70
10504	AF090931	Homo sapiens	PRO0483	88	80
10505	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	89	72
10506	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	121	81
10507	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	188	82
10508	AF130050	Homo sapiens	PRO0872	101	74
10509	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	176	68
10510	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	120	96
10511	AK026249	Homo sapiens	unnamed protein product	97	68
10512	X95276	Plasmodium falciparum	ORF91	75	29
10513	X17093	Homo sapiens	leukocyte antigen F	397	91
10514	W48351	Homo sapiens	Human breast cancer related protein	115	66

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2.		
10515	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	154	68
10516	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	86	47
10517	AF090944	Homo sapiens	PRO0663	118	48
10518	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	131	77
10519	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	230	58
10520	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10521	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	130	40
10522	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10523	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	139	69
10524	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	125	100
10525	J04495	Macaca mulatta	alpha-globin	144	90
10526	G02535	Homo sapiens	Human secreted protein, SEQ ID NO: 6616.	105	61
10527	AF130089	Homo sapiens	PRO2550	132	67
10528	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	90	53
10529	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	112	75
10530	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	157	79
10531	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	59
10532	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	121	63
10533	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	112	43
10534	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	131	65
10535	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	95	60
10536	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	157	79
10537	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	199	90
10538	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	113	75
10539	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	120	65
10540	AF130089	Homo sapiens	PRO2550	195	67
10541	Y60522	Homo sapiens	Human normal bladder tissue EST encoded protein 194.	73	72
10542	G01175	Homo sapiens	Human secreted protein, SEQ ID NO: 5256.	83	100
10543	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	81	54
10544	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	147	75
10545	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	109	66

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10546	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	123	46
10547	AF130089	Homo sapiens	PRO2550	133	63
10548	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	246	80
10549	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	122	51
10550	J02459	bacteriophage lambda	J (tail:host specificity;1132)	772	97
10551	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	158	80
10552	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	123	50
10553	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	184	71
10554	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	107	60
10555	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	140	69
10556	U49973	Homo sapiens	ORF2: function unknown	91	70
10557	AF151850	Homo sapiens	CGI-92 protein	459	63
10558	X66285	Mus musculus	HC1 ORF	92	30
10559	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	127	67
10560	AF130050	Homo sapiens	PRO0872	100	71
10561	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	335	80
10562	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	126	58
10563	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	127	76
10564	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	158	62
10565	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	118	77
10566	V00488	Homo sapiens	alpha globin	464	89
10567	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	162	81
10568	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	113	72
10569	G03040	Homo sapiens	Human secreted protein, SEQ ID NO: 7121.	127	47
10570	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	125	65
10571	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	79	88
10572	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	158	80
10573	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	138	56
10574	AF119900	Homo sapiens	PRO2822	154	55
10575	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	87	72
10576	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	131	66
10577	G03112	Homo sapiens	Human secreted protein, SEQ ID NO: 7193.	80	47
10578	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	121	53
10579	Y91577	Homo sapiens	Human secreted protein sequence	335	83

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded by gene 2 SEQ ID NO:250.		
10580	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	104	47
10581	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	324	68
10582	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	129	66
10583	AF090895	Homo sapiens	PRO0117	137	63
10584	L27428	Homo sapiens	reverse transcriptase	98	50
10585	G00418	Homo sapiens	Human secreted protein, SEQ ID NO: 4499.	101	68
10586	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	108	82
10587	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	166	76
10588	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	100	70
10589	X03145	Homo sapiens	pot. ORF I	120	43
10590	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	139	70
10591	AF144054	Homo sapiens	apoptosis related protein APR-4	92	50
10592	AK024455	Homo sapiens	FLJ00047 protein	111	75
10593	AL359782	Trypanosoma brucei	possible (hvh-6) u1102, variant a dna, complete virion genome.	143	58
10594	G03636	Homo sapiens	Human secreted protein, SEQ ID NO: 7717.	116	54
10595	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	196	57
10596	AF130089	Homo sapiens	PRO2550	140	66
10597	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	115	52
10598	G00481	Homo sapiens	Human secreted protein, SEQ ID NO: 4562.	79	71
10599	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	79
10600	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	119	67
10601	AF090895	Homo sapiens	PRO0117	106	68
10602	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	83	72
10603	AF090930	Homo sapiens	PRO0478	119	70
10604	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	120	83
10605	AF132949	Homo sapiens	CGI-15 protein	114	96
10606	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	176	77
10607	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	155	74
10608	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	127	63
10609	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	88	60
10610	AF130089	Homo sapiens	PRO2550	86	90
10611	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	149	72
10612	L27428	Homo sapiens	reverse transcriptase	311	52
10613	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	83	84
10614	D00570	Mus musculus	open reading frame (196 AA)	116	69



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10615	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	290	62
10616	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	125	51
10617	AF116695	Homo sapiens	PRO2221	131	56
10618	M64793	Rattus norvegicus	salivary proline-rich protein	101	48
10619	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	104	65
10620	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	112	58
10621	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	336	85
10622	AF118082	Homo sapiens	PRO1902	80	73
10623	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	136	50
10624	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	109	67
10625	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	92	75
10626	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	121	62
10627	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	104	52
10628	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	137	66
10629	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	67
10630	U93569	Homo sapiens	putative p150	104	52
10631	AF090895	Homo sapiens	PRO0117	136	70
10632	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	89	57
10633	AF113685	Homo sapiens	PRO0974	130	64
10634	AK024455	Homo sapiens	FLJ00047 protein	103	63
10635	M24732	Homo sapiens	lamin-like protein	80	65
10636	U49974	Homo sapiens	mariner transposase	116	72
10637	AK024455	Homo sapiens	FLJ00047 protein	158	67
10638	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	121	64
10639	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	137	57
10640	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	123	72
10641	L27428	Homo sapiens	reverse transcriptase	150	54
10642	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	68	81
10643	U93565	Homo sapiens	putative p150	282	57
10644	AF090942	Homo sapiens	PRO0657	153	74
10645	Y48333	Homo sapiens	Human prostate cancer-associated protein 30.	196	90
10646	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	242	73
10647	U79260	Homo sapiens	unknown	95	77
10648	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	149	64
10649	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	158	87
10650	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	339	89

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10651	U15183	Mycobacterium leprae	proline-rich antigen	102	37
10652	AF217536	Homo sapiens	truncated mevalonate kinase	138	70
10653	AF119855	Homo sapiens	PRO1847	74	100
10654	M15530	Homo sapiens	B-cell growth factor	94	52
10655	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	144	54
10656	M15317	Plasmodium falciparum	histidine-rich protein	124	51
10657	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	143	66
10658	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	114	77
10659	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	172	55
10660	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	150	78
10661	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10662	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	151	71
10663	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10664	AK000496	Homo sapiens	unnamed protein product	140	77
10665	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	147	75
10666	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10667	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	149	78
10668	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	303	78
10669	D00526	Rattus norvegicus	L-gulon-gamma-lactone oxidase	108	73
10670	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	143	65
10671	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	409	84
10672	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	110	65
10673	G00423	Homo sapiens	Human secreted protein, SEQ ID NO: 4504.	123	43
10674	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	85	36
10675	U93565	Homo sapiens	putative p150	115	45
10676	AF109907	Homo sapiens	SI64	205	65
10677	G02620	Homo sapiens	Human secreted protein, SEQ ID NO: 6701.	118	73
10678	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	106	62
10679	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10680	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	248	54
10681	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	88	52
10682	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	126	77
10683	S58722	Homo sapiens	X-linked retinopathy protein {C-	123	72

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			terminal, clone XEH.8c}		
10684	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	123	72
10685	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	99	40
10686	AF068294	Homo sapiens	HDCMB45P	182	54
10687	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	104	53
10688	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	277	76
10689	G00233	Homo sapiens	Human secreted protein, SEQ ID NO: 4314.	118	65
10690	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	143	71
10691	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	97	81
10692	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	160	68
10693	AF130089	Homo sapiens	PRO2550	133	56
10694	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	129	71
10695	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	123	71
10696	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	161	45
10697	G00648	Homo sapiens	Human secreted protein, SEQ ID NO: 4729.	88	56
10698	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	75	71
10699	G00517	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	92	38
10700	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	132	55
10701	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	118	54
10702	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	66	73
10703	S79410	Mus musculus	nuclear localization signal binding protein	124	44
10704	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	113	78
10705	S79410	Mus musculus	nuclear localization signal binding protein	119	50
10706	AK025116	Homo sapiens	unnamed protein product	160	84
10707	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10708	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10709	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	230	76
10710	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	96	45
10711	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	174	70
10712	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	127	50
10713	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	148	45
10714	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	151	80

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10715	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	157	67
10716	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	109	68
10717	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	151	52
10718	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	84	80
10719	M19973	Rattus norvegicus	cytochrome PB24	104	45
10720	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	103	72
10721	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	161	52
10722	L27428	Homo sapiens	reverse transcriptase	159	42
10723	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XE11.8c)	127	75
10724	Y00311	Homo sapiens	Human secreted protein encoded by gene 54.	84	50
10725	AF090895	Homo sapiens	PRO0117	170	71
10726	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	105	42
10727	K03205	Homo sapiens	salivary proline-rich protein precursor	123	38
10728	U93563	Homo sapiens	putative p150	162	64
10729	X14576	Murine leukemia virus	gag fusion protein	172	41
10730	AF090895	Homo sapiens	PRO0117	151	60
10731	AF119851	Homo sapiens	PRO1722	127	54
10732	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	152	61
10733	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	156	76
10734	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	135	73
10735	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	151	65
10736	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	141	75
10737	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	74
10738	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	124	69
10739	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	91	60
10740	AF130051	Homo sapiens	PRO0898	90	63
10741	AF090895	Homo sapiens	PRO0117	129	55
10742	AF119900	Homo sapiens	PRO2822	164	85
10743	AJ005560	Mus musculus	SPK2B protein	88	35
10744	Z79996	Homo sapiens	cB33F2.1 (PUTATIVE novel protein similar to C-terminal parts of APOL (apolipoprotein L) and TNF-inducible protein CG12-1)	185	100
10745	G03140	Homo sapiens	Human secreted protein, SEQ ID NO: 7221.	94	88
10746	X82208	Homo sapiens	beta-contractin	134	96
10747	D49744	Mus musculus	farnesyltransferase alpha subunit	228	60
10748	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	127	50
10749	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	153	62

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4523.		
10750	AF130089	Homo sapiens	PRO2550	147	62
10751	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	108	71
10752	D17652	Homo sapiens	HBp15/L22	416	72
10753	AB002389	Homo sapiens	KIAA0391	486	86
10754	G03093	Homo sapiens	Human secreted protein, SEQ ID NO: 7174.	238	73
10755	S79410	Mus musculus	nuclear localization signal binding protein	103	57
10756	AF130089	Homo sapiens	PRO2550	104	72
10757	X75421	Hypocrea jecorina	actin	197	66
10758	AF298594	Nicotiana glauca	arabinogalactan protein	107	30
10759	U94832	Homo sapiens	KSRP	95	40
10760	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	179	82
10761	Y86573	Homo sapiens	Human gene 91 - encoded protein fragment, SEQ ID NO:490.	271	80
10762	Z81528	Caenorhabditis elegans	predicted using GeneFinder - contains similarity to Pfam domain: PF00939 (Sodium:sulfate symporter transmembrane region), Score=2.8, E-value=1.2, N=1; PF01757 (Domain of unknown function), Score=556.0, E-value=8.1e-164, N=1	103	27
10763	V00662	Homo sapiens	ATPase 6	593	83
10764	A06977	Homo sapiens	albumin	610	81
10765	X67863	Mus musculus	T2	109	46
10766	AF137030	Homo sapiens	transmembrane protein 2	620	96
10767	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	101	66
10768	X15324	Homo sapiens	angiotensinogen	529	89
10769	M64983	Homo sapiens	fibrinogen beta chain	604	87
10770	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	381	83
10771	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	133	73
10772	M64110	Homo sapiens	caldesmon	346	94
10773	AB014566	Homo sapiens	KIAA0666 protein	145	78
10774	AL138810	Homo sapiens	dJ179L10.2 (Similar to CGI-29 protein)	216	90
10775	AJ223953	Homo sapiens	hPTTG	353	82
10776	U92288	Human herpesvirus 6	HN1	113	39
10777	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	143	78
10778	X12796	Bos taurus	HMG1 protein (AA 1 - 215)	435	96
10779	U86782	Homo sapiens	26S proteasome-associated pad1 homolog	477	89
10780	M60047	Homo sapiens	heparin binding protein	514	81
10781	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	99	48
10782	AF130079	Homo sapiens	PRO2852	175	48
10783	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	115	64
10784	M11147	Homo sapiens	ferritin light chain	439	83
10785	AF090931	Homo sapiens	PRO0483	145	55
10786	AF072441	Homo sapiens	calcineurin binding protein cabin 1	498	90
10787	AF116715	Homo sapiens	PRO2829	127	88

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10788	AF201949	Homo sapiens	60S ribosomal protein L30 isolog	631	91
10789	AC005253	Homo sapiens	R26445_1	403	84
10790	M15386	Homo sapiens	gamma-globin	617	82
10791	Y95005	Homo sapiens	Human secreted protein vc57_1, SEQ ID NO:50.	716	95
10792	G01285	Homo sapiens	Human secreted protein, SEQ ID NO: 5366.	165	52
10793	X67863	Mus musculus	T2	128	50
10794	Y82326	Homo sapiens	Human arginase I SEQ ID NO:17.	507	80
10795	Y00755	Homo sapiens	extracellular matrix protein BM-40 (AA 1 - 303)	559	87
10796	AF119851	Homo sapiens	PRO1722	117	71
10797	AF090930	Homo sapiens	PRO0478	146	63
10798	V00488	Homo sapiens	alpha globin	509	84
10799	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	131	42
10800	X83618	Homo sapiens	hydroxymethylglutaryl-CoA synthase	422	78
10801	AF132952	Homo sapiens	CGI-18 protein	341	88
10802	M17375	Gallus gallus	type XII collagen	88	42
10803	K02401	Homo sapiens	chorionic somatomammotropin	436	85
10804	K02401	Homo sapiens	chorionic somatomammotropin	410	86
10805	U61232	Homo sapiens	cofactor E	359	77
10806	D86438	Homo sapiens	Iba1 (ionized calcium binding adapter molecule 1)	406	77
10807	AF118082	Homo sapiens	PRO1902	105	38
10808	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	148	60
10809	AF090942	Homo sapiens	PRO0657	163	52
10810	U63332	Homo sapiens	super cysteine rich protein; SCRP	116	86
10811	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	104	45
10812	X61296	Rattus norvegicus	open reading frame 2	156	41
10813	U82303	Homo sapiens	unknown	103	64
10814	G01478	Homo sapiens	Human secreted protein, SEQ ID NO: 5559.	75	77
10815	U52077	Homo sapiens	mariner transposase	131	85
10816	D38112	Homo sapiens	ATPase subunit 6	251	74
10817	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	103	80
10818	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	102	52
10819	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	94	66
10820	Y21811	Homo sapiens	CPF polypeptide 36PRO.	200	62
10821	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	161	60
10822	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	70
10823	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	337	63
10824	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	122	61
10825	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	122	68
10826	J03634	Homo sapiens	erythroid differentiation protein precursor	222	68



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10867	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	99	75
10868	U79260	Homo sapiens	unknown	94	47
10869	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene product.	151	52
10870	AJ010025	Homo sapiens	unr-interacting protein	100	64
10871	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	110	44
10872	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	136	71
10873	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	126	61
10874	AF130089	Homo sapiens	PRO2550	115	88
10875	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	114	59
10876	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	83	48
10877	AF118086	Homo sapiens	PRO1992	145	82
10878	AF116712	Homo sapiens	PRO2738	110	55
10879	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	123	77
10880	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	111	61
10881	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	106	51
10882	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	107	67
10883	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	101	65
10884	U79260	Homo sapiens	unknown	111	56
10885	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	153	60
10886	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	107	57
10887	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	148	80
10888	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	142	58
10889	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	156	67
10890	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	105	52
10891	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	187	65
10892	A67510	Mus musculus	MUS MUSCULUS GENOMIC DNA CONTAINING N ALLELE OF FV1 GENE.	120	37
10893	AJ223410	Homo sapiens	EBI1-ligand chemokine	174	77
10894	D38112	Homo sapiens	cytochrome c oxidase subunit 1	475	83
10895	V00662	Homo sapiens	ATPase 6	316	95
10896	V00662	Homo sapiens	ATPase 6	427	82
10897	U09500	Homo sapiens	cytochrome b	403	92
10898	U93564	Homo sapiens	p40	215	91
10899	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	69	77
10900	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	159	60
10901	AC003058	Arabidopsis thaliana	unknown protein	93	43



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10902	M10546	Homo sapiens	cytochrome oxidase I	302	66
10903	G00447	Homo sapiens	Human secreted protein, SEQ ID NO: 4528.	102	58
10904	AK024455	Homo sapiens	FLJ00047 protein	118	74
10905	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	108	64
10906	AF090942	Homo sapiens	PRO0657	149	74
10907	J01415	Homo sapiens	cytochrome oxidase subunit 3	167	91
10908	D38112	Homo sapiens	ATPase subunit 6	355	68
10909	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	145	72
10910	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	114	72
10911	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	144	53
10912	V00662	Homo sapiens	ATPase 6	289	69
10913	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	93	51
10914	V00662	Homo sapiens	cytochrome oxidase III	509	86
10915	J03071	Homo sapiens	chorionic somatomammotropin CS-2	459	80
10916	G28029	Saccharomyces cerevisiae	ORF YKL030w	96	32
10917	G03102	Homo sapiens	Human secreted protein, SEQ ID NO: 7183.	94	56
10918	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	114	36
10919	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	88
10920	S58722	Homo sapiens	X-linked neuropathy protein {C-terminal, clone XEH.8c}	103	39
10921	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	99	95
10922	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	75	63
10923	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	125	85
10924	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	140	73
10925	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	77	38
10926	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	111	58
10927	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	139	75
10928	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	78
10929	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	77	57
10930	K02576	Homo sapiens	salivary proline-rich protein I	93	53
10931	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	83	54
10932	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	262	84
10933	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	113	72
10934	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	120	62
10935	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	69

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10936	J02963	Homo sapiens	platelet glycoprotein IIb precursor	120	56
10937	AB028893	Homo sapiens	ribosomal protein S11	279	53
10939	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	127	55
10940	AF119900	Homo sapiens	PRO2822	154	53
10941	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	127	62
10942	K02576	Homo sapiens	salivary proline-rich protein I	109	41
10943	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	61
10944	AF116715	Homo sapiens	PRO2829	119	69
10945	M10546	Homo sapiens	cytochrome oxidase I	303	95
10946	L27428	Homo sapiens	reverse transcriptase	112	51
10947	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	90
10948	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	121	83
10949	AF116715	Homo sapiens	PRO2829	134	67
10950	S58722	Homo sapiens	X-linked retinopathy protein [C-terminal, clone XEH.8c]	139	83
10952	AF130079	Homo sapiens	PRO2852	119	79
10953	Z38128	Mus musculus	histone H1	126	35
10954	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	135	53
10955	L22029	Glycine max	hydroxyproline-rich glycoprotein	126	37
10956	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	81	69
10957	AF118082	Homo sapiens	PRO1902	90	51
10958	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	116	53
10959	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	82	51
10960	U79260	Homo sapiens	unknown	97	52
10961	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	194	66
10962	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	124	48
10963	G03084	Homo sapiens	Human secreted protein, SEQ ID NO: 7165.	66	73
10964	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	87
10965	Z28029	Saccharomyces cerevisiae	ORF YKL030w	99	70
10966	V00672	Pan troglodytes	reading frame protein 5	107	70
10967	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	138	58
10968	K02401	Homo sapiens	chorionic somatomammotropin	478	77
10969	D38112	Homo sapiens	cytochrome c oxidase subunit 3	642	86
10970	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	156	57
10971	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	126	56
10972	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	103	51
10973	K02401	Homo sapiens	chorionic somatomammotropin	491	82
10974	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	93
10975	D38112	Homo sapiens	NADH dehydrogenase subunit 4	236	85
10976	Y02785	Homo sapiens	Human secreted protein encoded by	108	50

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gene 51 clone HUKEX85.		
10977	J03071	Homo sapiens	chorionic somatomammotropin CS-2	435	73
10978	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	119	74
10979	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	137	73
10980	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	133	63
10981	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	90	65
10982	X92485	Plasmodium vivax	pval	119	47
10983	Y15913	Homo sapiens	COL1A1 and PDGFB fusion transcript	64	47
10984	D38112	Homo sapiens	cytochrome c oxidase subunit I	463	77
10985	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	309	65
10986	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	145	87
10987	AF130089	Homo sapiens	PRO2550	88	31
10988	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	65
10989	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	137	75
10990	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	145	76
10991	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	118	72
10992	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	69
10993	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	120	92
10994	AJ277092	Oryctolagus cuniculus	translationally controlled tumor protein 3	172	49
10995	AF052831	Trypanosoma cruzi	unknown	92	37
10996	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	119	53
10997	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	123	43
10998	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	165	52
10999	S52010	Mus sp.	orf1 5' of EpoR	93	39
11000	AF130079	Homo sapiens	PRO2852	131	81
11001	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	111	75
11002	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	132	83
11003	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	151	60
11004	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	159	58
11005	K02401	Homo sapiens	chorionic somatomammotropin	579	89
11006	K02401	Homo sapiens	chorionic somatomammotropin	464	87
11007	M15894	Homo sapiens	chorionic somatomammotropin precursor	370	74
11008	K02401	Homo sapiens	chorionic somatomammotropin	467	88
11009	K02401	Homo sapiens	chorionic somatomammotropin	537	91
11010	K02401	Homo sapiens	chorionic somatomammotropin	475	87
11011	K02401	Homo sapiens	chorionic somatomammotropin	460	88

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11012	G03639	Homo sapiens	Human secreted protein, SEQ ID NO: 7720.	101	61
11013	AF266166	Gill/chthys mirabilis	ribosomal protein S13	223	54
11014	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	176	61
11015	AF116715	Homo sapiens	PRO2829	121	69
11016	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	92	75
11017	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	113	78
11018	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	114	40
11019	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	48
11020	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	151	51
11021	X14963	Homo sapiens	collagen-like protein (447 AA)	107	47
11022	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	72
11023	AF116715	Homo sapiens	PRO2829	140	75
11024	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	70
11025	AP000001	Pyrococcus horikoshii	58aa long hypothetical protein	99	52
11026	D38112	Homo sapiens	cytochrome c oxidase subunit 3	601	81
11027	D38112	Homo sapiens	cytochrome c oxidase subunit 3	434	74
11028	Z97333	Homo sapiens	RHCE protein	149	51
11029	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	113	48
11030	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	120	77
11031	U61234	Homo sapiens	cofactor C	226	63
11032	M10546	Homo sapiens	cytochrome oxidase I	116	88
11033	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	584	93
11034	L10910	Homo sapiens	splicing factor	108	58
11035	M26361	Mus musculus	LINE/g H-chain fusion protein	140	48
11036	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	79
11037	AK024455	Homo sapiens	FLJ00047 protein	122	48
11038	AF126163	Homo sapiens	HLA3 protein	96	68
11039	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	144	79
11040	AK024455	Homo sapiens	FLJ00047 protein	151	62
11041	L06498	Homo sapiens	ribosomal protein S20	321	73
11042	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	84
11043	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	125	68
11044	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	208	91
11045	G00552	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	79	62
11046	D38112	Homo sapiens	ATPase subunit 6	297	90
11047	D38112	Homo sapiens	cytochrome c oxidase subunit 3	416	73
11048	G00491	Homo sapiens	Human secreted protein, SEQ ID NO: 4572.	73	80
11049	AF090944	Homo sapiens	PRO0663	96	70
11050	AF130089	Homo sapiens	PRO2550	152	71
11051	Y02671	Homo sapiens	Human secreted protein encoded by	108	81



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11092	AF090930	Homo sapiens	PRO0478	146	75
11093	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	163	82
11094	V00662	Homo sapiens	ATPase 6	130	87
11095	B01372	Homo sapiens	Neuron-associated protein.	122	82
11096	D38112	Homo sapiens	ATPase subunit 6	132	62
11097	U18339	Variola virus	D4L	96	60
11098	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	60
11099	AF130089	Homo sapiens	PRO2550	128	75
11100	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	218	62
11101	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	232	79
11102	AF090930	Homo sapiens	PRO0478	154	73
11103	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	133	65
11104	K03036	Mus musculus	alpha-1 type I procollagen	103	43
11105	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	142	59
11106	L13129	Mus musculus	synexin	119	35
11107	AF280111	Homo sapiens	cytochrome P450 subfamily IIIA polypeptide 43	122	52
11108	J00314	Homo sapiens	beta-tubulin	606	94
11109	X05196	Homo sapiens	aldolase C	412	89
11110	D00570	Mus musculus	open reading frame (196 AA)	127	85
11111	D50532	Homo sapiens	macrophage lectin 2	165	65
11112	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	125	74
11113	M15530	Homo sapiens	B-cell growth factor	163	82
11114	V00662	Homo sapiens	ATPase 6	217	91
11115	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	100
11116	K02576	Homo sapiens	salivary proline-rich protein 1	119	36
11117	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	132	59
11118	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	103	67
11119	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	94	42
11120	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	127	75
11121	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	104	64
11122	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	90	59
11123	AF161356	Homo sapiens	HSPC093	119	64
11124	J02963	Homo sapiens	platelet glycoprotein IIb precursor	102	70
11125	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	149	60
11126	AF068294	Homo sapiens	HDCMB45P	272	59
11127	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	120	79
11128	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	101	78
11129	AF130089	Homo sapiens	PRO2550	124	80
11130	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	109	51
11131	U40265	Trypanosoma cruzi	ATPase subunit 6	102	31

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11132	X01677	Homo sapiens	glyceraldehyde-3-phosphate dehydrogenase	555	88
11133	K02576	Homo sapiens	salivary proline-rich protein 1	108	37
11134	M81757	Homo sapiens	S19 ribosomal protein	232	76
11135	U93565	Homo sapiens	putative p150	173	51
11136	AF061944	Homo sapiens	kinase deficient protein KDP	369	100
11137	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	145	61
11138	AB030255	Homo sapiens	serine/threonine phosphatase 1 gamma	404	83
11139	AL049610	Homo sapiens	dJ1053C14.2 (KIAA0026 (transcription factor-like protein MRGX))	248	77
11140	Y36421	Homo sapiens	Fragment of human secreted protein encoded by gene 8.	81	53
11141	M13692	Homo sapiens	alpha-1 acid glycoprotein precursor	112	41
11142	M16961	Homo sapiens	alpha-2-HS-glycoprotein	543	89
11143	D38112	Homo sapiens	cytochrome c oxidase subunit 3	605	88
11144	AF090944	Homo sapiens	PRO0663	137	67
11145	X92485	Plasmodium vivax	pva1	102	57
11146	AF130089	Homo sapiens	PRO2550	113	58
11147	U63542	Homo sapiens	FAP protein	154	57
11148	W03988	Homo sapiens	SH2 domain from human SH-PTP2 (amino acids 1-106).	162	73
11149	AF116695	Homo sapiens	PRO2221	173	44
11150	M15530	Homo sapiens	B-cell growth factor	105	45
11151	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	160	64
11152	M15530	Homo sapiens	B-cell growth factor	124	75
11153	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	117	67
11154	AF118082	Homo sapiens	PRO1902	79	52
11155	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	123	72
11156	Y27893	Homo sapiens	Human secreted protein encoded by gene No. 116.	266	96
11157	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	148	84
11158	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	72
11159	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	105	58
11160	X60376	Brassica napus	proline-rich protein	111	39
11161	S79410	Mus musculus	nuclear localization signal binding protein	111	37
11162	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	53
11163	AF090930	Homo sapiens	PRO0478	146	73
11164	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	90	60
11165	AF242772	Homo sapiens	mesenchymal stem cell protein DSCD28	141	51
11166	X82629	Homo sapiens	Mox-2	307	83
11167	D38112	Homo sapiens	NADH dehydrogenase subunit 4	168	91
11168	X55684	Lycopersicon esculentum	extensin (class I)	71	66
11169	AC079041	Arabidopsis thaliana	hypothetical protein	98	45
11170	AF090930	Homo sapiens	PRO0478	156	50

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11171	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	99	70
11172	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	124	54
11173	D38112	Homo sapiens	cytochrome c oxidase subunit I	587	82
11174	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	127	66
11175	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	157	68
11176	AF090931	Homo sapiens	PRO0483	146	87
11177	M15530	Homo sapiens	B-cell growth factor	153	75
11178	AF090930	Homo sapiens	PRO0478	129	52
11179	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	98	77
11180	AF194537	Homo sapiens	NAG13	165	48
11181	AF068294	Homo sapiens	HDCMB45P	146	53
11182	AF090931	Homo sapiens	PRO0483	153	78
11183	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	141	65
11184	Y13396	Homo sapiens	Amino acid sequence of protein PRO332.	452	92
11185	AF090930	Homo sapiens	PRO0478	132	51
11186	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	178	79
11187	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	237	70
11188	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	117	83
11189	AL080206	Homo sapiens	hypothetical protein	103	71
11190	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	77
11191	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	112	65
11192	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	127	54
11193	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	150	65
11194	M92046	Trypanosoma cruzi	surface antigen	160	26
11195	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	126	72
11196	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	98	75
11197	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	117	50
11198	D88548	Homo sapiens	24-kDa subunit of complex I	160	47
11199	AF090852	Antilocapra americana	prion protein	115	38
11200	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	136	62
11201	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	139	75
11202	U93563	Homo sapiens	putative p150	239	43
11203	U93570	Homo sapiens	putative p150	173	45
11204	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	166	68
11205	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	68
11206	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	87	56



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11207	W48808	Homo sapiens	Homo sapiens clone CG109_1 protein.	123	89
11208	D38112	Homo sapiens	cytochrome c oxidase subunit 3	619	87
11209	W48808	Homo sapiens	Homo sapiens clone CG109_1 protein.	125	89
11210	D38112	Homo sapiens	cytochrome c oxidase subunit 3	521	83
11211	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	90	76
11212	D38112	Homo sapiens	cytochrome c oxidase subunit 1	547	81
11213	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	92	74
11214	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	126	63
11215	AF162149	Mycoplasma bovis	variable surface lipoprotein	118	34
11216	AF130089	Homo sapiens	PRO2550	147	96
11217	AF090931	Homo sapiens	PRO0483	112	77
11218	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	70
11219	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	111	55
11220	AF130051	Homo sapiens	PRO0898	122	63
11221	AF130079	Homo sapiens	PRO2852	171	64
11222	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	146	55
11223	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	130	71
11224	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	69
11225	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	141	85
11226	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	103	90
11227	M15530	Homo sapiens	B-cell growth factor	122	55
11228	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	121	67
11229	M15317	Plasmodium falciparum	histidine-rich protein	116	43
11230	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	131	78
11231	W19932	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS55.	74	76
11232	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	134	67
11233	AK023045	Homo sapiens	unnamed protein product	100	69
11234	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	82
11235	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	125	65
11236	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	109	53
11237	AF029403	Homo sapiens	oxysterol 7alpha-hydroxylase	144	72
11238	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	112	44
11239	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	96
11240	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	127	43
11241	L36529	Homo sapiens	protein p84	343	90
11242	M15530	Homo sapiens	B-cell growth factor	122	55
11243	Y01158	Homo sapiens	Secreted protein encoded by gene 18	130	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HCAC81.		
11244	U92698	Rattus norvegicus	ribosomal protein S2	229	74
11245	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	116	41
11246	W75859	Homo sapiens	Human secretory protein of clone DM340-1.	123	37
11247	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	132	73
11248	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	93	56
11249	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	132	56
11250	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	72
11251	S79410	Mus musculus	nuclear localization signal binding protein	115	46
11252	AK021453	Homo sapiens	unnamed protein product	146	81
11253	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	88.	56
11254	S80916	Homo sapiens	parotid "a" protein, Po=salivary proline-rich protein (exon 3)	113	43
11255	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	136	45
11256	G02382	Homo sapiens	Human secreted protein, SEQ ID NO: 6463.	107	67
11257	AF194537	Homo sapiens	NAG13	153	76
11258	M15530	Homo sapiens	B-cell growth factor	130	70
11259	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	131	72
11260	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	104	59
11261	G02922	Homo sapiens	Human secreted protein, SEQ ID NO: 7003.	316	92
11262	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	111	81
11263	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	142	71
11264	AF130089	Homo sapiens	PRO2550	111	66
11265	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	118	71
11266	M15530	Homo sapiens	B-cell growth factor	158	76
11267	AF130079	Homo sapiens	PRO2852	124	68
11268	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	104	50
11269	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	57
11270	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	107	63
11271	AF118082	Homo sapiens	PRO1902	87	47
11272	M10546	Homo sapiens	cytochrome oxidase I	305	74
11273	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	108	53
11274	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	235	81
11275	U93570	Homo sapiens	putative p150	182	54
11276	X03145	Homo sapiens	pot. ORF V	144	60
11277	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	103	57
11278	AL035681	Homo sapiens	dJ756G23.1 (novel Leucine Rich	269	100

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			Protein)		
11279	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	103	61
11280	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	115	70
11281	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	87	71
11282	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	162	81
11283	AF116715	Homo sapiens	PRO2829	141	71
11284	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	111	76
11285	U52077	Homo sapiens	mariner transposase	198	78
11286	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	120	62
11287	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	103	45
11288	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	63	60
11289	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	123	72
11290	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	120	70
11291	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	106	46
11292	AF116715	Homo sapiens	PRO2829	130	63
11293	AF090930	Homo sapiens	PRO0478	134	60
11294	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	119	65
11295	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	102	50
11296	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	141	49
11297	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	154	72
11298	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	126	54
11299	AK025270	Homo sapiens	unnamed protein product	150	54
11300	AF118078	Homo sapiens	PRO1848	121	63
11301	AF090942	Homo sapiens	PRO0657	81	43
11302	AF116715	Homo sapiens	PRO2829	131	60
11303	AF090931	Homo sapiens	PRO0483	121	71
11304	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	108	82
11305	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	122	59
11306	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	93	89
11307	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	108	65
11308	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	114	51
11309	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	67	55
11310	J02963	Homo sapiens	platelet glycoprotein IIb precursor	105	71
11311	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	104	73
11312	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	88	73

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11313	U40265	Trypanosoma cruzi	ATPase subunit 6	94	31
11314	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	157	53
11315	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	113	54
11316	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	165	90
11317	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	149	74
11318	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	144	55
11319	AF161356	Homo sapiens	HSPC093	112	56
11320	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	102	53
11321	AF116661	Homo sapiens	PRO1438	131	74
11322	AK000496	Homo sapiens	unnamed protein product	137	59
11323	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	74	57
11324	U63542	Homo sapiens	FAP protein	151	79
11325	M15530	Homo sapiens	B-cell growth factor	192	45
11326	AF116715	Homo sapiens	PRO2829	164	78
11327	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	127	62
11328	AF090895	Homo sapiens	PRO0117	116	69
11329	AF090942	Homo sapiens	PRO0657	132	62
11330	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	190	72
11331	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	112	49
11332	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	119	38
11333	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	52
11334	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	145	53
11335	X92485	Plasmodium vivax	pval	105	38
11336	M15530	Homo sapiens	B-cell growth factor	148	73
11337	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	126	100
11338	AF118086	Homo sapiens	PRO1992	123	80
11339	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	79	66
11340	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	162	73
11341	AF130079	Homo sapiens	PRO2852	145	80
11342	M19419	Mus musculus	proline-rich salivary protein	104	44
11343	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	123	62
11344	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	120	91
11345	U94832	Homo sapiens	KSRP	122	51
11346	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	139	56
11347	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	188	87
11348	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	173	59
11349	W48351	Homo sapiens	Human breast cancer related protein	111	68

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2.		
11350	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	149	62
11351	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	267	68
11352	AF161356	Homo sapiens	HSPC093	134	51
11353	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	139	47
11354	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	115	64
11355	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	126	67
11356	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	123	59
11357	AF130089	Homo sapiens	PRO2550	114	62
11358	AK000496	Homo sapiens	unnamed protein product	126	41
11359	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	173	81
11360	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	128	64
11361	AF130056	Homo sapiens	PRO1367	74	57
11362	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	116	63
11363	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	104	91
11364	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	137	53
11365	Z30643	Homo sapiens	chloride channel (putative)	409	98
11366	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	107	68
11367	AF068294	Homo sapiens	HDCMB45P	281	57
11368	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	110	71
11369	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	136	89
11370	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	129	79
11371	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	137	57
11372	U18339	Variola virus	D4L	95	61
11373	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	100	52
11374	M15530	Homo sapiens	B-cell growth factor	135	61
11375	X92485	Plasmodium vivax	pva1	111	50
11376	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	177	71
11377	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	111	68
11378	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	96	53
11379	G02567	Homo sapiens	Human secreted protein, SEQ ID NO: 6648.	83	54
11380	AP000616	Oryza sativa	similar to RING-H2 finger protein R1A1a (AF078683)	110	85
11381	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	156	64
11382	R96800	Homo sapiens	Human histocyte-secreted factor HSF.	121	79
11383	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncogene.	104	41

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11384	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	86	53
11385	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	40
11386	AF068294	Homo sapiens	HDCMB45P	158	48
11387	B08976	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:133.	136	46
11388	AF090931	Homo sapiens	PRO0483	123	74
11389	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	156	75
11390	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	102	48
11391	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	117	54
11392	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	134	43
11393	S79410	Mus musculus	nuclear localization signal binding protein	111	46
11394	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	49
11395	AF090930	Homo sapiens	PRO0478	148	70
11396	AF210651	Homo sapiens	NAG18	100	62
11397	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	121	56
11398	AF063243	Bos taurus	ribosomal protein L30	165	77
11399	AF162149	Mycoplasma bovis	variable surface lipoprotein	104	37
11400	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	175	71
11401	D38112	Homo sapiens	NADH dehydrogenase subunit 4	341	92
11402	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	137	90
11403	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	115	70
11404	M10126	Leishmania tarentolae	NH2 terminus uncertain	101	41
11405	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	126	69
11406	X82385	Homo sapiens	RNA polymerase II subunit	296	100
11407	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	68
11408	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	141	44
11409	J02963	Homo sapiens	platelet glycoprotein IIb precursor	118	77
11410	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	169	77
11411	AL390114	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	169	82
11412	AK025116	Homo sapiens	unnamed protein product	133	44
11413	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	113	63
11414	AK024455	Homo sapiens	FLJ00047 protein	127	65
11415	AK024455	Homo sapiens	FLJ00047 protein	87	63
11416	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH &c}	94	57
11417	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	123	58
11418	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	148	69

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11419	S79410	Mus musculus	nuclear localization signal binding protein	113	53
11420	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	166	68
11421	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	124	51
11422	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	113	70
11423	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	88	62
11424	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	136	72
11425	AK002154	Homo sapiens	unnamed protein product	292	75
11426	Y02887	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	98	75
11427	R13556	Homo sapiens	Protein encoded downstream of hhe_M oncoprotein.	143	64
11428	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	131	81
11429	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	130	81
11430	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	172	61
11431	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	112	74
11432	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	52
11433	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	128	58
11434	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	147	63
11435	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	139	83
11436	X53220	Bos taurus	NADH dehydrogenase	154	57
11437	AF090895	Homo sapiens	PRO0117	122	59
11438	J04655	Ascaris suum	collagen	90	46
11439	AF090942	Homo sapiens	PRO0657	166	52
11440	AK024455	Homo sapiens	FLJ00047 protein	100	35
11441	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	116	49
11442	M15530	Homo sapiens	B-cell growth factor	105	75
11443	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	133	64
11444	Y19730	Homo sapiens	SEQ ID NO 448 from WO9922243.	115	67
11445	AF090895	Homo sapiens	PRO0117	79	61
11446	AF118086	Homo sapiens	PRO1992	109	63
11447	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	160	80
11448	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	97	75
11450	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	136	72
11451	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	89	55
11452	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	144	71
11453	AF090931	Homo sapiens	PRO0483	140	78
11454	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	129	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11455	G00383	Homo sapiens	Human secreted protein, SEQ ID NO: 4464.	104	63
11456	AF118086	Homo sapiens	PRO1992	151	71
11457	U73168	Homo sapiens	partial CDS, human putative tumor suppressor (U23946)	121	95
11458	S79410	Mus musculus	nuclear localization signal binding protein	96	73
11459	AK000496	Homo sapiens	unnamed protein product	233	63
11460	AK024453	Homo sapiens	FLJ00047 protein	90	73
11461	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	132	64
11462	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	103	86
11463	K03207	Homo sapiens	salivary proline-rich protein precursor	135	36
11464	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	127	88
11465	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	104	77
11466	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	141	48
11467	AF090942	Homo sapiens	PRO0657	89	58
11468	AC005698	Arabidopsis thaliana	T3P18.6	128	47
11469	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	101	48
11470	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	136	81
11471	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	91	45
11472	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	102	77
11473	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	145	55
11474	AF210651	Homo sapiens	NAG18	117	57
11475	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	117	62
11476	AF116715	Homo sapiens	PRO2829	124	77
11477	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	45
11478	G02828	Homo sapiens	Human secreted protein, SEQ ID NO: 6909.	85	78
11479	X91940	Homo sapiens	WNT-8B protein	204	97
11480	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	131	71
11481	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	117	63
11482	X92485	Plasmodium vivax	pval	98	52
11483	AF217518	Homo sapiens	uncharacterized bone marrow protein BM042	895	100
11484	U79260	Homo sapiens	unknown	104	80
11485	L27428	Homo sapiens	reverse transcriptase	169	52
11486	M15530	Homo sapiens	B-cell growth factor	122	67
11487	U49974	Homo sapiens	mariner transposase	156	62
11488	AF090942	Homo sapiens	PRO0657	110	44
11489	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	156	65
11490	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	52
11491	G03133	Homo sapiens	Human secreted protein, SEQ ID NO:	95	51



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7214.		
11492	AF090530	Homo sapiens	PRO0478	145	58
11493	X63726	Phoca vitulina	cytochrome c oxidase subunit I	556	87
11494	AL021897	Mycobacterium tuberculosis	pra	119	56
11495	X98485	Plasmodium vivax	putative	92	35
11496	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCAC381.	156	73
11497	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	129	72
11498	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	115	66
11499	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	58
11500	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	113	36
11501	AE003568	Drosophila melanogaster	CG12566 gene product	105	32
11502	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	141	78
11503	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	102	51
11504	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	138	60
11505	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	109	85
11506	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	101	59
11507	M81321	Macaca fascicularis	proline-rich protein	128	48
11508	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	110	78
11509	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	98	60
11510	X07882	Homo sapiens	Po protein	118	41
11511	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	133	79
11512	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	68
11513	AF000381	Homo sapiens	non-functional folate binding protein	203	93
11514	X92485	Plasmodium vivax	pva1	115	44
11515	S58722	Homo sapiens	X-linked retinopathy protein [C-terminal, clone XEH.8c]	109	51
11516	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	141	78
11517	AF090894	Homo sapiens	PRO0113	108	58
11518	M15530	Homo sapiens	B-cell growth factor	93	72
11519	G03084	Homo sapiens	Human secreted protein, SEQ ID NO: 7165.	66	73
11520	AF117065	Homo sapiens	male-specific lethal-3 homolog 1	200	61
11521	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	335	87
11522	M15530	Homo sapiens	B-cell growth factor	104	74
11523	AF116715	Homo sapiens	PRO2829	122	64
11524	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	145	68
11525	Y02671	Homo sapiens	Human secreted protein encoded by	103	61

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gene 22 clone HMSJW18.		
11526	X92485	Plasmodium vivax	pval	111	42
11527	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	101	80
11528	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	134	58
11529	AF090931	Homo sapiens	PRO0483	163	76
11530	AF119900	Homo sapiens	PRO2822	139	44
11531	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	126	73
11532	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	126	50
11533	S79410	Mus musculus	nuclear localization signal binding protein	107	46
11534	AF090930	Homo sapiens	PRO0478	120	81
11535	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	105	64
11536	X92485	Plasmodium vivax	pval	123	56
11537	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	122	72
11538	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	108	64
11539	AE003834	Drosophila melanogaster	CG8054 gene product	456	84
11540	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	135	53
11541	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	99	70
11542	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	77	63
11543	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	123	73
11544	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	78	58
11545	U79260	Homo sapiens	unknown	128	43
11546	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	122	56
11547	X92485	Plasmodium vivax	pval	116	46
11548	S79410	Mus musculus	nuclear localization signal binding protein	111	55
11549	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	95	75
11550	U67056	Acanthamoeba castellanii	myosin I heavy chain kinase	111	44
11551	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	159	60
11552	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	127	50
11553	Z34975	Homo sapiens	IdlCp	470	86
11554	AF210651	Homo sapiens	NAG18	101	65
11555	X78677	Homo sapiens	ketoheokinase	241	92
11556	G04039	Homo sapiens	Human secreted protein, SEQ ID NO: 8120.	254	72
11557	AB032976	Homo sapiens	KIAA1150 protein	565	75
11558	U93572	Homo sapiens	p40	127	37

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11559	U27488	Pseudorabies virus	glycoprotein gX	88	38
11560	R80095	Homo sapiens	Human superoxide-dismutase-4 polypeptide.	113	63
11561	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	83	65
11562	AF130089	Homo sapiens	PRO2550	111	33
11563	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	146	60
11564	AF090895	Homo sapiens	PRO0117	172	77
11566	V01512	Homo sapiens	c-fos	416	82
11567	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	72	33
11568	X16074	Mus sp.	L-34 protein (AA 1-264)	117	35
11569	Y45381	Homo sapiens	Human secreted protein fragment encoded from gene 28.	131	77
11570	AK025395	Homo sapiens	unnamed protein product	683	98
11571	D78255	Mus musculus	PAP-1	134	80
11572	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	110	70
11573	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	131	78
11574	J01415	Homo sapiens	cytochrome oxidase subunit 3	141	59
11575	S79410	Mus musculus	nuclear localization signal binding protein	102	58
11576	AC007842	Homo sapiens	BC331191.1	409	86
11577	Z22636	Sinorhizobium meliloti	Thi	103	36
11578	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	83	36
11579	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	115	60
11580	AF162149	Mycoplasma bovis	variable surface lipoprotein	167	44
11581	AF130079	Homo sapiens	PRO2852	117	77
11582	AF229067	Homo sapiens	PADI-H protein	136	75
11583	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	132	72
11584	Z70292	Homo sapiens	chemokine CC-1	386	93
11585	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	107	67
11586	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	134	75
11587	X05006	Homo sapiens	S-protein	237	100
11588	Y21850	Homo sapiens	Human signal peptide-containing protein (SIGP) (clone ID 1880830).	365	77
11589	U43959	Homo sapiens	beta 4 adducin	114	54
11590	AF030162	Homo sapiens	inner mitochondrial membrane translocase Tim23	104	95
11591	X03557	Homo sapiens	56-KDa protein (aa 1-478)	491	74
11592	AF151074	Homo sapiens	HSPC240	151	73
11593	AF116719	Homo sapiens	PRO2987	558	89
11594	AF090942	Homo sapiens	PRO0657	120	41
11595	X55039	Homo sapiens	centromere autoantigen B (CENP-B)	160	32
11596	X98475	Mus musculus	vasodilator-stimulated phosphoprotein	101	43
11597	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	140	73

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11598	U07151	Homo sapiens	ARL3	113	35
11599	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	123	79
11600	AL050084	Homo sapiens	hypothetical protein	119	100
11601	AF090931	Homo sapiens	PRO0483	124	73
11602	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	132	60
11603	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	156	82
11604	AF224494	Mus musculus	arsenite inducible RNA associated protein	473	79
11605	M60047	Homo sapiens	heparin binding protein	597	95
11606	G00933	Homo sapiens	Human secreted protein, SEQ ID NO: 5014.	721	97
11607	W12091	Homo sapiens	C57S derivative of antigen non-specific human GIF.	573	98
11608	AF229439	Mus musculus	zinc finger protein 289	535	80
11609	M86637	Brugia pahangi	unknown	104	38
11610	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	93	70
11611	G02224	Homo sapiens	Human secreted protein, SEQ ID NO: 6305.	508	94
11612	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	108	51
11613	AK024372	Homo sapiens	unnamed protein product	105	77
11614	Y94918	Homo sapiens	Human secreted protein clone dd504_18 protein sequence SEQ ID NO:42.	310	62
11615	Y48547	Homo sapiens	Human breast tumour-associated protein 8.	641	96
11616	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	108	81
11617	L34081	Homo sapiens	bile acid CoA: Amino acid N-acyltransferase	356	82
11618	G01399	Homo sapiens	Human secreted protein, SEQ ID NO: 5480.	570	98
11619	AF020038	Homo sapiens	NADP-dependent isocitrate dehydrogenase	272	83
11620	AB051901	Homo sapiens	VDUP1	247	98
11621	Y48547	Homo sapiens	Human breast tumour-associated protein 8.	691	92
11622	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	382	71
11623	A06977	Homo sapiens	albumin	562	92
11624	X73460	Homo sapiens	ribosomal protein L3	502	84
11625	AL035398	Homo sapiens	dJ796117.1 (PUTATIVE novel protein)	373	98
11626	D50310	Homo sapiens	cyclin I	175	100
11627	AF000950	Archaeoglobus fulgidus	thermosome, subunit alpha (thsA)	131	25
11628	D88315	Mus musculus	tetracycline transporter-like protein	137	81
11629	Y36204	Homo sapiens	Human secreted protein #76.	406	100
11630	AF130089	Homo sapiens	PRO2550	110	63
11631	J02982	Homo sapiens	glycophorin B precursor	95	100
11632	AF116719	Homo sapiens	PRO2587	558	93
11633	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	137	92
11634	U09823	Oryctolagus	elongation factor I alpha	483	85

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		cuniculus			
11635	G01922	Homo sapiens	Human secreted protein, SEQ ID NO: 6003.	157	73
11636	AF116719	Homo sapiens	PRO2987	491	90
11637	D14421	Rattus norvegicus	b isotype of B regulatory subunit of protein phosphatase 2A	208	86
11638	AF116719	Homo sapiens	PRO2987	544	93
11639	AF130079	Homo sapiens	PRO2852	127	81
11640	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	150	59
11641	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	100	66
11642	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	119	71
11643	Y86574	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:491.	64	100
11644	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	82	70
11645	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	109	74
11646	AF130089	Homo sapiens	PRO2550	128	52
11647	AK024455	Homo sapiens	FLJ00047 protein	138	61
11648	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	73	84
11649	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	128	60
11650	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	83	78
11651	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	105	64
11652	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	103	62
11653	AF130089	Homo sapiens	PRO2550	116	69
11654	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	176	54
11655	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	129	63
11656	AF130089	Homo sapiens	PRO2550	135	77
11657	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	146	93
11658	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	123	61
11659	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	117	47
11660	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	92	84
11661	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	70	75
11662	U00029	Saccharomyces cerevisiae	Yhr217cp	101	50
11663	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	107	88
11664	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	110	90
11665	U63542	Homo sapiens	FAP protein	119	69
11666	AF130114	Homo sapiens	PRO2459	78	38
11667	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	106	64
11668	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	137	66

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4478.		
11669	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	77	63
11670	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	116	68
11671	AK021618	Homo sapiens	unnamed protein product	97	43
11672	G02482	Homo sapiens	Human secreted protein, SEQ ID NO: 6563.	108	55
11673	S75997	Rattus sp.	nucleoporin p62 homolog	95	40
11674	AF129163	Homo sapiens	natural resistance-associated macrophage protein 1	104	54
11675	M15530	Homo sapiens	B-cell growth factor	89	81
11676	M92357	Homo sapiens	B94 protein	143	100
11677	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	132	74
11678	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	126	64
11679	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	66
11680	U16359	Rattus norvegicus	nitric oxide synthase	108	85
11681	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	145	92
11682	M15530	Homo sapiens	B-cell growth factor	127	64
11683	AF090931	Homo sapiens	PRO0483	152	60
11684	AF130087	Homo sapiens	PRO2411	150	68
11685	U18339	Varicella virus	D4L	94	70
11686	S58722	Homo sapiens	X-linked retinopathy protein [C-terminal, clone XEH.8c]	104	80
11687	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	134	68
11688	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	131	70
11689	AF090944	Homo sapiens	PRO0663	129	73
11690	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	111	67
11691	U79260	Homo sapiens	unknown	98	44
11692	W78226	Homo sapiens	Fragment of human secreted protein encoded by gene 1.	361	64
11693	G00962	Homo sapiens	Human secreted protein, SEQ ID NO: 5043.	269	100
11694	AL359782	Trypanosoma brucei	possible (hly-v) u1102, variant a dna, complete virion genome.	132	83
11695	Y94526	Homo sapiens	Human lysine-rich statherin protein.	136	82
11696	AF116637	Homo sapiens	PRO1489	232	95
11697	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	108	50
11698	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	120	81
11699	G00476	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	150	80
11700	AK024455	Homo sapiens	FLJ00047 protein	148	68
11701	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	131	72
11702	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	105	45
11703	AC005545	Homo sapiens	delta-adaptin, partial CDS	127	38
11704	S58722	Homo sapiens	X-linked retinopathy protein [C-terminal, clone XEH.8c]	143	81

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11705	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	67
11706	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	153	67
11707	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	129	88
11708	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	89	69
11709	AB047600	Macaca fascicularis	hypothetical protein	95	63
11710	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	100	76
11711	J02963	Homo sapiens	platelet glycoprotein IIb precursor	112	80
11712	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	117	58
11713	AF008196	Homo sapiens	bax epsilon	140	71
11714	R13556	Homo sapiens	Protein encoded downstream of hnc_M oncoprotein.	113	56
11715	G00397	Homo sapiens	Human secreted protein; SEQ ID NO: 4478.	125	67
11716	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	121	74
11717	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	125	51
11718	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	96	81
11719	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	106	85
11720	AJ243883	Periplaneta americana	putative transcription factor	118	57
11721	AF220264	Homo sapiens	MOST-1	121	74
11722	AF130051	Homo sapiens	PRO0898	169	72
11723	K02401	Homo sapiens	chorionic somatomammotropin	507	95
11724	K02401	Homo sapiens	chorionic somatomammotropin	461	85
11725	U93564	Homo sapiens	p40	340	90
11726	AF130089	Homo sapiens	PRO2550	107	73
11727	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	128	79
11728	J02963	Homo sapiens	platelet glycoprotein IIb precursor	109	90
11729	Y51824	Homo sapiens	Human OSBH protein.	182	89
11730	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	107	80
11731	K02401	Homo sapiens	chorionic somatomammotropin	459	94
11732	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	93	42
11733	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	111	67
11734	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	103	43
11735	S79410	Mus musculus	nuclear localization signal binding protein	98	75
11736	AF090931	Homo sapiens	PRO0483	123	88
11737	K02401	Homo sapiens	chorionic somatomammotropin	340	92
11738	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	73
11739	G02624	Homo sapiens	Human secreted protein, SEQ ID NO: 6705.	131	57
11740	X55695	Lycopersicon esculentum	glycine-rich protein	164	48
11741	AK024455	Homo sapiens	FLJ00047 protein	89	77

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11742	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2. SEQ ID NO:125.	415	90
11743	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	105	94
11744	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	116	87
11745	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	131	69
11746	W13831	Homo sapiens	Human cyclin E delta 9 mutant.	140	52
11747	AB001431	Mus musculus	motor domain of KIF14	179	84
11748	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	141	72
11749	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	99	63
11750	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	88	64
11751	AF090931	Homo sapiens	PRO0483	118	68
11752	AF150105	Homo sapiens	small zinc finger-like protein	194	68
11753	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	127	69
11754	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	100	80
11755	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	109	65
11756	K02401	Homo sapiens	chorionic somatomammotropin	427	87
11757	U52077	Homo sapiens	mariner transposase	113	82
11758	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	133	54
11759	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	111	80
11760	AF090944	Homo sapiens	PRO0663	143	76
11761	D38112	Homo sapiens	NADH dehydrogenase subunit 6	529	99
11762	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	171	58
11763	AF132200	Homo sapiens	PRO1751	127	66
11764	AK025116	Homo sapiens	unnamed protein product	141	80
11765	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	75	62
11766	AF090930	Homo sapiens	PRO0478	106	59
11767	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	127	80
11768	AF090931	Homo sapiens	PRO0483	164	60
11769	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	102	81
11770	AF161356	Homo sapiens	HSPC093	131	68
11771	AF130089	Homo sapiens	PRO2550	160	82
11772	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	140	79
11773	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	136	71
11774	AF090942	Homo sapiens	PRO0657	153	78
11775	AJ223410	Homo sapiens	EBI1-ligand chemokine	108	52
11776	K02401	Homo sapiens	chorionic somatomammotropin	395	91
11777	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	107	70
11778	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	99	62
11779	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	84	64



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11780	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 1433.	116	68
11781	AF194537	Homo sapiens	NAG13.	201	65
11782	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	139	68
11783	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	149	59
11784	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	112	78
11785	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	99	68
11786	AF130089	Homo sapiens	PRO2550	108	83
11787	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	124	88
11788	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	103	100
11789	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	146	60
11790	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	73
11791	AL035494	Homo sapiens	dj635G19.2.3 (novel protein (PUTATIVE PARTIAL isoform 3))	106	56
11792	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	100	66
11793	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	125	61
11794	A20770	synthetic construct	(Asp1-Thr161)-EPI	95	76
11795	S74221	Homo sapiens	IK factor=cytokine down-regulating HLA class II	108	61
11796	K01664	Drosophila melanogaster	Bkm-like protein	96	77
11797	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	111	65
11798	Y75995	Homo sapiens	Human skin cell protein, SEQ ID NO:173.	324	87
11799	J03071	Homo sapiens	chlorionic somatomammotropin CS-5	120	75
11800	L00693	Homo sapiens	carcinoembryonic antigen	96	85
11801	AL160493	Leishmania major	probable (bhv-6) u1102, variant a DNA, complete virion genome	80	44
11802	AL339782	Trypanosoma brucei	possible (bhv-6) u1102, variant a dna, complete virion genome.	125	64
11803	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	142	82
11804	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	107	85
11805	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	152	80
11806	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	122	61
11807	U91985	Homo sapiens	DNA fragmentation factor-45	585	92
11808	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	60
11809	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	170	89
11810	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	191	76
11811	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	100

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11812	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	156	55
11813	P92219	Homo sapiens (human)	CR1 protein.	121	84
11814	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	107	75
11815	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	74	78
11816	M15530	Homo sapiens	B-cell growth factor	148	68
11817	AF090942	Homo sapiens	PRO0657	139	60
11818	W90847	Homo sapiens	Human lymphocyte targeted peptide #15.	117	100
11819	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	73
11820	Z72853	Saccharomyces cerevisiae	ORF YGR069w	94	42
11821	G03710	Homo sapiens	Human secreted protein, SEQ ID NO: 7791.	176	65
11822	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	60
11823	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	104	68
11824	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	99	51
11825	W90172	Homo sapiens	Human heart muscle specific protein.	256	34
11826	AB017007	Homo sapiens	PMS2L16	248	89
11827	AL160371	Leishmania major	probable (bhv-6) u1102, variant a DNA, complete virion genome	127	86
11828	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	135	71
11829	AF119851	Homo sapiens	PRO1722	129	60
11830	AF132200	Homo sapiens	PRO1751	120	77
11831	Y08061	Homo sapiens	Human c-myc protein fragment.	133	83
11832	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	128	64
11833	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	152	100
11834	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	73
11835	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	88
11836	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	95
11837	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	411	91
11838	AK000496	Homo sapiens	unnamed protein product	113	78
11839	AF119855	Homo sapiens	PRO1847	84	68
11840	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	88
11841	S79410	Mus musculus	nuclear localization signal binding protein	113	69
11842	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	151	55
11843	AF090942	Homo sapiens	PRO0657	139	65
11844	AF220264	Homo sapiens	MOST-1	88	69
11845	AF184612	Drosophila melanogaster	split ends	95	47
11846	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	136	82

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11847	AB017007	Homo sapiens	PMS2L16	310	100
11848	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	100	79
11849	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	111	61
11850	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	110	72
11851	AF090931	Homo sapiens	PRO0483	164	80
11852	AF116661	Homo sapiens	PRO1438	124	67
11853	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	119	72
11854	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	135	59
11855	U63332	Homo sapiens	super cysteine rich protein; SCRP	100	84
11856	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	120	54
11857	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	68
11858	AK024455	Homo sapiens	FLJ00047 protein	123	69
11859	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	66
11860	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	94	66
11861	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	108	75
11862	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	108	86
11863	AF130050	Homo sapiens	PRO0872	81	58
11864	AF119900	Homo sapiens	PRO2822	152	90
11865	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	78	45
11866	J03071	Homo sapiens	chorionic somatomammotropin CS-2	526	93
11867	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	80
11868	G00591	Homo sapiens	Human secreted protein, SEQ ID NO: 4672.	119	58
11869	Y10830	Homo sapiens	Amino acid sequence of a human secreted protein.	246	100
11870	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	101	59
11871	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	120	59
11872	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	84
11873	D28113	Homo sapiens	MOBP	458	80
11874	D28114	Homo sapiens	MOBP	306	68
11875	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	101	85
11876	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	110	64
11877	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	57
11878	M15530	Homo sapiens	B-cell growth factor	98	62
11879	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	100
11880	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	99	70
11881	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	101	53

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11882	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	219	75
11883	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	131	61
11884	U93563	Homo sapiens	putative p150	139	75
11885	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hbcn) gene product.	154	52
11886	AF090944	Homo sapiens	PRO0663	149	80
11887	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	107	94
11888	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	138	62
11889	L26953	Homo sapiens	chromosomal protein	123	75
11890	U16359	Rattus norvegicus	nitric oxide synthase	105	69
11891	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	129	83
11892	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	126	78
11893	G00481	Homo sapiens	Human secreted protein, SEQ ID NO: 4562.	82	70
11894	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	149	90
11895	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	118	75
11896	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	167	86
11897	D38112	Homo sapiens	NADH dehydrogenase subunit 6	136	77
11898	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	126	58
11899	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	158	78
11900	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	137	71
11901	G00613.	Homo sapiens	Human secreted protein, SEQ ID NO: 4694.	85	62
11902	G02558	Homo sapiens	Human secreted protein, SEQ ID NO: 6639.	242	73
11903	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	127	59
11904	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	182	85
11905	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	135	75
11906	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	128	79
11907	U93574	Homo sapiens	putative p150	169	64
11908	AF090944	Homo sapiens	PRO0663	128	75
11909	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	100	84
11910	AF090930	Homo sapiens	PRO0478	159	76
11911	J03071	Homo sapiens	chorionic somatomammotropin CS-2	496	88
11912	J03071	Homo sapiens	chorionic somatomammotropin CS-2	551	92
11913	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	168	76
11914	K02401	Homo sapiens	chorionic somatomammotropin	450	85
11915	K02401	Homo sapiens	chorionic somatomammotropin	478	87
11916	K02401	Homo sapiens	chorionic somatomammotropin	454	82

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11917	G02382	Homo sapiens	Human secreted protein, SEQ ID NO: 6463.	121	73
11918	X65121	Mus musculus	alpha1 (X) collagen	112	35
11919	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	115	62
11920	AK024455	Homo sapiens	FLJ00047 protein	102	76
11921	AF150087	Homo sapiens	small zinc finger-like protein	181	52
11922	U55376	Caenorhabditis elegans	F16H11.2 gene product	122	78
11923	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	256	80
11924	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	127	74
11925	AF090944	Homo sapiens	PRO0663	144	75
11926	A1223475	Escherichia coli	InsA protein	477	100
11927	M15386	Homo sapiens	gamma-globin	616	92
11928	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	105	72
11929	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	122	92
11930	AF090895	Homo sapiens	PRO0117	80	71
11931	AF130089	Homo sapiens	PRO2550	129	68
11932	AK025116	Homo sapiens	unnamed protein product	113	53
11933	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	114	70
11934	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	69	76
11935	AF116695	Homo sapiens	PRO2221	336	70
11936	AF090931	Homo sapiens	PRO0483	153	77
11937	AF130089	Homo sapiens	PRO2550	135	72
11938	L06237	Homo sapiens	microtubule-associated protein 1B	143	36
11939	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	124	72
11940	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	158	76
11941	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	130	53
11942	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	111	65
11943	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	106	59
11944	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	65
11945	D28113	Homo sapiens	MOBP	186	62
11946	D38112	Homo sapiens	NADH dehydrogenase subunit 1	353	76
11947	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	113	72
11948	D38112	Homo sapiens	NADH dehydrogenase subunit 6	139	87
11949	A1006591	Homo sapiens	cysteine-rich protein	148	76
11950	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	113	88
11951	AF116695	Homo sapiens	PRO2221	205	57
11952	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	158	75
11953	AF113685	Homo sapiens	PRO0974	107	72
11954	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	107	80
11955	AK026107	Homo sapiens	unnamed protein product	129	84
11956	AF109907	Homo sapiens	S164	140	96

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11957	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	99	100
11958	K02576	Homo sapiens	salivary proline-rich protein 1	124	41
11959	K02401	Homo sapiens	chorionic somatomammotropin	497	90
11960	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	155	69
11961	J02963	Homo sapiens	platelet glycoprotein IIb precursor	126	85
11962	M15530	Homo sapiens	B-cell growth factor	114	86
11963	K02401	Homo sapiens	chorionic somatomammotropin	472	87
11964	AK024455	Homo sapiens	FLJ00047 protein	95	61
11965	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	145	78
11966	L27428	Homo sapiens	reverse transcriptase	144	50
11967	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	187	76
11968	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	124	81
11969	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	112	64
11970	AK024455	Homo sapiens	FLJ00047 protein	120	70
11971	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	105	61
11972	R13556	Homo sapiens	Protein encoded downstream of hlic_M oncoprotein.	106	70
11973	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	70	75
11974	G00491	Homo sapiens	Human secreted protein, SEQ ID NO: 4572.	86	60
11975	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	161	72
11976	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	105	42
11977	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	121	58
11978	AK024372	Homo sapiens	unnamed protein product	104	80
11979	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	137	77
11980	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	96	90
11981	S79410	Mus musculus	nuclear localization signal binding protein	100	56
11982	R59842	Homo sapiens	ApoE41 protease.	129	62
11983	K01664	Drosophila melanogaster	Bkm-like protein	132	53
11984	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	105	90
11985	M15530	Homo sapiens	B-cell growth factor	117	43
11986	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	99	65
11987	R59843	Homo sapiens	ApoE41.x2 protease.	117	84
11988	L26953	Homo sapiens	chromosomal protein	124	79
11989	U93564	Homo sapiens	p40	523	88
11990	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO: 163.	155	82
11991	AF090894	Homo sapiens	PRO0113	126	56
11992	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	129	63
11993	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	144	67
11994	U71363	Homo sapiens	zinc finger protein zfp6	213	68

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11995	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	82	65
11996	AF130089	Homo sapiens	PRO2550	145	68
11997	R95913	Homo sapiens	Neural thread protein.	114	88
11998	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	122	56
11999	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	147	81
12000	AF090931	Homo sapiens	PRO0483	152	81
12001	AF090931	Homo sapiens	PRO0483	145	81
12002	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	124	64
12003	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	103	78
12004	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	133	51
12005	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	108	63
12006	L19527	Homo sapiens	ribosomal protein L27	547	93
12007	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	127	82
12008	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	127	82
12009	M55409	Homo sapiens	pancreatic tumor-related protein	257	98
12010	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	127	64
12011	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	291	89
12012	X03717	Homo sapiens	pot. unidentified reading frame	126	43
12013	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	131	80
12014	AB011148	Homo sapiens	KIAA0576 protein	135	84
12015	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	114	87
12016	AK024455	Homo sapiens	FLJ00047 protein	102	70
12017	L27428	Homo sapiens	reverse transcriptase	144	87
12018	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	135	87
12019	D38112	Homo sapiens	NADH dehydrogenase subunit 1	137	93
12020	AK001363	Homo sapiens	unnamed protein product	490	100
12021	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	111	79
12022	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	106	87
12023	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	157	58
12024	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	87	66
12025	R95913	Homo sapiens	Neural thread protein.	157	45
12026	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	138	52
12027	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	116	60
12028	V00488	Homo sapiens	alpha globin	191	100
12029	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	102	87
12030	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	114	79
12031	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	142	86
12032	X01703	Homo sapiens	alpha-tubulin	534	93
12033	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	557	90

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12034	X01703	Homo sapiens	alpha-tubulin	619	94
12035	AF255556	Nototheria coriiceps	alpha tubulin	430	85
12036	X53618	Paracentrotus lividus	alpha-tubulin (AA 1-452)	437	87
12037	M62810	Homo sapiens	mitochondrial transcription factor 1	433	95
12038	Y36156	Homo sapiens	Human secreted protein #28.	157	75
12039	X01703	Homo sapiens	alpha-tubulin	604	97
12040	X01703	Homo sapiens	alpha-tubulin	517	90
12041	S70154	Homo sapiens	cytosolic acetoacetyl-coenzyme A thiolase, CT [EC 2.3.1.9]	533	94
12042	X01703	Homo sapiens	alpha-tubulin	472	85
12043	M23613	Homo sapiens	nucleophosmin	428	80
12044	AL031174	Schizosaccharomyces pombe	hypothetical protein	102	52
12045	Y94653	Homo sapiens	Human netrin-like protein (NEL) amino acid sequence.	152	82
12046	AF016507	Homo sapiens	C-terminal binding protein 2	172	100
12047	X05196	Homo sapiens	aldolase C	454	93
12048	X03796	Mus musculus	aldolase C (aa 1-227)	351	74
12049	X05196	Homo sapiens	aldolase C	408	88
12050	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	147	70
12051	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XFH.8c}	169	55
12052	AF090944	Homo sapiens	PRO0663	119	59
12053	V01577	Homo sapiens	variable region	223	93
12054	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	144	74
12055	AF090931	Homo sapiens	PRO0483	121	74
12056	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	105	76
12057	U18339	Variola virus	D4L	100	52
12058	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	135	62
12059	AB001684	Chlorella vulgaris	ORF41c	81	75
12060	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	128	74
12061	AK024455	Homo sapiens	FLJ00047 protein	70	46
12062	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	130	69
12063	AF090944	Homo sapiens	PRO0663	110	66
12064	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	109	53
12065	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	94	79
12066	AF090931	Homo sapiens	PRO0483	123	70
12067	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	111	75
12068	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	144	77
12069	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	145	76
12070	G03639	Homo sapiens	Human secreted protein, SEQ ID NO: 7720.	114	81
12071	AF116715	Homo sapiens	PRO2829	138	63
12072	J02963	Homo sapiens	platelet glycoprotein IIb precursor	127	82
12073	U79260	Homo sapiens	unknown	98	73
12074	W88627	Homo sapiens	Secreted protein encoded by gene 94	132	80



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HPMBQ32.		
12075	J02459	bacteriophage lambda	T (tail component;144)	555	98
12076	AK024455	Homo sapiens	FLJ00047 protein	127	65
12077	X00911	Rattus norvegicus	pot. MSA-precursor	190	73
12078	AF164797	Homo sapiens	ribosomal protein L17 isolog	538	95
12079	A06977	Homo sapiens	albumin	602	87
12080	AF000198	Caenorhabditis elegans	Similar to cuticular collagen	118	38
12081	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	142	86
12082	AL339782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	103	50
12083	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	142	86
12084	G00413	Homo sapiens	Human secreted protein, SEQ ID NO: 4494.	64	54
12085	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	132	53
12086	A14829	Homo sapiens	preproapolipoprotein	619	82
12087	AF119900	Homo sapiens	PRO2822	107	76
12088	U52077	Homo sapiens	mariner transposase	277	74
12089	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	126	100
12090	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	92
12091	W05278	Homo sapiens	Tumour necrosis factor-related gene product CL6.5.40.	115	42
12092	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	112	81
12093	G03343	Homo sapiens	Human secreted protein, SEQ ID NO: 7424.	114	64
12094	A1237660	Bacteriophage 21	Ren protein	187	94
12095	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	135	80
12096	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	49
12097	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	122	92
12098	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	148	59
12099	AF090942	Homo sapiens	PRO0657	115	70
12100	AF090931	Homo sapiens	PRO0483	112	74
12101	AF090944	Homo sapiens	PRO0663	103	37
12102	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	76	58
12103	J02963	Homo sapiens	platelet glycoprotein IIb precursor	130	80
12104	AL160493	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	106	84
12105	R95913	Homo sapiens	Neural thread protein.	105	75
12106	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	149	75
12107	Y09561	Homo sapiens	ATP receptor	188	85
12108	AF090895	Homo sapiens	PRO0117	107	83
12109	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	117	65
12110	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 130	130	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6292.		
12111	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	117	69
12112	Y12478	Homo sapiens	congenital heart disease 5 protein	291	62
12113	AF220264	Homo sapiens	MOST-1	142	76
12114	Y12077	Homo sapiens	Human 5' EST secreted protein SEQ ID NO: 390.	109	95
12115	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	171	63
12116	AF064869	Rattus norvegicus	brain-enriched guanylate kinase-associated protein 2; BEGA2	294	98
12117	S79410	Mus musculus	nuclear localization signal binding protein	128	36
12119	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	102	73
12120	U79260	Homo sapiens	unknown	98	65
12121	AF161356	Homo sapiens	HSPC093	118	67
12122	AF130087	Homo sapiens	PRO2411	115	80
12123	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	280	75
12124	S48406	Mus sp.	alpha 1 (XII) collagen {triple-helical domain Col.2}	59	41
12125	AB030816	Homo sapiens	H-REV107 protein-related protein	420	79
12126	R96418	Homo sapiens	Partial human transforming growth factor beta receptor type II.	169	100
12127	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	91	46
12128	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	109	83
12129	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	127	57
12130	AF119900	Homo sapiens	PRO2822	108	79
12131	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	70
12132	AF303828	Mus musculus	ubc-like protein MMS2	131	43
12133	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	127	58
12134	U49974	Homo sapiens	mariner transposase	124	80
12135	X52164	Mus musculus	Q300 protein (AA 1-77)	106	94
12136	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	151	69
12137	AF192913	Homo sapiens	zinc finger protein ZNF180	581	94
12138	X58907	Homo sapiens	steroid 21-monooxygenase	128	58
12139	AF090931	Homo sapiens	PRO0483	121	70
12140	AK024455	Homo sapiens	FLJ00047 protein	84	60
12141	AF090931	Homo sapiens	PRO0483	122	71
12142	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	153	60
12143	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	121	100
12144	G02922	Homo sapiens	Human secreted protein, SEQ ID NO: 7003.	191	62
12145	U57092	Homo sapiens	Rab30	257	87
12146	AF130089	Homo sapiens	PRO2550	129	74
12147	AF090931	Homo sapiens	PRO0483	138	80
12148	G02382	Homo sapiens	Human secreted protein, SEQ ID NO: 6463.	135	60
12149	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	138	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12150	U51723	Plasmodium vivax	V-SERA I	107	37
12151	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	82	68
12152	Y23884	Homo sapiens	Amino acid sequence of FK506 binding protein 65 (FKBP65).	124	69
12153	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	93	70
12154	AF229067	Homo sapiens	PADI-H protein	162	68
12155	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	125	85
12157	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	113	39
12158	U89439	Bos taurus	ubiquitin-like protein	146	76
12159	G03725	Homo sapiens	Human secreted protein, SEQ ID NO: 7806.	677	98
12160	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	124	90
12161	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	109	80
12162	AF090931	Homo sapiens	PRO0483	125	76
12163	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	191	64
12164	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	96	61
12165	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	115	68
12166	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	219	93
12167	AF118086	Homo sapiens	PRO1992	155	78
12168	X12789	Mus musculus	cytokeratin 8 (AA 1 - 489)	174	63
12169	S79410	Mus musculus	nuclear localization signal binding protein	94	48
12170	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	57
12171	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	78
12172	AF068294	Homo sapiens	HDCMB45P	184	56
12173	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	116	50
12174	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	107	59
12175	X92485	Plasmodium vivax	pval	108	44
12176	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	102	84
12177	X83703	Homo sapiens	nuclear protein	330	68
12178	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	147	50
12179	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	103	73
12180	AF132200	Homo sapiens	PRO1751	131	64
12181	AC005514	Homo sapiens	CTF5	261	90
12182	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	156	75
12183	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	137	75
12184	P92219	Homo sapiens (human)	CR1 protein.	101	74
12185	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	156	56

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12186	G02213	Homo sapiens	Human secreted protein, SEQ ID NO: 6294.	626	97
12187	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	96	51
12188	AF118067	Homo sapiens	PRO1578	89	73
12189	M63154	Homo sapiens	intrinsic factor	130	96
12190	AF090942	Homo sapiens	PRO0657	144	72
12191	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	76
12192	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	134	63
12193	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	159	76
12194	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	76
12195	AF090931	Homo sapiens	PRO0483	134	62
12196	AF130089	Homo sapiens	PRO2550	117	74
12197	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	113	57
12198	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	126	70
12199	J02459	bacteriophage lambda	Fi (DNA packaging;117)	203	95
12200	Y08061	Homo sapiens	Human c-myc protein fragment.	135	58
12201	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	132	86
12202	AF119900	Homo sapiens	PRO2822	148	68
12203	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	59
12204	R59842	Homo sapiens	ApoE4L1 protease.	118	91
12205	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	121	72
12206	S75997	Rattus sp.	nucleoporin p62 homolog	131	65
12207	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	145	65
12208	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	145	86
12209	AJ242956	Homo sapiens	E1 fusion protein	96	88
12210	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	132	78
12211	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	81
12212	K03179	Homo sapiens	pro-alpha-1 type-I collagen	96	37
12213	G01895	Homo sapiens	Human secreted protein, SEQ ID NO: 5976.	310	57
12214	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	493	82
12215	R13144	Homo sapiens	Deleted in Colorectal Carcinomas.	700	98
12216	AF132200	Homo sapiens	PRO1751	109	61
12217	A3013897	Homo sapiens	HKR1	324	64
12218	AF071172	Homo sapiens	HERC2	123	86
12219	L38593	Homo sapiens	integral membrane protein	78	62
12220	AF036233	Homo sapiens	cdc25B phosphatase	204	51
12221	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	107	60
12222	AL049795	Homo sapiens	dJ622L5.9 (eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) (TRIP-1, TGF-beta receptor interacting protein 1))	163	86
12223	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	120	76

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12224	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	64
12225	AF130079	Homo sapiens	PRO2852	103	80
12226	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	163	86
12227	AF119855	Homo sapiens	PRO1847	96	78
12228	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	195	87
12229	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	103	90
12230	U49957	Homo sapiens	LIM protein	212	100
12231	AK022759	Homo sapiens	unnamed protein product	646	100
12232	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	110	70
12233	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	109	74
12234	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	123	76
12235	AF220264	Homo sapiens	MOST-1	104	85
12236	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	113	87
12237	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	143	84
12238	AF090942	Homo sapiens	PRO0657	103	66
12239	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	129	72
12240	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	135	75
12241	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA 1a (AF078683)	136	95
12242	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	148	72
12243	K02576	Homo sapiens	salivary proline-rich protein 1	118	39
12244	AL390114	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	78	100
12245	AC005200	Homo sapiens	plasmalemmal porin	131	79
12246	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	150	65
12247	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	90	55
12248	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	77	64
12249	U63542	Homo sapiens	FAP protein	108	56
12250	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	75
12251	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	139	63
12252	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	122	71
12253	AF118086	Homo sapiens	PRO1992	73	70
12254	AF083929	Mus musculus	ES18	108	44
12255	AF130089	Homo sapiens	PRO2550	124	88
12256	AF090931	Homo sapiens	PRO0483	132	80
12257	X95190	Homo sapiens	branched chain acyl-CoA oxidase	166	86
12258	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	131	53
12259	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	124	88
12260	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	128	85

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4409.		
12261	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	133	72
12262	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	110	70
12263	Y08061	Homo sapiens	Human c-myc protein fragment.	125	85
12264	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	126	65
12265	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	95
12266	AK024455	Homo sapiens	FLJ00047 protein	108	63
12267	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	166	73
12268	AF090931	Homo sapiens	PRO0483	108	82
12269	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	120	68
12270	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	120	66
12271	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	74
12272	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	129	60
12273	AF130089	Homo sapiens	PRO2550	134	79
12274	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	118	80
12275	AF194537	Homo sapiens	NAG13	151	52
12276	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	75	68
12277	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	113	60
12278	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	111	70
12279	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	119	92
12280	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	108	90
12281	U66464	Homo sapiens	hematopoietic progenitor kinase	102	83
12282	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	118	65
12283	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	162	82
12284	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	130	77
12285	AF116661	Homo sapiens	PRO1438	104	74
12286	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	98	66
12287	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	105	74
12288	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	129	78
12289	X53581	Rattus norvegicus	ORF7	111	47
12290	AF090931	Homo sapiens	PRO0483	147	87
12291	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	106	69
12292	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	137	53
12293	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	56

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12294	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	60
12295	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	112	66
12296	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	140	62
12297	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	144	70
12298	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	95	51
12299	S79410	Mus musculus	nuclear localization signal binding protein	108	70
12300	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	122	85
12301	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	117	73
12302	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	115	62
12303	AF130051	Homo sapiens	PRO0898	116	65
12304	J02963	Homo sapiens	platelet glycoprotein IIb precursor	119	60
12305	Y00662	Homo sapiens	ATPase 6	118	100
12306	AF107406	Homo sapiens	GW128	98	66
12307	A05308	synthetic construct	glioblastoma-derived T-cell suppressor factor	376	93
12308	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	173	71
12309	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	140	74
12310	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	98	47
12311	Y27571	Homo sapiens	Human secreted protein encoded by gene No. 5.	130	42
12312	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	134	76
12313	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	98	82
12314	U79260	Homo sapiens	unknown	97	64
12315	L27428	Homo sapiens	reverse transcriptase	214	44
12316	D00570	Mus musculus	open reading frame (196 AA)	115	83
12317	AF090931	Homo sapiens	PRO0483	104	74
12318	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	123	84
12319	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	107	70
12320	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	97	62
12321	S79410	Mus musculus	nuclear localization signal binding protein	95	58
12322	G00362	Homo sapiens	Human secreted protein, SEQ ID NO: 4443.	104	59
12323	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	115	75
12324	AF286472	Homo sapiens	retinitis pigmentosa GTPase regulator	121	53
12325	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	162	75
12326	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	129	75
12327	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	125	88

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12328	AF090944	Homo sapiens	PRO0663	122	76
12329	AF090931	Homo sapiens	PRO0483	156	81
12330	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	107	80
12331	AF115715	Homo sapiens	PRO2829	127	72
12332	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	145	49
12333	S80862	Western equine encephalomyelitis virus/Western equine encephalomyelitis virus, Peptide Partial, 259 aa	nucleocapsid gene C	108	35
12334	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	141	83
12335	AK024455	Homo sapiens	FLJ00047 protein	133	71
12336	AF090944	Homo sapiens	PRO0663	139	84
12337	J02963	Homo sapiens	platelet glycoprotein IIb precursor	124	71
12338	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	102	69
12339	AL359782	Trypanosoma brucei	possible (hly-6) u1102, variant a dna, complete virion genome.	121	81
12340	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	149	54
12341	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	134	66
12342	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	102	60
12343	AF118086	Homo sapiens	PRO1992	80	63
12344	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	104	80
12345	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	145	72
12346	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	143	75
12347	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	116	37
12348	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	176	76
12349	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	103	48
12350	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	81
12351	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	108	70
12352	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	101	84
12353	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	105	42
12354	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	147	66
12355	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	125	65
12356	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	96	68
12357	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	122	43
12358	AL160493	Leishmania major	probable (hly-6) u1102, variant a DNA, complete virion genome	132	38
12359	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	94	90



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4478.		
12360	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	56
12361	AB001684	Chlorella vulgaris	ORF49b	92	44
12362	U93564	Homo sapiens	p40	257	84
12363	U60269	Homo sapiens	putative envelope protein, orf similar to env of Type A and Type B retroviruses and to class II HERVs	427	84
12364	G03064	Homo sapiens	Human secreted protein, SEQ ID NO: 7145.	102	73
12365	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	102	68
12366	AF090944	Homo sapiens	PRO0663	94	45
12367	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	150	55
12368	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	105	85
12369	AF130089	Homo sapiens	PRO2550	112	78
12370	AF090895	Homo sapiens	PRO0117	125	64
12371	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	121	95
12372	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	145	72
12373	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	72
12374	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	133	79
12375	AP000001	Pyrococcus horikoshii	58aa long hypothetical protein	96	51
12376	U16359	Rattus norvegicus	nitric oxide synthase	105	76
12377	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	123	78
12378	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	126	83
12379	Y53643	Homo sapiens	A bone marrow secreted protein designated BMS6.	329	98
12380	U64094	Homo sapiens	soluble type II interleukin-1 receptor	114	100
12381	J02459	bacteriophage lambda	D (head-DNA stabilization;110)	467	100
12382	L10908	Mus musculus	Gcap1 gene product	100	89
12383	AF220264	Homo sapiens	MOST-1	113	68
12384	U79260	Homo sapiens	unknown	94	60
12385	B01372	Homo sapiens	Neuron-associated protein.	148	52
12386	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	116	63
12387	G00952	Homo sapiens	Human secreted protein, SEQ ID NO: 5033.	125	92
12388	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	130	65
12389	S79410	Mus musculus	nuclear localization signal binding protein	150	62
12390	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	102	38
12391	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	113	56
12392	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	73	92

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12393	M69297	Homo sapiens	ORF 3	167	75
12394	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	142	43
12395	AF220264	Homo sapiens	MOST-1	131	57
12396	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	139	62
12397	AF130089	Homo sapiens	PRO2550	120	62
12398	AK023117	Homo sapiens	unnamed protein product	529	97
12399	AF123652	Homo sapiens	FEZ1	157	96
12400	D38112	Homo sapiens	NADH dehydrogenase subunit 6	139	87
12401	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	306	60
12402	AC005051	Homo sapiens	neuronal apoptosis inhibitory protein	143	96
12403	J03071	Homo sapiens	chorionic somatomammotropin CS-2	585	100
12405	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	125	100
12406	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hbcn) gene product.	150	63
12407	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	157	85
12408	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	120	75
12409	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	141	50
12410	G03465	Homo sapiens	Human secreted protein, SEQ ID NO: 7546.	103	51
12411	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	147	71
12412	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	159	70
12413	SS8722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	129	79
12414	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	156	72
12415	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	74	72
12416	AL390114	Leishmania major	probable (hvh-6) u1 102, variant a DNA, complete virion genome	102	50
12417	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	171	75
12418	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	137	55
12419	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	111	52
12420	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	129	53
12421	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	110	55
12422	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	126	87
12423	U93564	Homo sapiens	p40	350	93
12424	M17885	Homo sapiens	acidic ribosomal phosphoprotein (P0)	484	88
12425	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	130	69
12426	X60376	Brassica napus	proline-rich protein	89	47
12427	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	83	88
12428	SS8722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	117	75
12429	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	107	67

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12430	AK027208	Homo sapiens	unnamed protein product	108	64
12431	Y07693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	154	68
12432	AF130089	Homo sapiens	PRO2550	118	88
12433	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	90	55
12434	AK024455	Homo sapiens	FLJ00047 protein	113	75
12435	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	107	80
12436	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	114	75
12437	AC005498	Homo sapiens	R31665_2	163	75
12438	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
12439	G03116	Homo sapiens	Human secreted protein, SEQ ID NO: 7197.	145	84
12440	AK024455	Homo sapiens	FLJ00047 protein	136	73
12441	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	122	69
12442	AF090942	Homo sapiens	PRO0657	120	72
12443	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	159	53
12444	AF130089	Homo sapiens	PRO2550	110	73
12445	AL021395	Homo sapiens	dJ269M15.1 (similar to peptidylprolyl isomerase (cyclophilin))	225	64
12446	AF090931	Homo sapiens	PRO0483	155	79
12447	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	130	81
12448	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	122	74
12449	AF119855	Homo sapiens	PRO1847	88	72
12450	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	147	84
12451	AK024455	Homo sapiens	FLJ00047 protein	78	68
12452	AF116712	Homo sapiens	PRO2738	118	62
12453	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	109	67
12454	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	59
12455	AK024455	Homo sapiens	FLJ00047 protein	146	64
12456	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	72
12457	AF090944	Homo sapiens	PRO0663	129	79
12458	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	119	70
12459	R22278	Homo sapiens	Human gp.-specific component phenotype Gc1.	250	65
12460	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	143	58
12461	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	111	61
12462	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	147	84
12463	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	94	38
12464	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	134	74
12465	AF200715	Homo sapiens	PTB domain adaptor protein CED-6	332	95
12466	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	139	64

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7867.		
12467	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	55
12468	AF199023	Homo sapiens	phospholipid scramblase 4	476	98
12469	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	104	89
12470	AF108841	Homo sapiens	pol protein	306	87
12471	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	111	79
12472	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	124	78
12473	U18339	Variola virus	D4L	117	60
12474	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	124	63
12475	AF130089	Homo sapiens	PRO2550	105	52
12476	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	80	62
12477	M91242	Rattus norvegicus	calcium channel alpha-1 subunit	156	68
12478	AF130089	Homo sapiens	PRO2550	154	79
12479	M15530	Homo sapiens	B-cell growth factor	154	70
12480	U39904	Mus musculus	citron	718	97
12481	R99364	Homo sapiens	Human REST protein DNA binding domain.	229	37
12482	AL160371	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	97	54
12483	AF161356	Homo sapiens	HSPC093	94	55
12484	Y69166	Homo sapiens	A mature human N-acetylglucosaminyl transferase protein.	97	75
12485	AF090942	Homo sapiens	PRO0657	103	55
12486	U79260	Homo sapiens	unknown	98	74
12487	AL160493	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	96	53
12488	U37100	Homo sapiens	aldose reductase-like peptide	400	97
12489	U93569	Homo sapiens	putative p150	141	56
12490	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	104	66
12491	R59842	Homo sapiens	ApoE4L1 protease.	86	89
12492	Y00876	Homo sapiens	Human LAPH-1 protein sequence.	219	45
12493	AK024455	Homo sapiens	FLJ00047 protein	85	53
12494	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	95	63
12495	Y36722	Homo sapiens	Fragment of human secreted protein encoded by gene 98.	216	60
12496	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	102	57
12497	Y77551	Homo sapiens	C-terminal domain of beta1c integrin.	132	67
12498	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	122	69
12499	AF161356	Homo sapiens	HSPC093	98	51
12500	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	150	81
12501	G00492	Homo sapiens	Human secreted protein, SEQ ID NO: 4573.	97	52
12502	AF132200	Homo sapiens	PRO1751	94	69
12503	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	76	65
12504	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	99	75

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12505	M19651	Rattus norvegicus	fos-related antigen	132	92
12506	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	113	48
12507	U94832	Homo sapiens	KSRP	117	48
12508	W47029	Homo sapiens	Human N-proteinase (70 kDa short form).	121	62
12509	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	66
12510	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	90	80
12511	AF042384	Homo sapiens	BC-2 protein	516	98
12512	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	96	50
12513	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	121	45
12514	AL162044	Homo sapiens	hypothetical protein	174	48
12515	AF130079	Homo sapiens	PRO2852	96	73
12516	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	113	77
12517	D32202	Homo sapiens	alpha 1C adrenergic receptor isoform 2	164	86
12518	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	99	85
12519	U00694	Gallus gallus	vitamin D3 hydroxylase associated protein	187	45
12520	AB030829	Rattus norvegicus	carbonic anhydrase III	503	63
12521	J04204	Bos taurus	32 kd accessory protein	618	95
12522	M36341	Homo sapiens	ADP-ribosylation factor 4	374	93
12523	AF090931	Homo sapiens	PRO0483	163	82
12524	AB007925	Homo sapiens	KIAA0456 protein	130	62
12525	G02314	Homo sapiens	Human secreted protein, SEQ ID NO: 6395.	162	79
12526	AF178948	Homo sapiens	TALE homeobox protein Meis2a	321	93
12527	AL359782	Trypanosoma brucei	possible (hvh-6) u1102, variant a dna, complete virion genome.	156	85
12528	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	126	57
12529	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	145	68
12530	AK024372	Homo sapiens	unnamed protein product	112	56
12531	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	76	65
12532	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	132	66
12533	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	146	53
12534	AF090942	Homo sapiens	PRO0657	83	60
12535	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	136	65
12536	R95913	Homo sapiens	Neural thread protein.	106	52
12537	AF130089	Homo sapiens	PRO2550	148	84
12538	AF102826	Homo sapiens	RD114/simian type D retrovirus receptor	605	91
12539	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	143	52
12540	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	87	65
12541	G03600	Homo sapiens	Human secreted protein, SEQ ID NO: 7681.	209	92

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12542	M31964	Saimiriine herpesvirus 2	collagen-like protein	92	52
12543	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	76
12544	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	72
12545	AC004912	Homo sapiens	similar to CR16, SH3 domain binding protein; similar to 2205340A (PID:g1587070)	442	98
12546	V00662	Homo sapiens	URF A61, (NADH dehydrogenase subunit)	175	91
12547	AF130089	Homo sapiens	PRO2550	112	40
12548	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	48
12549	X35110	Homo sapiens	neurite outgrowth-promoting protein	479	72
12550	X98296	Homo sapiens	ubiquitin hydrolase	500	88
12551	R94317	Homo sapiens	Hepatocyte proliferation substance HP-041V.	390	92
12552	G01623	Homo sapiens	Human secreted protein, SEQ ID NO: 5704.	142	90
12553	D86966	Homo sapiens	similar to human ZFY protein.	161	56
12554	D00570	Mus musculus	open reading frame (196 AA)	122	67
12555	AF130089	Homo sapiens	PRO2550	94	88
12556	AF043184	Homo sapiens	T cell receptor beta chain	607	84
12557	U93564	Homo sapiens	p40	154	100
12558	U42026	Homo sapiens	plasma membrane Ca2+-ATPase variant 4a PMCA4a	200	97
12559	S79410	Mus musculus	nuclear localization signal binding protein	103	50
12560	U90552	Homo sapiens	butyrophilin	356	98
12561	K02576	Homo sapiens	salivary proline-rich protein 1	156	37
12562	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	138	41
12563	X16454	Homo sapiens	carcinoembryonic antigen subdomain B	353	98
12564	AL031186	Homo sapiens	bK984G1.4 (Ewing sarcoma breakpoint region 1 protein)	119	100
12565	M68941	Homo sapiens	protein-tyrosine phosphatase	223	93
12566	Y14487	Homo sapiens	cytosolic serine hydroxymethyltransferase	145	84
12567	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	149	61
12568	AB005047	Homo sapiens	SH3 binding protein	124	52
12569	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	102	53
12570	X68142	Oryctolagus cuniculus	elongation factor 1 gamma	678	93
12571	L20315	Mus musculus	MPS1 protein	337	77
12572	AL359782	Trypanosoma brucei	possible (hiv-6) u1102, variant a dna, complete virion genome.	114	50
12573	AF130089	Homo sapiens	PRO2550	124	71
12574	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	146	51
12575	AF005902	Monodelphis domestica	kinesin homolog	534	82
12576	Y56021	Homo sapiens	Human CD40 receptor interacting protein 4C4.	711	96
12577	Y99662	Homo sapiens	Human GTPase associated protein-13.	634	100
12578	Z48008	Saccharomyces cerevisiae	Sok1p	225	100

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12579	AF112207	Homo sapiens	translation initiation factor eIF-2b delta subunit	195	97
12580	M22538	Homo sapiens	NADH-ubiquinone reductase	224	82
12581	AB034730	Mus musculus	This gene is isolated by means of differential display method using tw, an excellent mouse model for ectopic ossification.; similar to megakaryocyte stimulating factor precursor and cartilage superficial zone protein	112	44
12582	U93567	Homo sapiens	p40	364	93
12583	AY007233	Homo sapiens	phosphoinositol 3-phosphate binding protein-1	475	100
12584	L07592	Homo sapiens	peroxisome proliferator activated receptor	113	81
12585	AE003682	Drosophila melanogaster	CG8135 gene product	191	38
12586	AF119851	Homo sapiens	PRO1722	88	64
12587	AF090895	Homo sapiens	PRO0117	144	59
12588	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	144	57
12589	U75199	Mus musculus	Rho-guanine nucleotide exchange factor	111	32
12590	J04615	Homo sapiens	small nuclear ribonucleoprotein	383	97
12591	L77967	Ovis aries	small proline-rich protein with paired repeat	60	33
12592	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	118	78
12593	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	123	83
12594	AF090944	Homo sapiens	PRO0663	152	82
12595	Y15243	Homo sapiens	ULBP-3 amino acid sequence.	852	100
12596	X98235	Drosophila melanogaster	type 1	159	42
12597	AF191309	Mus musculus	zinc finger protein	407	66
12598	W82841	Homo sapiens	Human cerebral protein-1.	107	91
12599	AF070664	Homo sapiens	HSPC008	128	89
12600	U03688	Homo sapiens	cytochrome P450	257	96
12601	AB015798	Homo sapiens	DnaJ homolog	226	73
12602	AC003058	Arabidopsis thaliana	unknown protein	88	40
12603	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	80	35
12604	AF200187	cercopithicine herpesvirus 15	EBNA2-like protein	109	28
12605	AF161532	Homo sapiens	HSPC047	720	100
12606	M21302	Homo sapiens	small proline rich protein	60	59
12607	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	107	47
12608	AJ302650	Rattus norvegicus	RP59 protein	599	54
12609	J05401	Homo sapiens	sarcomeric mitochondrial creatine kinase precursor (EC 2.7.3.2)	763	96
12610	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	216	87
12611	W78175	Homo sapiens	Human secreted protein encoded by gene 50 clone HSTAG52.	337	100
12612	S79410	Mus musculus	nuclear localization signal binding protein	145	66
12613	AF119855	Homo sapiens	PRO1847	157	61

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12614	U82303	Homo sapiens	unknown	107	62
12615	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	146	49
12616	AF130051	Homo sapiens	PRO0898	254	56
12617	AF057350	Rattus norvegicus	NF-E2-related factor 2	807	59
12618	Y02168	Homo sapiens	A facilitative glucose transporter protein GLUT8.	452	100
12619	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	158	84
12620	G03812	Homo sapiens	Human secreted protein, SEQ ID NO: 7893.	246	60
12621	X55683	Lycopersicon esculentum	extensin (class I)	79	43
12622	AF109907	Homo sapiens	S164	93	40
12623	Y36156	Homo sapiens	Human secreted protein #28.	114	61
12624	AF116712	Homo sapiens	PRO2758	104	48
12625	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	81	65
12626	AF113685	Homo sapiens	PRO0974	104	43
12627	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	116	45
12628	AF107406	Homo sapiens	GW128	133	58
12629	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	100	57
12630	AB047600	Macaca fascicularis	hypothetical protein	172	66
12631	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	136	63
12632	AF118082	Homo sapiens	PRO1902	138	45
12633	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	151	62
12634	X52164	Mus musculus	Q300 protein (AA 1-77)	95	58
12635	AF064597	Homo sapiens	LINE-1 like protein	108	46
12636	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	116	49
12637	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	110	52
12638	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	79	70
12639	M29622	Mus musculus	open reading frame 2	81	60
12640	M26460	Homo sapiens	retinoblastoma 1	100	45
12641	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	110	63
12642	AB047936	Macaca fascicularis	hypothetical protein	100	52
12643	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	146	41
12644	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	143	48
12645	AF090942	Homo sapiens	PRO0657	157	54
12646	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	130	56
12647	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	267	65
12648	AF130079	Homo sapiens	PRO2852	109	57
12649	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	99	61
12650	X55686	Lycopersicon	extensin (class II)	65	35



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		esculentum			
12651	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	87	84
12652	AF119851	Homo sapiens	PRO1722	150	70
12653	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	133	50
12654	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	146	70
12655	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	136	63
12656	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	93	52
12657	U93563	Homo sapiens	putative p150	1046	50
12658	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	346	70
12659	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	104	70
12660	AF119851	Homo sapiens	PRO1722	98	56
12661	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	90	65
12662	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	59	64
12663	AF118082	Homo sapiens	PRO1902	91	66
12664	L10908	Mus musculus	Gcap1 gene product	113	50
12665	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	124	37
12666	AF090895	Homo sapiens	PRO0117	76	57
12667	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	103	43
12668	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	90	61
12669	M15530	Homo sapiens	B-cell growth factor	90	80
12670	AF198447	Aspergillus nidulans	60S ribosomal protein L3	217	69
12671	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	137	51
12672	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	77	68
12673	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	67	40
12674	X79417	Sus scrofa	40S ribosomal protein S12	377	75
12675	AF107406	Homo sapiens	GW128	74	51
12676	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	99	62
12677	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	127	65
12678	G00590	Homo sapiens	Human secreted protein, SEQ ID NO: 4671.	99	62
12679	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	128	85
12680	AF194537	Homo sapiens	NAG13	142	59
12681	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	155	77
12682	AF161356	Homo sapiens	HSPC093	104	50
12683	AF107406	Homo sapiens	GW128	84	54
12684	U83303	Homo sapiens	line-1 reverse transcriptase	90	39
12685	V40883_cdl	Homo sapiens	03-DEC-1997 Coding sequence of clone BG366_2.	728	100
12686	M24732	Homo sapiens	lamin-like protein	94	54
12687	X00824	Gallus gallus	collagen	66	42

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12688	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	184	64
12689	AF118086	Homo sapiens	PRO1992	140	61
12690	AL390114	Leishmania major	probable (hvh-6) u1102, variant a DNA, complete virion genome	131	54
12691	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	180	72
12692	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	104	72
12693	AF130089	Homo sapiens	PRO2550	204	51
12694	K01664	Drosophila melanogaster	Bkm-like protein	92	52
12695	AL390114	Leishmania major	probable (hvh-6) u1102, variant a DNA, complete virion genome	110	52
12696	L39103	Homo sapiens	glycoprotein Ib alpha	61	45
12697	M15530	Homo sapiens	B-cell growth factor	121	64
12698	M36913	Zea mays	cell wall protein (put.); putative	75	40
12699	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	68
12700	M24732	Homo sapiens	lamin-like protein	95	35
12701	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	67	50
12702	AF298594	Nicotiana glauca	arabinogalactan protein	105	30
12703	X92485	Plasmodium vivax	pva1	97	38
12704	AF210651	Homo sapiens	NAG18	89	64
12705	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	190	53
12706	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	93	78
12707	U52077	Homo sapiens	mariner transposase	451	51
12708	AC003058	Arabidopsis thaliana	unknown protein	244	77
12709	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	138	65
12710	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	99	82
12711	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	104	34
12712	AF242772	Homo sapiens	mesenchymal stem cell protein DSCD28	106	45
12713	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	116	36
12714	AF116715	Homo sapiens	PRO2829	139	68
12715	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	89	62
12716	X55684	Lycopersicon esculentum	extensin (class I)	86	54
12717	Z93891	Hegeter politus	cytochrome oxidase	72	48
12718	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	105	46
12719	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	74	46
12720	U30221	Citridia fasciculata	NADH dehydrogenase subunit 5	92	39
12721	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	131	82
12722	AF107406	Homo sapiens	GW128	72	54
12723	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 131	131	55

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6720.		
12724	AF116661	Homo sapiens	PRO1438	145	59
12725	Y53871	Homo sapiens	A human brain-derived signalling factor polypeptide.	584	98
12726	L10908	Mus musculus	Gcap1 gene product	95	37
12727	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	124	37
12728	X55686	Lycopersicon esculentum	extensin (class II)	66	36
12729	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	110	55
12730	L23852	Homo sapiens	Putative 3' end of coding region; putative	83	37
12731	Y13141	Bromheadia finlaysoniana	extensin	59	48
12732	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	88	69
12733	AF090895	Homo sapiens	PRO0117	130	55
12734	R95913	Homo sapiens	Neural thread protein.	162	45
12735	U72355	Homo sapiens	Hsp27 ERE-TATA-binding protein	972	57
12736	AF247039	porcine adenovirus 3	163R*	108	35
12737	M22332	Homo sapiens	unknown protein	148	45
12738	AF090895	Homo sapiens	PRO0117	89	72
12739	B08525	Homo sapiens	Protein encoded by a novel gene associated with colon disease.	296	86
12740	X90872	Homo sapiens	associated to Golgi apparatus	116	54
12741	M26460	Homo sapiens	retinoblastoma 1	75	37
12742	S52010	Mus sp.	orf1 5' of EpoR	104	31
12743	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	88	50
12744	AB047600	Macaca fascicularis	hypothetical protein	111	47
12745	AF090944	Homo sapiens	PRO0663	152	65
12746	Y21106	Homo sapiens	Human bcl2 proto-oncogene wild type protein fragment 3.	62	64
12747	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	97	76
12748	X66861	Mus musculus	Hox-1.4	92	34
12749	AF166125	Homo sapiens	selenoprotein N	978	98
12750	W87504	Homo sapiens	Human N-methyl-D-aspartate receptor subunit encoded by clone NMDA24.	98	29
12751	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	91	78
12752	X72963	Nicotiana tabacum	pAP8 product	80	45
12753	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	123	61
12754	AF146191	Homo sapiens	FRG1	208	85
12755	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	154	75
12756	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	72	48
12757	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	111	51
12758	U83280	Leishmania donovani	39 kDa antigen	106	60
12759	AF116661	Homo sapiens	PRO1438	73	48
12760	AF164615	Homo sapiens	envelope protein.	257	83

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12761	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	135	70
12762	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	111	50
12763	M29622	Mus musculus	open reading frame 2	73	68
12764	L27428	Homo sapiens	reverse transcriptase	111	60
12765	S79410	Mus musculus	nuclear localization signal binding protein	106	45
12766	AK024455	Homo sapiens	FLJ00047 protein	108	66
12767	M36914	Zea mays	cell wall protein (put.); putative	78	36
12768	L27428	Homo sapiens	reverse transcriptase	159	59
12769	AJ005567	Mus musculus	SPR21 protein	55	39
12770	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	115	82
12771	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	76	64
12772	AF217374	Acanthaster planci	cytochrome oxidase subunit I	126	85
12773	AF130114	Homo sapiens	PRO2459	129	50
12774	AF010144	Homo sapiens	neuronal thread protein AD7/c-NTP	220	71
12775	AF287482	Chlorobium tepidum	Orf122	166	68
12776	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	84	50
12777	AF130079	Homo sapiens	PRO2852	258	58
12778	AF090931	Homo sapiens	PRO0483	65	76
12779	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	152	66
12780	AB047948	Macaca fascicularis	hypothetical protein	59	37
12781	AF119900	Homo sapiens	PRO2822	132	59
12782	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	97	51
12783	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	77	77
12784	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	93	84
12785	L27428	Homo sapiens	reverse transcriptase	183	39
12786	AF119851	Homo sapiens	PRO1722	128	61
12787	AF116715	Homo sapiens	PRO2829	111	72
12788	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	147	77
12789	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	84	66
12790	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	155	71
12791	AF124729	Mus musculus	acinusS'	122	50
12792	AC003058	Arabidopsis thaliana	unknown protein	86	52
12793	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	108	74
12794	M62415	Pseudopleuronectes americanus	HPLC6	82	35
12795	Y36156	Homo sapiens	Human secreted protein #28.	133	48
12796	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	74
12797	L22030	Glycine max	hydroxyproline-rich glycoprotein	170	32
12798	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	114	43
12799	Y76184	Homo sapiens	Human secreted protein encoded by	90	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gene 61.		
12800	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	102	38
12801	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	98	69
12802	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	177	69
12803	AF130089	Homo sapiens	PRO2550	94	74
12804	S77772	Homo sapiens	aspartylglucosaminidase, AGA {C-terminal, alternatively spliced} (EC 3.5.1.26)	83	68
12805	AF063866	Melanoplus sanguinipes entomopoxvirus	ORF MSV233 hypothetical protein	82	28
12806	AF026689	Homo sapiens	prostate-specific transglutaminase	80	60
12807	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	122	47
12808	X03145	Homo sapiens	pot. ORF V	150	34
12809	L10908	Mus musculus	Gcap1 gene product	111	34
12810	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	170	55
12811	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	101	62
12812	AJ233591	Mus musculus	reverse transcriptase	287	67
12813	U82303	Homo sapiens	unknown	149	52
12814	AF107406	Homo sapiens	GW128	103	58
12815	U82303	Homo sapiens	unknown	93	83
12816	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	161	54
12817	B01390	Homo sapiens	Neuron-associated protein.	81	38
12818	AF287482	Chlorobium tepidum	Orf122	174	69
12819	AE003499	Drosophila melanogaster	CG12706 gene product	166	28
12820	M15530	Homo sapiens	B-cell growth factor	124	71
12821	U83303	Homo sapiens	line-1 reverse transcriptase	161	53
12822	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	150	77
12823	G00497	Homo sapiens	Human secreted protein, SEQ ID NO: 4578.	103	66
12824	AF064597	Homo sapiens	LINE-1 like protein	64	45
12825	X71442	Rattus norvegicus	ORF 1; putative	113	45
12826	U62039	Elephantulus edwardii	reverse transcriptase	74	46
12827	M15530	Homo sapiens	B-cell growth factor	127	54
12828	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	94	84
12829	U63332	Homo sapiens	super cysteine rich protein; SCRIP	59	57
12830	AF229067	Homo sapiens	PADI-H protein	184	61
12831	K02576	Homo sapiens	salivary proline-rich protein 1	69	34
12832	AF144054	Homo sapiens	apoptosis related protein APR-4	83	46
12833	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	168	61
12834	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	142	40
12835	U19098	Lycopersicon chilense	proline-rich protein	81	38
12836	R96800	Homo sapiens	Human histocyte-secreted factor HSF.	229	68

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12837	Y13141	Bromheadia finlaysoniana	extensin	81	60
12838	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	88	71
12839	X72963	Nicotiana tabacum	pAP8 product	94	40
12840	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	315	56
12841	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	94	55
12842	AK025947	Homo sapiens	unnamed protein product	124	57
12843	AF159055	Homo sapiens	leucine zipper-like protein	69	55
12844	AF040257	Homo sapiens	TNF receptor homolog	98	50
12845	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	94	76
12846	X88799	Oryza sativa	DNA binding protein	94	37
12847	AL359782	Trypanosoma brucei	possible (hvh-6) u1102, variant a dna, complete virion genome.	98	48
12848	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	164	56
12849	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	75	59
12850	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	122	54
12851	M31964	Saimiriinc herpesvirus 2	collagen-like protein	79	50
12852	AF118082	Homo sapiens	PRO1902	94	77
12853	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	139	54
12854	R59842	Homo sapiens	ApoE4L1 protease.	108	82
12855	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	99	66
12856	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	89	56
12857	D29833	Homo sapiens	proline rich peptide P-B	64	52
12858	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	155	80
12859	G02482	Homo sapiens	Human secreted protein, SEQ ID NO: 6563.	88	61
12860	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	66	33
12861	Y13141	Bromheadia finlaysoniana	extensin	75	47
12862	M29622	Mus musculus	open reading frame 2	74	62
12863	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	141	70
12864	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	117	54
12865	AF090894	Homo sapiens	PRO0113	108	63
12866	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	121	54
12867	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	103	44
12868	S68106	Ascaris suum, Peptide Partial, 100 aa	type IV collagen alpha 2 chain, alpha 2 (IV) (alternatively spliced)	75	35
12869	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	97	56
12870	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	146	62

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12871	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	78	76
12872	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	105	56
12873	A03050234	Canis familiaris	D4 dopamine receptor	61	58
12874	M22332	Homo sapiens	unknown protein	128	41
12875	U05313	Trypanosoma brucei	CR3	67	48
12876	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	115	65
12877	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	66	54
12878	X55684	Lycopersicon esculentum	extensin (class I)	78	34
12879	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	51
12880	AF130079	Homo sapiens	PRO2852	125	75
12881	AF090895	Homo sapiens	PRO1117	142	59
12882	AF181251	Rattus norvegicus	lung Kruppel-like factor	93	39
12883	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	167	74
12884	M26460	Homo sapiens	retinoblastoma 1	136	41
12885	AJ277557	Homo sapiens	mitochondrial 5(3')-deoxyribonucleotidase (dNT-2)	280	100
12886	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	119	62
12887	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	145	43
12888	AF119851	Homo sapiens	PRO1722	94	50
12889	K02576	Homo sapiens	salivary proline-rich protein 1	121	39
12890	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	95	68
12891	AK024455	Homo sapiens	FLJ00047 protein	77	51
12892	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	115	83
12893	L27428	Homo sapiens	reverse transcriptase	89	29
12894	Y01154	Homo sapiens	Protein sequence Seq Id 54 from WO9901020.	112	72
12895	G02597	Homo sapiens	Human secreted protein, SEQ ID NO: 6678.	72	62
12896	AK023563	Homo sapiens	unnamed protein product	260	64
12897	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	76	66
12898	AC002304	Arabidopsis thaliana	F14J16.29	111	36
12899	Y86445	Homo sapiens	Human gene 42-encoded protein fragment, SEQ ID NO:360.	83	53
12900	AF116638	Homo sapiens	PRO1546	123	57
12901	AB010361	Mus musculus	msz47	64	43
12902	R59842	Homo sapiens	ApoE4L1 protease.	130	86
12903	L06498	Homo sapiens	ribosomal protein S20	249	56
12904	L13635	Rattus norvegicus	growth response protein	176	69
12905	AF156961	Homo sapiens	gag	183	44
12906	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	207	67
12907	AF107406	Homo sapiens	GW128	99	50
12908	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	93	75

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12909	AF263540	Homo sapiens	MIB006	1809	100
12910	Y48292	Homo sapiens	Human prostate cancer-associated protein 78.	60	50
12911	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	179	87
12912	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	108	72
12913	Z72499	Homo sapiens	herpesvirus associated ubiquitin-specific protease (HAUSP)	5242	99
12914	AF092136	Homo sapiens	PTD015	297	100
12915	AF161356	Homo sapiens	HSPC093	123	42
12916	AF044670	Homo sapiens	33 kDa Vamp-associated protein; VAP-33	506	90
12917	W27087	Homo sapiens	Human transforming growth factor alpha HIII.	1243	100
12918	Y59807	Homo sapiens	Human normal ovarian tissue derived protein 84.	111	43
12919	AJ388518	Canis familiaris	non-histone chromosomal protein HM-G-17	108	84
12920	AK023392	Homo sapiens	unnamed protein product	119	60
12921	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	104	87
12922	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	124	81
12923	X78444 cd1	Homo sapiens	21-MAY-1997 Human UCSF-2 cDNA.	1090	100
12924	AF116661	Homo sapiens	PRO1438	89	52
12925	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	82	80
12926	AF119855	Homo sapiens	PRO1847	120	63
12927	AF090931	Homo sapiens	PRO0483	92	90
12928	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	119	88
12929	Y91429	Homo sapiens	Human secreted protein sequence encoded by gene 21 SEQ ID NO:150.	108	38
12930	Y12661	Homo sapiens	neuro-endocrine specific protein VGF	2506	99
12931	Y84546	Homo sapiens	Amino acid sequence of a fragment of human collagen type 1 protein.	61	50
12932	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	121	53
12933	G00481	Homo sapiens	Human secreted protein, SEQ ID NO: 4562.	104	52
12934	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	104	60
12935	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	331	77
12936	M15530	Homo sapiens	B-cell growth factor	83	71
12937	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	146	64
12938	R59842	Homo sapiens	ApoB4L1 protease.	112	61
12939	AF090895	Homo sapiens	PRO0117	94	80
12940	X73459	Homo sapiens	signal recognition particle subunit 14	549	98
12941	L23545	Homo sapiens	putative	141	45
12942	AF054178	Homo sapiens	Cl-B14.5a homolog	238	84
12943	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	55
12944	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	143	55
12945	D00570	Mus musculus	open reading frame (251 AA)	166	34
12946	U62039	Elephantulus	reverse transcriptase	63	50



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		edwardii			
12947	AE003499	Drosophila melanogaster	CG12706 gene product	104	31
12948	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	65	100
12949	X70343	Nicotiana glauca	extensin	102	38
12950	G02332	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	103	45
12951	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	85	56
12952	AF090895	Homo sapiens	PRO0117	139	68
12953	AF090896	Homo sapiens	PRO0131	93	85
12954	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	101	75
12955	M96982	Homo sapiens	U2 snRNP auxiliary factor small subunit	292	68
12956	X71087	Homo sapiens	monocyte chemoattractant protein (MCP-3)	408	96
12957	S80864	Homo sapiens	cytochrome c-like polypeptide	591	68
12958	AF109907	Homo sapiens	SI64	188	63
12959	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	173	50
12960	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	168	62
12961	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	98	56
12962	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	106	84
12963	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	125	44
12964	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	107	57
12965	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	71	65
12966	AC009853	Arabidopsis thaliana	hypothetical protein	102	44
12967	AF090942	Homo sapiens	PRO0657	99	62
12968	M15530	Homo sapiens	B-cell growth factor	90	65
12969	AF090895	Homo sapiens	PRO0117	83	54
12970	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	119	54
12971	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	123	57
12972	L32558	Homo sapiens	sequence is expressed in human Tera-2 clone 13 (embryonal carcinoma) cells. The sequence may contain mismatches (one strand sequenced only once). 97% identical in 320 bp overlap with human 54 kDa prot; ORF	426	85
12973	AF008196	Homo sapiens	bax epsilon	78	87
12974	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	96	80
12975	AL031848	Homo sapiens	dJ20208.2.2 (novel rodent HES2 (hairly and Enhancer of Split 2) LIKE protein (isoform 2))	176	100
12976	AJ245905	Chlorocebus aethiops	HSBP1-like protein	94	100
12977	AF067519	Homo sapiens	PITSLRE protein kinase beta SV1 isoform	1923	93

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12978	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	168	73
12979	X52154	Mus musculus	Q300 protein (AA 1-77)	105	39
12980	Y13141	Bromheadia finlaysoniana	extensin	53	36
12981	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	87	77
12982	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	83	89
12983	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	92	46
12984	AF113685	Homo sapiens	PRO0974	111	67
12985	U31086	Gallus gallus	neuron-glia adhesion molecule	52	50
12986	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	132	68
12987	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	91	71
12988	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	135	81
12989	AB029042	Homo sapiens	ATPase inhibitor precursor	364	100
12990	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	174	72
12991	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	174	57
12992	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	158	57
12993	AF118082	Homo sapiens	PRO1902	77	78
12994	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	76	60
12995	M15530	Homo sapiens	B-cell growth factor	105	76
12996	AJ005562	Mus musculus	SPR2D protein	104	36
12997	Y48346	Homo sapiens	Human prostate cancer-associated protein 43.	184	77
12998	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	82	53
12999	L11645	Homo sapiens	alpha-tubulin	196	68
13000	AF113685	Homo sapiens	PRO0974	123	52
13001	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	78	53
13002	AJ005564	Mus musculus	SPR2F protein	76	44
13003	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	101	76
13004	AL159178	Streptomyces coelicolor A3(2)	putative secreted protein	89	37
13005	L77967	Ovis aries	small proline-rich protein with paired repeat	64	36
13006	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	85	70
13007	AF068294	Homo sapiens	HDCMB45P	237	52
13008	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	128	50
13009	AF144054	Homo sapiens	apoptosis related protein APR-4	100	75
13010	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	148	67
13011	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	152	66
13012	B01390	Homo sapiens	Neuron-associated protein.	99	32
13013	A27282	Homo sapiens	TGR-CL3C	69	42
13014	G00689	Homo sapiens	Human secreted protein, SEQ ID NO:	135	46

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4770.		
13015	AF130089	Homo sapiens	PRO2550	88	60
13016	AF266223	Gillichthys mirabilis	ribosomal protein L27	122	50
13017	S79410	Mus musculus	nuclear localization signal binding protein	116	40
13018	U82303	Homo sapiens	unknown	64	60
13019	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	70	57
13020	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	169	91
13021	V00488	Homo sapiens	alpha globin	213	100
13022	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	59
13023	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	109	86
13024	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	151	84
13025	U82303	Homo sapiens	unknown	86	52
13026	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	124	61
13027	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	83	50
13028	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	74	63
13029	Y84546	Homo sapiens	Amino acid sequence of a fragment of human collagen type 1 protein.	59	46
13030	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	96	68
13031	S71494	Mus sp.	SmD homolog {Gly-Arg repeat}	93	55
13032	AF113685	Homo sapiens	PRO0974	100	48
13033	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	242	85
13034	AL390114	Leishmania major	extremely cysteine/valine rich protein	178	41
13035	G01129	Homo sapiens	Human secreted protein, SEQ ID NO: 5210.	228	81
13036	X66285	Mus musculus	HCl ORF	103	44
13037	AF026689	Homo sapiens	prostate-specific transglutaminase	90	55
13038	U47924	Homo sapiens	RPL13-2	424	63
13039	AF090942	Homo sapiens	PRO0657	111	44
13040	AK025116	Homo sapiens	unnamed protein product	131	52
13041	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	92	72
13042	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	100	69
13043	AF130089	Homo sapiens	PRO2550	109	45
13044	G02879	Homo sapiens	Human secreted protein, SEQ ID NO: 6960.	116	52
13045	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	162	70
13046	L10908	Mus musculus	Gcap1 gene product	162	40
13047	L02321	Homo sapiens	glutathione S-transferase GSTM5-5	1072	93
13048	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	89	60
13049	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	153	60
13050	U33547	Homo sapiens	MHC class II antigen	69	85
13051	AC006014	Homo sapiens	similar to mismatch repair proteins; similar to P1D:g1304125	652	91

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13052	A27282	Homo sapiens	TGR-CL3C	65	51
13053	Y69166	Homo sapiens	A mature human N-acetylglucosaminyl transferase protein.	106	60
13054	M20030	Homo sapiens	small proline rich protein	57	33
13055	AF022117	Balaena mysticetus	metallothionein	119	62
13056	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	78	43
13057	R20305	Homo sapiens	Val(1) to Met, His(2) deleted, Ala(76) to Lys beta-globin mutant.	274	98
13058	X55686	Lycopersicon esculentum	extensin (class II)	56	39
13059	U10696	Zea mays	Ec metallothionein class II protein	66	26
13060	Y40417	Homo sapiens	A human N-acetylneuraminase lyase (hNANL) protein.	1183	80
13061	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	125	41
13062	AF002210	Homo sapiens	copper chaperone for superoxide dismutase	702	61
13063	AF118086	Homo sapiens	PRO1992	69	84
13064	M24097	Homo sapiens	MHC HLA-C-alpha-2 chain	1550	96
13065	AC003113	Arabidopsis thaliana	F24O1.6	51	40
13066	AF161531	Homo sapiens	HSFC046	488	97
13067	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	141	50
13068	AL359782	Trypanosoma brucei	possible (hlv-6) u1102, variant a dna, complete virion genome.	116	46
13069	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	145	69
13070	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	224	71
13071	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	153	52
13072	AF216965	Homo sapiens	ancient conserved domain protein 3	876	100
13073	Y15917	Homo sapiens	COLIA1 and PDGFB fusion transcript	108	35
13074	X77664	Homo sapiens	retinoic acid receptor beta isoform 1	53	71
13075	AF156961	Homo sapiens	gag	136	37
13076	R59842	Homo sapiens	ApoE4L1 protease.	117	75
13077	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	121	65
13078	U23183	Caenorhabditis elegans	gene lies in inverted repeat and exon 1 overlaps tRNA; may be pseudogene	100	79
13079	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	56
13080	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	138	65
13081	Y12473	Homo sapiens	centrin	359	79
13082	G01518	Homo sapiens	Human secreted protein, SEQ ID NO: 5599.	375	98
13083	Y57891	Homo sapiens	Human transmembrane protein HTMPN-15.	1030	99
13084	AB046765	Homo sapiens	KIAA1545 protein	161	93
13085	X55686	Lycopersicon esculentum	extensin (class II)	66	40
13086	AF130079	Homo sapiens	PRO2852	137	45
13087	K01664	Drosophila melanogaster	Bkm-like protein	86	33
13088	G03812	Homo sapiens	Human secreted protein, SEQ ID NO:	105	44

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7893.		
13089	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	114	63
13090	AL121905	Homo sapiens	dJ534B8.3 (novel protein similar to an aspartic protease)	963	100
13091	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	95	47
13092	AB030236	Canis familiaris	D4 dopamine receptor	65	38
13093	AF161356	Homo sapiens	HSPC093	119	48
13094	Z14014	Nicotiana tabacum	Pistil extensin like protein, partial CDS only	67	50
13095	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	124	56
13096	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	73
13098	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	62
13099	AF130051	Homo sapiens	PRO0898	194	61
13100	Y86445	Homo sapiens	Human gene 42-encoded protein fragment, SEQ ID NO:360.	80	70
13101	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	111	43
13102	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	120	71
13103	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	116	63
13104	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	90	64
13105	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	176	56
13106	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR-A41726)	101	75
13107	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	100	65
13108	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	137	77
13109	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	94	88
13110	AF119855	Homo sapiens	PRO1847	103	49
13111	AF119851	Homo sapiens	PRO1722	142	80
13112	Y00311	Homo sapiens	Human secreted protein encoded by gene 54.	107	51
13113	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	104	54
13114	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	144	71
13115	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	138	50
13116	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	110	56
13117	AK025653	Homo sapiens	unnamed protein product	188	100
13118	AF130089	Homo sapiens	PRO2550	129	68
13119	AF161356	Homo sapiens	HSPC093	131	59
13120	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	121	45
13121	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	82	55
13122	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 87	87	45

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4718.		
13123	Y38394	Homo sapiens	Human secreted protein encoded by gene No. 9.	213	100
13124	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	108	55
13125	AF119855	Homo sapiens	PRO1847	109	45
13126	R95913	Homo sapiens	Neural thread protein.	137	47
13127	B01390	Homo sapiens	Neuron-associated protein.	101	47
13128	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	122	67
13129	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	105	52
13130	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	170	72
13131	D38112	Homo sapiens	NADH dehydrogenase subunit 3	500	90
13132	AF138957	Bos taurus	type II collagen cyanogen bromide fragment CB8	99	38
13133	AF084256	Homo sapiens	beta glucuronidase isoform d	157	69
13134	U92817	Homo sapiens	unnamed HERV-H protein	113	48
13135	Y19743	Homo sapiens	SEQ ID NO 461 from WO9922243.	967	99
13136	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	155	52
13137	AF090928	Homo sapiens	PRO0470	133	69
13138	AF090931	Homo sapiens	PRO0483	150	60
13139	AF116661	Homo sapiens	PRO1438	146	57
13140	AL022318	Homo sapiens	bK150C2.2 (Phorbol 3)	443	56
13141	S79410	Mus musculus	nuclear localization signal binding protein	114	80
13142	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	86	43
13143	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	62
13144	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	146	66
13145	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	123	71
13146	AF107406	Homo sapiens	GW128	120	50
13147	L10908	Mus musculus	Gcap1 gene product	91	42
13148	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	66
13149	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	119	67
13150	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	168	86
13151	G00418	Homo sapiens	Human secreted protein, SEQ ID NO: 4499.	74	58
13152	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	108	61
13153	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	131	67
13154	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	113	54
13155	AF000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	84
13156	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	167	80
13157	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	125	68
13158	D38112	Homo sapiens	cytochrome c oxidase subunit 3	514	71
13159	Y86248	Homo sapiens	Human secreted protein HC1HPF68.	130	66

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SEQ ID NO:163.		
13160	AF116661	Homo sapiens	PRO1438	152	63
13161	AB046048	Macaca fascicularis	unnamed protein product	105	53
13162	AF107406	Homo sapiens	GW128	159	62
13163	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	132	59
13164	M15530	Homo sapiens	B-cell growth factor	97	80
13165	K02576	Homo sapiens	salivary proline-rich protein 1	67	36
13166	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	126	57
13167	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	95	53
13168	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	96	57
13169	AL049795	Homo sapiens	dJ622L5.7.2 (novel protein (isoform 2))	250	95
13170	G00366	Homo sapiens	Human secreted protein, SEQ ID NO: 4447.	116	56
13171	L10908	Mus musculus	Gcap1 gene product	75	53
13172	S73853	Homo sapiens	NF2-neurofibromatosis type 2 {alternatively spliced, form A4}	160	73
13173	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	76
13174	A52568	Homo sapiens	HMGL-C	84	44
13175	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	91	49
13176	AK025116	Homo sapiens	unnamed protein product	130	44
13177	AF090901	Homo sapiens	PRO0195	103	84
13178	AF090894	Homo sapiens	PRO0113	92	62
13179	AF130079	Homo sapiens	PRO2852	118	38
13180	AK025047	Homo sapiens	unnamed protein product	141	67
13181	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	87	59
13182	AC003058	Arabidopsis thaliana	unknown protein	220	74
13183	S79980	Bos taurus	ribosomal protein L37	186	94
13184	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	90
13185	AF155232	Pisum sativum	extensin	95	36
13187	U16359	Rattus norvegicus	nitric oxide synthase	90	78
13188	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	113	79
13189	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	158	53
13190	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	130	59
13191	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	131	66
13192	D38112	Homo sapiens	NADH dehydrogenase subunit 3	439	86
13193	Z66499	Caenorhabditis elegans	T01B7.8	127	35
13194	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	126	61
13195	Y13141	Bromheadia finlaysoniana	extensin	58	43
13196	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	95	76
13197	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	116	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13198	X58236	Homo sapiens	36/8-8 fusion protein with epitope for anti-lectin antibody	98	41
13199	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	102	58
13200	AF220264	Homo sapiens	MOST-1	141	45
13201	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	112	58
13202	Y17221	Homo sapiens	Human secreted protein (clone fl317-3).	115	57
13203	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	91	39
13204	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	126	65
13205	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	98	68
13206	M15530	Homo sapiens	B-cell growth factor	105	76
13207	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	84	45
13208	L27428	Homo sapiens	reverse transcriptase	205	49
13209	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XRL8c}	77	57
13210	M81321	Macaca fascicularis	proline-rich protein	104	48
13211	X55685	Lycopersicon esculentum	extensin (class I)	122	33
13212	M15530	Homo sapiens	B-cell growth factor	159	61
13213	AF130089	Homo sapiens	PRO2550	126	56
13214	AF210651	Homo sapiens	NAG18	125	68
13215	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	114	76
13216	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5527.	157	70
13217	R59842	Homo sapiens	ApoE4L1 protease.	102	72
13218	K01664	Drosophila melanogaster	Bcm-like protein	123	37
13219	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	101	55
13220	D14167	Gallus gallus	ribosomal protein L37a	126	40
13221	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	178	82
13222	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	141	55
13223	L10908	Mus musculus	Gcap1 gene product	114	53
13224	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	216	73
13225	G03259	Homo sapiens	Human secreted protein, SEQ ID NO: 7340.	104	76
13226	AF130079	Homo sapiens	PRO2852	158	66
13227	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	60
13228	S77772	Homo sapiens	aspartylglucosaminidase, AGA {C-terminal, alternatively spliced} {EC 3.5.1.26}	100	46
13229	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	72
13230	M15530	Homo sapiens	B-cell growth factor	162	72
13231	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	161	66
13232	AL160371	Leishmania major	probable (hiv-6) u1102, variant a DNA, complete virion genome	80	52



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13233	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	126	51
13234	AF126163	Homo sapiens	HLA3 protein	131	78
13235	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	125	85
13236	AB001684	Chlorella vulgaris	ORF49b	55	45
13237	M15530	Homo sapiens	B-cell growth factor	114	66
13238	AL335929	Neurospora crassa	conserved hypothetical protein	99	46
13239	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	63
13240	S79410	Mus musculus	nuclear localization signal binding protein	110	40
13241	AF119851	Homo sapiens	PRO1722	167	63
13242	S79410	Mus musculus	nuclear localization signal binding protein	147	68
13243	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	95	65
13244	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	99	84
13245	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSAWA27.	104	62
13246	AF161356	Homo sapiens	HSPC093	116	67
13247	X61046	Hydra sp.	mini-collagen	108	49
13248	V00662	Homo sapiens	URF 3 (NADH dehydrogenase subunit)	458	89
13249	M11900	Mus musculus	15-kDa proline-rich salivary protein	92	37
13250	AB017362	Bombyx mori	fibroin H-chain	70	43
13251	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	125	58
13252	G00360	Homo sapiens	Human secreted protein, SEQ ID NO: 4441.	122	58
13253	AF210651	Homo sapiens	NAG18	151	73
13254	AF224494	Mus musculus	arsenite inducible RNA associated protein	299	50
13255	AK026107	Homo sapiens	unnamed protein product	102	60
13256	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	113	61
13257	AK024455	Homo sapiens	FLJ00047 protein	115	59
13258	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	155	51
13259	AJ251579	Arabidopsis thaliana	cef protein	115	39
13260	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	360	82
13261	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	151	61
13262	D38112	Homo sapiens	NADH dehydrogenase subunit 3	413	87
13263	D23661	Homo sapiens	ribosomal protein L37	487	94
13264	AF130079	Homo sapiens	PRO2852	153	43
13265	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	109	61
13266	Y01154	Homo sapiens	Protein sequence Seq Id 54 from WO9901020.	133	79
13267	L10908	Mus musculus	Gcap1 gene product	103	43
13268	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	151	70
13269	G04064	Homo sapiens	Human secreted protein, SEQ ID NO: 8145.	97	51

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13270	AF130089	Homo sapiens	PRO2550	95	47
13271	AF130075	Homo sapiens	PRO2532	90	60
13272	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	103	54
13273	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	77	91
13274	AF130089	Homo sapiens	PRO2550	104	57
13275	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	94	45
13276	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	122	52
13277	AF113685	Homo sapiens	PRO0974	98	36
13278	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	85	68
13279	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	139	89
13280	G01129	Homo sapiens	Human secreted protein, SEQ ID NO: 5210.	243	79
13281	AF116715	Homo sapiens	PRO2829	108	56
13282	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	105	60
13283	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	194	78
13284	AL359782	Trypanosoma brucei	probable granule cell antiserum positive 8	104	47
13285	S79410	Mus musculus	nuclear localization signal binding protein	104	72
13286	AF130089	Homo sapiens	PRO2550	147	58
13287	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	133	58
13288	AF119855	Homo sapiens	PRO1847	115	45
13289	AF161356	Homo sapiens	HSPC093	131	50
13290	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	104	43
13291	K01664	Drosophila melanogaster	Bkm-like protein	112	49
13292	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	150	69
13293	M36647	Homo sapiens	mitochondrial hinge protein precursor	284	76
13294	D38112	Homo sapiens	NADH dehydrogenase subunit 3	444	85
13295	D38112	Homo sapiens	cytochrome c oxidase subunit 3	633	93
13296	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	164	76
13297	AL359782	Trypanosoma brucei	possible (hly-6) u1102, variant a dna, complete virion genome.	147	80
13298	Y13141	Bromheadia finlaysoniana	extensin	84	38
13299	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	139	49
13300	AF130079	Homo sapiens	PRO2852	98	60
13301	AF090894	Homo sapiens	PRO0113	114	52
13302	AF130079	Homo sapiens	PRO2852	161	83
13303	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	154	76
13304	AF118086	Homo sapiens	PRO1992	120	75
13305	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	100	73
13306	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	108	56

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13307	Y74110	Homo sapiens	Human prostate tumor EST fragment derived protein #297.	448	100
13308	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	85	65
13309	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	104	47
13310	AF116715	Homo sapiens	PRO2829	124	76
13311	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	142	63
13312	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	155	61
13313	AF116661	Homo sapiens	PRO1438	142	67
13314	AF161356	Homo sapiens	HSPC093	121	46
13315	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	169	52
13316	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	98	90
13317	AF130079	Homo sapiens	PRO2852	109	58
13318	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	113	80
13319	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	81	61
13320	AF130089	Homo sapiens	PRO2550	106	77
13321	AF090931	Homo sapiens	PRO0483	143	63
13322	D29833	Homo sapiens	proline rich peptide P-B	59	33
13323	D38112	Homo sapiens	NADH dehydrogenase subunit 3	417	78
13324	AF000616	Oryza sativa	similar to RING-H2 finger protein RH1A1a (AF078683)	119	82
13325	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	168	59
13326	A31038	Nicotiana glauca	PRP3	88	41
13327	AF090895	Homo sapiens	PRO0117	87	55
13328	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	88	51
13329	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	103	66
13330	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	101	67
13331	AF090930	Homo sapiens	PRO0478	93	36
13332	AF159055	Homo sapiens	leucine zipper-like protein	118	71
13333	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	89	57
13334	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	121	80
13335	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	160	73
13336	AJ005562	Mus musculus	SPR2D protein	86	44
13337	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	169	66
13338	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	78	57
13339	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	102	91
13340	AF090895	Homo sapiens	PRO0117	137	47
13341	K01664	Drosophila melanogaster	Bkm-like protein	115	46
13342	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	100	76
13343	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 134	134	65

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7795.		
13344	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	76	76
13345	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	72
13346	G00552	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	143	69
13347	AF119900	Homo sapiens	PRO2822	93	58
13348	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	169	75
13349	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	83	68
13350	AF116715	Homo sapiens	PRO2829	134	64
13351	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	115	65
13352	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	118	59
13353	Y02887	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	139	77
13354	AF116661	Homo sapiens	PRO1438	112	75
13355	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	170	73
13356	AF126163	Homo sapiens	HHLA3 protein	116	55
13357	U18339	Variola virus	D4L	101	58
13358	AF130089	Homo sapiens	PRO2550	127	52
13359	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	184	82
13360	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	78	50
13361	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	126	71
13362	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	174	76
13363	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	176	51
13364	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	99	41
13365	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	118	56
13366	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	158	50
13367	Y19467	Homo sapiens	Amino acid sequence of a human secreted protein.	65	64
13368	M15530	Homo sapiens	B-cell growth factor	132	77
13369	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	63
13370	AF130079	Homo sapiens	PRO2852	108	61
13371	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	150	76
13372	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	117	65
13373	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	118	57
13374	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	121	63
13375	AF118086	Homo sapiens	PRO1992	147	74
13376	AF130089	Homo sapiens	PRO2550	149	48
13377	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	123	55

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13378	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	120	53
13379	AF090894	Homo sapiens	PRO0113	101	52
13380	AF107406	Homo sapiens	GW128	126	51
13381	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	156	84
13382	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	119	80
13383	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSAWA27.	84	70
13384	S79410	Mus musculus	nuclear localization signal binding protein	107	53
13385	S79410	Mus musculus	nuclear localization signal binding protein	107	53
13386	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	141	65
13387	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	113	63
13388	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	155	77
13389	AF130089	Homo sapiens	PRO2550	159	62
13390	AF161356	Homo sapiens	HSPC093	154	74
13391	AC006135	Arabidopsis thaliana	putative vicilin storage protein (globulin-like)	171	28
13392	AF113685	Homo sapiens	PRO0974	226	57
13393	AF118082	Homo sapiens	PRO1902	69	68
13394	D23661	Homo sapiens	ribosomal protein L37	498	96
13395	AF130079	Homo sapiens	PRO2852	109	54
13396	AF119851	Homo sapiens	PRO1722	107	57
13397	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	165	68
13398	AF130089	Homo sapiens	PRO2550	145	68
13399	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	134	54
13400	J03798	Homo sapiens	small nuclear riboprotein Sm-D	451	93
13401	D29833	Homo sapiens	proline rich peptide P-B	64	39
13402	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	99	76
13403	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	159	76
13404	AF090894	Homo sapiens	PRO0113	152	70
13405	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	45
13406	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	172	72
13407	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	135	84
13408	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	63
13409	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	138	58
13410	AF130089	Homo sapiens	PRO2550	101	70
13411	AK024455	Homo sapiens	FLJ00047 protein	112	73
13412	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	145	48
13413	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	95	50
13414	AF090942	Homo sapiens	PRO0657	171	72
13415	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	120	64

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13416	M15530	Homo sapiens	B-cell growth factor	121	45
13417	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	115	58
13418	AF026689	Homo sapiens	prostate-specific transglutaminase	146	70
13419	Y01181	Homo sapiens	Polypeptide fragment encoded by gene 12.	85	64
13420	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	77	73
13421	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	149	62
13422	AF130089	Homo sapiens	PRO2550	111	39
13423	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	106	42
13424	AF119882	Homo sapiens	PRO2492	110	70
13425	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	104	59
13426	AF118082	Homo sapiens	PRO1902	129	48
13427	X70771	Chironomus tentans	Sp17	95	56
13428	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	66
13429	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	149	80
13430	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	103	63
13431	AF116661	Homo sapiens	PRO1438	128	54
13432	AK024455	Homo sapiens	FLJ00047 protein	117	69
13433	Y13141	Bromheadia finlaysoniana	extensin	91	40
13434	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	118	64
13435	AF090944	Homo sapiens	PRO0663	115	50
13436	X55687	Lycopersicon esculentum	extensin (class II)	73	32
13437	AF090942	Homo sapiens	PRO0657	77	50
13438	AP000061	Aeropyrum pernix	104aa long hypothetical protein	82	41
13439	G00481	Homo sapiens	Human secreted protein, SEQ ID NO: 4562.	94	51
13440	AF161356	Homo sapiens	HSPC093	115	53
13441	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	125	44
13442	Y59784	Homo sapiens	Human normal ovarian tissue derived protein 61.	1096	100
13443	U33547	Homo sapiens	MHC class II antigen	120	73
13444	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	106	71
13445	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	115	34
13446	G02256	Homo sapiens	Human secreted protein, SEQ ID NO: 6337.	486	100
13447	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	155	60
13448	AF130079	Homo sapiens	PRO2852	167	56
13449	AB047890	Macaca fascicularis	hypothetical protein	171	62
13450	AK025326	Homo sapiens	unnamed protein product	111	67
13451	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	93	76

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13452	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	109	91
13453	U65650	Arabidopsis thaliana	blue-copper binding protein III	103	35
13454	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	123	69
13455	AF090894	Homo sapiens	PRO0113	122	56
13456	D38585	Homo sapiens	TSC-22	710	99
13457	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	113	45
13458	X55686	Lycopersicon esculentum	extensin (class II)	64	51
13459	AF107406	Homo sapiens	GW128	162	54
13460	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	145	65
13461	X61045	Hydra sp.	mini-collagen	107	34
13462	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	130	46
13463	Y35970	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 219.	189	80
13464	L47668	Homo sapiens	alpha-2 collagen type I	64	39
13465	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	155	65
13466	Y27858	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	76
13467	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSAWA27.	109	70
13468	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	144	69
13469	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	121	39
13470	M15530	Homo sapiens	B-cell growth factor	144	57
13471	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	116	85
13472	V00488	Homo sapiens	alpha globin	704	96
13473	AJ012166	Canis familiaris	brain-specific synapse associated protein, Bassoon	56	45
13474	AF116661	Homo sapiens	PRO1438	128	45
13475	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	99	78
13476	V00488	Homo sapiens	alpha globin	278	91
13477	W65762	Homo sapiens	Human HDCAP protein.	490	98
13478	AB033767	Homo sapiens	brain-selective and closely mapped on the counter allele of CMAP in cystatin cluster	2184	97
13479	AB033767	Homo sapiens	brain-selective and closely mapped on the counter allele of CMAP in cystatin cluster	2184	97
13480	Y42382	Homo sapiens	Amino acid sequence of fx317_11.	613	95
13481	D29833	Homo sapiens	proline rich peptide P-B	61	58
13482	AK023277	Homo sapiens	unnamed protein product	488	98
13483	X67703	Drosophila melanogaster	Mst84Da	53	60
13484	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	135	54
13485	AF210550	Sceloporus siniferus	NADH dehydrogenase subunit 4	149	79
13486	Y14544	Danio rerio	Hoxc8 protein	98	36
13487	AP002032	Arabidopsis		111	27

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		thaliana			
13488	AB047846	Homo sapiens	gamma1-COP	4463	100
13489	M37194	Rattus norvegicus	clathrin-associated protein 17	739	100
13490	Y59743	Homo sapiens	Human normal ovarian tissue derived protein 20.	138	96
13491	U01317	Homo sapiens	G-gamma globin	198	90
13492	W04180	Homo sapiens	Cellubrevin-1.	459	98
13493	AL121583	Homo sapiens	bA504H3.1 (SNX5 (sorting nexin 5))	2058	100
13494	X53777	Homo sapiens	putative ribosomal protein (AA 1-184)	970	100
13495	AJ271881	Homo sapiens	bromodomain containing protein	3378	99
13496	AF132970	Homo sapiens	CGI-36 protein	878	100
13497	V73498 cd1	Homo sapiens	21-AUG-1997 Human S100P1 DNA.	273	100
13498	AL121583	Homo sapiens	bA504H3.1 (SNX5 (sorting nexin 5))	2058	100
13499	X82456	Homo sapiens	LIM and SH3 domain protein	1420	100
13500	AJ277932	Homo sapiens	RPB1 la protein	588	98
13501	Y33569	Homo sapiens	Consensus sequence for human RAD1 binding proteins.	633	84
13502	W73434	Homo sapiens	Human secreted protein encoded by Gene No. 2.	1903	100
13503	AJ005981	Sus scrofa	cAMP-regulated phosphoprotein	577	100
13504	AF116715	Homo sapiens	PRO2829	143	65
13505	U97553	murid herpesvirus 4	unknown	84	35
13506	X06323	Homo sapiens	put. ribosomal protein L3 (AA 1 - 348)	1903	100
13507	W82397	Homo sapiens	Human UBP protein #3.	4264	99
13508	M86246	Homo sapiens	EHS-2	110	71
13509	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	121	50
13510	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	91	44
13511	G03812	Homo sapiens	Human secreted protein, SEQ ID NO: 7893.	591	100
13512	Y04369	Homo sapiens	Human HUCEP-14 protein.	1389	100
13513	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	136	60
13514	AE000232	Escherichia coli K12	orf, hypothetical protein	1480	100
13515	X76717	Homo sapiens	MT-11 protein	382	100
13516	Y00919	Homo sapiens	Human Rab protein, RABP-2, protein sequence.	1039	100
13517	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	136	67
13518	AF090895	Homo sapiens	PRO0117	109	56
13519	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	109	65
13520	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	145	71
13521	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	93	60
13522	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	140	72
13523	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	130	73
13524	M15530	Homo sapiens	B-cell growth factor	112	67
13525	AF119851	Homo sapiens	PRO1722	135	57
13526	G00541	Homo sapiens	Human secreted protein, SEQ ID NO: 4622.	98	82
13527	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	117	41



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13528	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	100
13529	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	79	78
13530	AJ000536	Arabidopsis thaliana	COP1 protein	98	32
13531	U50403	Homo sapiens	breast cancer suppressor element Ishmael Upper RP2	101	62
13532	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	156	56
13533	Z80779	Homo sapiens	histone H2B	628	100
13534	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	62
13535	M11759	Lycopersicon esculentum	cell wall hydroxypoline-rich glycoprotein	82	63
13536	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	93	56
13537	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	139	81
13538	AF130051	Homo sapiens	PRO0898	90	53
13539	X16832	Homo sapiens	preprocathepsin H (AA ~22 to 314)	1835	99
13540	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	100	80
13541	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	131	82
13542	G00452	Homo sapiens	Human secreted protein, SEQ ID NO: 4533.	94	65
13543	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPM8Q32.	141	86
13544	AF130089	Homo sapiens	PRO2550	107	72
13545	M36647	Homo sapiens	mitochondrial hinge protein precursor	435	89
13546	U63810	Homo sapiens	WD40 protein C101	505	100
13547	AF090931	Homo sapiens	PRO0483	126	73
13548	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	143	65
13549	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	82	62
13550	AF113685	Homo sapiens	PRO0974	126	48
13551	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	89	53
13552	AF116661	Homo sapiens	PRO1438	109	69
13553	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	101	85
13554	X16832	Homo sapiens	preprocathepsin H (AA ~22 to 314)	1835	99
13555	Y73435	Homo sapiens	Human secreted protein clone yd73_1 protein sequence SEQ ID NO:92.	528	84
13556	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	126	65
13557	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	67
13558	G03093	Homo sapiens	Human secreted protein, SEQ ID NO: 7174.	189	75
13559	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	131	53
13560	AF118086	Homo sapiens	PRO1992	157	71
13561	Y00320	Homo sapiens	Human secreted protein encoded by gene 64.	101	64
13562	AF159055	Homo sapiens	leucine zipper-like protein	119	74

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13563	AF118082	Homo sapiens	PRO1902	83	86
13564	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	234	97
13565	Y59778	Homo sapiens	Human normal ovarian tissue derived protein 55.	66	100
13566	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	103	60
13567	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	96
13568	X83703	Homo sapiens	nuclear protein	1633	99
13569	G02473	Homo sapiens	Human secreted protein, SEQ ID NO: 6554.	242	45
13570	G00521	Homo sapiens	Human secreted protein, SEQ ID NO: 4602.	105	90
13571	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	80
13572	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	46
13573	X92744	Homo sapiens	hBD-1	290	83
13574	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	107	68
13575	AF107406	Homo sapiens	GW128	356	100
13576	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	101	48
13577	AF220264	Homo sapiens	MOST-1	95	73
13578	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	68
13579	AK024455	Homo sapiens	FLJ00047 protein	81	76
13580	AF130051	Homo sapiens	PRO0898	128	64
13581	AF084256	Homo sapiens	beta glucuronidase isoform d	142	58
13582	AF118082	Homo sapiens	PRO1902	85	51
13583	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	114	52
13584	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	66	54
13585	X52164	Mus musculus	Q300 protein (AA 1-77)	109	64
13586	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	109	77
13587	AF090901	Homo sapiens	PRO0195	114	53
13588	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	95	66
13589	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	117	58
13590	AK000321	Homo sapiens	unnamed protein product	1313	100
13591	AL357374	Homo sapiens	bA353C18.2 (novel protein)	421	100
13592	AL357374	Homo sapiens	bA353C18.2 (novel protein)	421	100
13593	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	139	62
13594	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	103	56
13595	U16359	Rattus norvegicus	nitric oxide synthase	109	76
13596	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	88
13597	G00325	Homo sapiens	Human secreted protein, SEQ ID NO: 4406.	275	100
13598	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	108	63
13599	AF116661	Homo sapiens	PRO1438	128	64

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13600	X55682	Lycopersicon esculentum	extensin (class I)	58	43
13601	X52164	Mus musculus	Q300 protein (AA 1-77)	106	45
13602	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	122	92
13603	AF149419	Oryctolagus cuniculus	eye sodium bicarbonate cotransport protein NBC2	126	75
13604	AJ005567	Mus musculus	SPR21 protein	63	40
13605	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	150	96
13606	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	121	60
13607	G02867	Homo sapiens	Human secreted protein, SEQ ID NO: 6948.	85	60
13608	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	57	35
13609	AF107406	Homo sapiens	GW128	108	42
13610	D82345	Homo sapiens	NB thymosin beta	167	100
13611	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	59
13612	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	50
13613	Y32193	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 044150.	490	80
13614	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	57
13615	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	124	58
13616	AF119900	Homo sapiens	PRO2822	95	53
13617	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	124	58
13618	S79978	Homo sapiens	prion protein, PrP {octapeptide repeats}	88	42
13619	AF220264	Homo sapiens	MOST-1	130	81
13620	U16359	Rattus norvegicus	nitric oxide synthase	95	65
13621	AL132841	Caenorhabditis elegans	Y15E3A.3	168	85
13622	K01664	Drosophila melanogaster	Bkm-like protein	118	65
13623	M86246	Homo sapiens	EHS-2	100	63
13624	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	104	46
13625	AF067205	Homo sapiens	vesicle transport related protein	198	69
13626	U39529	Echinometa mathaei	bindin	72	47
13627	S79410	Mus musculus	nuclear localization signal binding protein	102	52
13628	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	123	54
13629	K01664	Drosophila melanogaster	Bkm-like protein	113	46
13630	AF161536	Homo sapiens	HSPC051	582	100
13631	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	158	87
13632	AF130089	Homo sapiens	PRO2550	105	66
13633	AF116661	Homo sapiens	PRO1438	116	53
13634	AF116715	Homo sapiens	PRO2829	101	60

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13635	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	139	63
13636	U33547	Homo sapiens	MHC class II antigen	154	79
13637	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	107	75
13638	AF090895	Homo sapiens	PRO0117	87	62
13639	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	131	69
13640	AF026689	Homo sapiens	prostate-specific transglutaminase	128	60
13641	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	128	81
13642	AC003058	Arabidopsis thaliana	unknown protein	210	67
13643	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	287	76
13644	Y73483	Homo sapiens	Human secreted protein clone y118.1 protein sequence SEQ ID NO:188.	376	88
13645	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	130	85
13646	Y87212	Homo sapiens	Human secreted protein sequence SEQ ID NO:251.	423	97
13647	U50403	Homo sapiens	breast cancer suppressor element Ishmael Upper RP2	103	86
13648	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	128	55
13649	X58521	Homo sapiens	nucleoporin p62	2610	98
13650	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	69
13651	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	111	81
13652	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	140	60
13653	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	121	46
13654	U13066	Nicotiana glauca	arabinogalactan-protein precursor	92	33
13655	S79410	Mus musculus	nuclear localization signal binding protein	134	50
13656	Y07766	Homo sapiens	Human secreted protein fragment encoded from gene 23.	156	100
13657	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	124	48
13658	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	171	80
13659	AK000017	Homo sapiens	unnamed protein product	611	100
13660	U90446	Mus musculus	RNAse L inhibitor	3100	99
13661	AE000882	Methanothermobacter thermoautotrophicus	phosphoenolpyruvate synthase	88	38
13662	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	65
13663	K01664	Drosophila melanogaster	Bkm-like protein	97	34
13664	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	77	41
13665	Y94890	Homo sapiens	Human protein clone HP02798.	325	98
13666	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	65
13667	AF090930	Homo sapiens	PRO0478	119	88
13668	AF130089	Homo sapiens	PRO2350	120	77

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13669	AC006693	Caenorhabditis elegans	Hypothetical protein W02H5.e	165	85
13670	W80293	Homo sapiens	Human translocation associated protein designated Gp25L-H.	1003	95
13671	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	113	91
13672	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	160	60
13673	AL132841	Caenorhabditis elegans	Y15E3A.3	178	75
13674	AF118086	Homo sapiens	PRO1992	85	75
13675	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	132	55
13676	AF220264	Homo sapiens	MOST-1	133	85
13677	Y19730	Homo sapiens	SEQ ID NO 448 from WO9922243.	122	51
13678	Y65416	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1577.	467	98
13679	Y16589	Homo sapiens	A protein that interacts with presenilins.	2286	99
13680	AL160371	Leishmania major	probable (hvh-6) u1102, variant a DNA, complete virion genome	104	52
13681	AF090931	Homo sapiens	PRO0483	117	67
13682	X55686	Lycopersicon esculentum	extensin (class II)	60	56
13683	AF090944	Homo sapiens	PRO0663	93	90
13684	AL096770	Homo sapiens	bA150A6.2 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein (hs6M1-21))	178	52
13685	AF116661	Homo sapiens	PRO1438	115	60
13686	U62039	Elephantulus edwardii	reverse transcriptase	86	53
13687	Y13141	Bromheadia finlaysoniana	extensin	77	36
13688	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	114	60
13689	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	53
13690	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	107	51
13691	AC003058	Arabidopsis thaliana	unknown protein	178	85
13692	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	94	35
13693	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	143	78
13694	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	98	50
13695	D63163	Rattus sp.	cyclin C	111	86
13696	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	118	95
13697	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	80
13698	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	70
13699	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	93	58
13700	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	100	73
13701	M76744	Homo sapiens	BGP	112	52

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13702	Y15155	Homo sapiens	phosphorylase kinase beta-subunit	206	100
13703	AF090901	Homo sapiens	PRO0195	100	70
13704	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	131	79
13705	R95913	Homo sapiens	Neural thread protein.	106	36
13706	M15073	Homo sapiens	MHC HLA-DR-beta-1 chain	74	77
13707	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	35
13708	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	150	56
13709	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	89	77
13710	X70775	Chironomus cinclus	Sp12 gene homologue	85	38
13711	X80265	Hordeum vulgare	structural protein	96	41
13712	AB007922	Homo sapiens	KIAA0453 protein	147	64
13713	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	124	60
13714	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	108	65
13715	AF116661	Homo sapiens	PRO1438	120	77
13716	AF118086	Homo sapiens	PRO1992	127	64
13717	AK024453	Homo sapiens	FLJ00047 protein	93	56
13718	AF116661	Homo sapiens	PRO1438	137	55
13719	W48352	Homo sapiens	Human breast cancer related protein BCFL1.	93	59
13720	AF119851	Homo sapiens	PRO1722	94	58
13721	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	124	45
13722	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	117	58
13723	AF161361	Homo sapiens	HSFC098	115	50
13724	Y95829	Homo sapiens	Native human Tie receptor signal peptide.	108	100
13725	AF118086	Homo sapiens	PRO1992	166	75
13726	AF116636	Homo sapiens	PRO1488	95	70
13727	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	70
13728	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	60
13730	G00673	Homo sapiens	Human secreted protein, SEQ ID NO: 4754.	118	63
13731	U33547	Homo sapiens	MHC class II antigen	123	69
13732	R59843	Homo sapiens	ApoE4Lx2 protease.	135	88
13733	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	138	75
13734	AF026204	Caenorhabditis elegans	C30E1.1 gene product	102	51
13735	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	117	63
13736	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	112	87
13737	AL359782	Trypanosoma brucei	possible (hly-6) u1102, variant a dna, complete virion genome.	115	58
13738	AF130089	Homo sapiens	PRO2550	122	70
13739	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	124	74
13740	AF130051	Homo sapiens	PRO0898	85	70

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13741	AF093748	Homo sapiens	KH type splicing regulatory protein; KSRP	91	51
13742	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	150	77
13743	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	124	82
13744	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	91	48
13745	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	116	64
13746	AB001684	Chlorella vulgaris	ORF54d	70	66
13747	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	140	60
13748	AF090901	Homo sapiens	PRO0195	92	39
13749	AF090895	Homo sapiens	PRO0117	148	67
13750	AF119882	Homo sapiens	PRO2492	91	45
13751	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	60
13752	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	129	65
13753	AF161356	Homo sapiens	HSPC093	99	48
13754	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	124	70
13755	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	120	51
13756	AF130089	Homo sapiens	PRO2550	142	96
13757	AF130089	Homo sapiens	PRO2550	132	86
13758	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	50
13759	Y19609	Homo sapiens	SEQ ID NO 327 from WO9922243.	92	60
13760	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	154	52
13761	U62040	Elephantulus edwardii	reverse transcriptase	134	51
13762	AB001684	Chlorella vulgaris	ORF49b	100	45
13763	AF118082	Homo sapiens	PRO1902	129	50
13764	AF220264	Homo sapiens	MOST-1	129	66
13765	R59842	Homo sapiens	ApoE4L1 protease.	135	50
13766	AF220264	Homo sapiens	MOST-1	115	71
13767	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	139	73
13768	AF130089	Homo sapiens	PRO2550	97	34
13769	U80739	Homo sapiens	CAGH26	564	100
13770	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	128	55
13771	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	102	68
13772	AE004507	Pseudomonas aeruginosa	hypothetical protein of bacteriophage P1	93	44
13773	AB044885	Canis familiaris	dopamine receptor D4	78	52
13774	AF026246	Homo sapiens	HERV-E envelope glycoprotein	108	53
13775	S71805	Homo sapiens	RNA-binding protein=TLS/FUS-ERG	126	100
13776	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	82
13777	AB015727	Mus musculus	truncated granzyme M	86	37
13778	G02832	Homo sapiens	Human secreted protein, SEQ ID NO:	74	52

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6913.		
13779	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	137	61
13780	M14123	Homo sapiens	neutral protease large subunit	246	55
13781	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	99	67
13782	AF132972	Homo sapiens	CGI-38 protein	902	99
13783	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	147	63
13784	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	68
13785	AF130051	Homo sapiens	PRO0898	138	72
13786	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	95
13787	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	92	53
13788	U12206	Homo sapiens	unknown	84	42
13789	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	118	58
13790	S79410	Mus musculus	nuclear localization signal binding protein	102	50
13791	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	137	76
13792	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	104	72
13793	AB006006	Bos taurus	neurocalcin alpha	1000	100
13794	U63332	Homo sapiens	super cysteine rich protein; SCRP	183	95
13795	W34499	Homo sapiens	Obesity receptor C protein.	120	85
13796	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	127	67
13797	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	182	83
13798	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	112	71
13799	U63332	Homo sapiens	super cysteine rich protein; SCRP	91	84
13800	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	105	67
13801	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	154	72
13802	AF119900	Homo sapiens	PRO2822	131	50
13803	AK024433	Homo sapiens	FLJ00025 protein	117	95
13804	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	142	53
13805	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	48
13806	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	98	66
13807	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	98	66
13808	AL359782	Trypanosoma brucei	possible (hlyv-6) u1102, variant a dna, complete virion genome.	150	54
13809	M37679	Mus musculus	Ig heavy chain precursor	70	100
13810	AL451015	Neurospora crassa	putative protein	96	55
13811	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	88	77
13812	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	128	71



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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13813	AF130089	Homo sapiens	PRO2550	93	75
13814	K01664	Drosophila melanogaster	Bkm-like protein	119	60
13815	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	64
13816	AJ011435	Blackstonia imperfoliata	maturase	93	48
13817	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	130	76
13818	AF119851	Homo sapiens	PRO1722	141	50
13819	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	74	60
13820	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	76	72
13821	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	135	50
13822	K01664	Drosophila melanogaster	Bkm-like protein	95	52
13823	L10908	Mus musculus	Gcap1 gene product	103	50
13824	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	146	62
13825	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	125	83
13826	L10908	Mus musculus	Gcap1 gene product	96	43
13827	G02971	Homo sapiens	Human secreted protein, SEQ ID NO: 7052.	102	64
13828	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	135	53
13829	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	142	70
13831	AP000060	Aeropyrum pernix	101aa long hypothetical protein	79	50
13832	AF119900	Homo sapiens	PRO2822	94	46
13833	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	145	40
13834	AF218028	Homo sapiens	unknown	117	57
13835	L10908	Mus musculus	Gcap1 gene product	79	45
13836	Z26876	Homo sapiens	ribosomal protein	129	93
13837	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	124	76
13838	AF044311	Homo sapiens	gamma-synuclein	603	99
13839	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	100	82
13840	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	154	46
13841	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	64
13842	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	92	62
13843	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	93	60
13844	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	63
13845	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	145	79
13846	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	50
13847	G03469	Homo sapiens	Human secreted protein, SEQ ID NO: 7550.	101	68

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13848	G03240	Homo sapiens	Human secreted protein, SEQ ID NO: 7321.	107	43
13849	U05313	Trypanosoma brucei	CR3	98	40
13850	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	100	65
13851	AF159055	Homo sapiens	leucine zipper-like protein	103	55
13852	R59842	Homo sapiens	ApoE4L1 protease.	99	71
13853	V01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	142	65
13854	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	79
13855	R59842	Homo sapiens	ApoE4L1 protease.	93	69
13856	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	114	76
13857	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	94	57
13858	U63332	Homo sapiens	super cysteine rich protein; SCRP	105	58
13859	AF289022	Homo sapiens	forminotransferase cyclodeaminase form C	467	100
13860	AF078844	Homo sapiens	hqp0376 protein	488	100
13861	A032436	Homo sapiens	brain-specific Na-dependent inorganic phosphate cotransporter	2968	100
13862	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	91	72
13863	AF130079	Homo sapiens	PRO2852	131	63
13864	Z29701_cd1	Homo sapiens	29-MAY-1998 Wild-type human c-Src tyrosine kinase cDNA.	2380	100
13865	L77967	Ovis aries	small proline-rich protein with paired repeat	80	33
13866	AL030318	Homo sapiens	dJ977B1.5 (myosin regulatory light chain 2, smooth muscle isoform)	904	100
13867	U37690	Homo sapiens	RNA polymerase II subunit	358	100
13868	X13923	Homo sapiens	cytochrome c oxidase subunit VIb (AA 1-86)	491	100
13869	L13848	Homo sapiens	RNA helicase A	6669	99
13870	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	133	46
13871	K02064	Bos taurus	cytochrome c oxidase subunit IV precursor EC 1.9.3.1	96	72
13872	D31763	Homo sapiens	ha0946 protein is Kruppel-related.	4606	96
13873	Z14014	Nicotiana glauca	Pistil extensin like protein, partial CDS only	83	43
13874	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	117	70
13875	Z52203_cd1	Homo sapiens	17-SEP-1998 Human PRO217 protein encoding cDNA, UNQ191.	2135	99
13876	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	106	64
13877	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	143	50
13878	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	104	60
13879	L25404	Brassica napus	cyclin	124	42
13880	AL390114	Leishmania major	extremely cysteine/valine rich protein	139	59
13881	AC003113	Arabidopsis thaliana	F24O1.6	70	64

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SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13882	AB000098	Rattus norvegicus	MIPP65	905	50
13883	Z95114	Homo sapiens	bK212A2.1 (TNF-inducible protein CG12-1 (similar to apolipoprotein L))	1639	100
13884	AF132984	Homo sapiens	Nuclear pore complex interacting protein NP1P	551	82
13885	AF121862	Homo sapiens	Sorting nexin 13	1453	99
13886	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	83	69
13887	K01664	Drosophila melanogaster	Bkm-like protein	109	77
13888	AF217197	Homo sapiens	FBP interacting repressor	2725	99
13889	D38112	Homo sapiens	NADH dehydrogenase subunit 6	187	94
13890	AF118086	Homo sapiens	PRO1992	85	62
13891	M58664	Homo sapiens	Signal transducer CD24	371	97
13892	AK023443	Homo sapiens	Unnamed protein product	125	45
13893	AB040972	Homo sapiens	KIAA1539 protein	2271	99
13894	U03750	Escherichia coli	DeaD	95	48
13895	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	73	53
13896	AF078851	Homo sapiens	Secretogranin III	2384	99
13897	U62039	Elephantulus edwardii	Reverse transcriptase	109	48
13898	X07816	Human herpesvirus 4	Epitope C13 (57 AA)	55	53
13899	AF116661	Homo sapiens	PRO1438	146	48
13900	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	77	60
13901	Y28643	Homo sapiens	Human serine protease inhibitor from cDNA clone HETDK50.	2191	100

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TABLE 3

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
1	13902	A	1	114	434	AIFKCVBGMFRIAHVNVCFVSSGLLI* PLTY/GVYDEWTHFAYMTIDLLLEIPITG SHPVVNLALFCLGAP/WISPTNGSFAYP VTPKSLIAHDFAVEATMPYTRLSST
2	13903	A	2	124	466	KSNTPNLGDGMSLFNRC/SWRSSLA VNDITYSSKKSNAETFTFHADLCITLSDK RPITITQALARIKVKHKPKATYEQILAVI DEF/ANFLKIKWIKAYDKENLFCBEG*KL CAASN
3	13904	A	4	1	427	EGFLELLRTNHSNSQLQLTGTIGLFLN EGKLVKFLSDV*K*YHSETFTVNFSD TE*AMKHINDYVEKQFQKGVLDVYKLE RDTVFDLANKIFFGKWKORPFVNDTEE SDPHVDQVSTVNEPIMKLLS/VMLNTHPC FKL
4	13905	A	5	1	464	KIKSFVASKOTIKRNRVTDNKKIYAY*Y SDKELIFTLRLTKT*K*KGKPNLKNQ EI*VPISPDIOIAHK/VLHGNSTSLVS ELAPCEAPV/RHPLTGLTAGLQGGREA GRLVGRWGC*W/VHFP*EKI/WQF*SK LHISLPYDPTTPLLGTCSR
5	13906	A	6	308	3	HFVTHSKHDLATAHLGY/PREMKT*VH TKTCT*IFTVALSVLARNWQGRPLCS EWL/KIMVHTMS*HSAIKRINRYRYQNC VNLFLGITLSBKSGTQNVY
6	13907	A	7	587	2	FLTRTGDPTRKSSSHANTQSRFPFDDP PA/PIANNLGNTHGGRRAJRCPTGPDG PAQCGQPRCWPSSHLATD*GPGSR LGMNREGAGPAGFTACSLSGCRTPTTH HFPASRMSCHLNCASPRYRSQNGRCE RVAQGSQAGGERGAKSQVVPAPARNK DPAKCRKPRNRRPNSGQVVRVAYRROR
7	13908	A	8	1	474	RIINNEHKGKYEELHE*EYKMLHYTESPA FTDLHLCYQKDMGLSTASSPAVGTG MDMDDEDDFISKWIFYSPHSYDK*LT FKTESRVRVRESDEVQIKVNDDEVISGL LTSKLDNVLKATGVLYDAYK/VLCERT RSLKESSLKLERNLQNH
8	13909	A	9	3	539	SQCSFFISPAISLTALSETHRALVRHPR LCLSPNLAPSSGPPRPPELAPCPSPSQA GLRTHCSWVKGHLQPLPVASGMSKTFCN KITTCYPPPP/PLCPNHSNPLATLDPDS VTHAVFE/L*SPSAPSSSTA*ILGSPS VCGASPCHPSPHSGICPTPPGLNPVCP CAPRAKWDGTCQT
9	13910	A	10	2	453	RL*GLGVALVKTPTKV*HGGPPTTY YIVLLISYALHQVVEYSVMVSIAPVAX VSDPLIVGTMYTLNIVSNLIGWPSV SLWLVNPLTVKSCV*TSYQNCCTPDAAE LCKKIGSGCYTALDGYVYESICVSIAP V/W*VFLVHKFK
10	13911	A	11	20	475	KMGVPLMLSDNRLFLPKNPLREKRTIS PKTTF*PLKINVKQVNLPLGPPGPKI FFPVFKFFFFFFFF/RDRVSLYHPGNSA VSQSELTAALTSPGSGQVILPSQPPK* ENHNILGGRGCSERPLPRAEFLDLRSFS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
11	13912	A	12	392	63	ITIVFP HINAD\GLEPKFSAKTGLGPE\GCCTMN KLGAGSATQSLGSGSQLSWQLSRREQEL EQARWFAQ\QVETLCRVYRKEMAKHEH AGLAVQLAA\ASBHGRTVSEETHLQ
12	13913	A	13	18	338	APHFOY\QMPFHL\PRTRTGQ\PSLPS RHGGHLS\GKMBHETS\VTLCGSPFPPTP PRDPDPGP*ARRAPCPRRPT*AHPRALS RAAPQ\PRALAGPRARHPTCPGSL
13	13914	A	14	2	371	TIKQ*RDNP\IQTGAKOLKRRHFKEDQW ASMT\KRSLS\SLVSRMWH\KITRMAGI KKSDNNKH*GRGEIRT\LLRCWMDCKV VQLLWKT\WQFL*GLYQYI\PHDPVISRL GISLILYIALRTF
14	13915	A	15	443	1	SRTPLDT\DKSMRGPRAS*NRQTLLLGA NAAGD\KIKAMLT\NNSENKILQNYVKC TLMPLYK\NNKNNMTAYLFTTQCTSYFK PTVETHCSEKKISF\KILL\TYWAPGHL RALMQIYKEIHHVVFVNPVNSILQPIVQ NVISTFKS
15	13916	A	16	375	38	HQNGSFLKKD\PTALLCLQETPRF\CKDT KRIKVRRY\QPNSSQKRA\VFLLIDSK IDPTKKI\PMILGLTLINT*AGNTEVP KSMQKLAGLKEZNDNSVINWGGPSYFV SIRK
16	13917	A	17	448	189	NRDRVSLCCPGAS*TPGLKRS\PHGLPK CNDYRRD\Y*LL\PARHTQ\NISTHS*QT TNTCSYPAF*KSRR*BPGYNTHTPSS DML
17	13918	A	18	1	426	GVSHHARSL\INQLFKKCS\TLFVL\REM QIKSLLASSSSSSSRNSVSGQGFETVGT HCGQCKL\QVFF\WKAV*YLLKLN\VF LFLIYNRAHLEDTCENVDRALFVIVKN WKLKYP\PGVQWR\IKLNYSHSVESSTAV LPIV
18	13919	A	19	2	423	YFETPQFLRLRLGYQCTFFFF\KPNSSC LGIEYNSGPDSCA*FFLQNGQIRLVNSAN IKLAMMTLKTNQVALAQFLCKESDQOF CKGYTHVKARTGWA*F*SAQSCDLLQNL QNVQ\GAKIPLVV*GFENRPTQRA*K HF
19	13920	A	20	10	443	LKVDSDGSEVRVYVFLQHTITLMLCSAYN NOLINIFVRPSLLAVALHMT\PGFTKSDV YSCEFRLRDVFEDEFIFL\GNIT\DFER SCYLLCKSEAIQVTTKDLFTEKGNIVL *FLVGLFKPF\VESYHICKSLLDEK*A PFIERP
20	13921	A	21	11	426	VLVETNNLRMSQVYN*PELFD\SPDAN TLSDSPSQKIGHAQ\KYSILKKNYTE DWAQACLEDTSKYEQVTOI\PMAPNDATL /PSS/AHLAFTAS*GAPSDS*LRNTLGL ICDGST\KPSSTN*KQTVIALQSHAGLN MKEC
21	13922	A	22	1147	1768	QLGMSHGYSKSMFQKLMCLFNHHLQK GHECLPKVIANSNPPPIIKYLAQLDMLL SGYSPRRQSVFSLSQPGGHPHNWTAIS RCKNLLKGMTQKLLIYQRAATNGRVS SSYVBP\PKLNSPEETAPQTPKSSQMPR



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
						EEATGTRAAIPWVPFPAQAQQLREEGPM EAEAQPMAPPEGRKSLANGPMAGSQP GQPSGRKRSRARDAAEFSDWDDYD FAPREPEVKAGARLELPPS*KITPSFWE NRNTPFLWQGLKIFY
45	13946	A	48	116	442	PONMOMERKPGPFKGLWAGGLDLENLG VMSVGLSLSPDDAVIWRPRTKGLIKQ FLRNGITGEKVDYFNGDQLGTSDHEISS VATWAKAHLGERGAFTFPQRVSLRE
46	13947	A	49	434	3	FTVPGPLLTVPITFISKVPFKSLPQIF NFTPGFPQIRV*TIIPISLRFRRKKP LFFF*HKVPLCSPYWNSIARSWVPAAS VFQV/KESFYLNLISVPPQVPLNVFLTF FFFFFLQRDR/SLPILPRMVNSWAQAI LPLNL
47	13948	A	50	1	482	EKPQYCSDFGKAFRMKTQ/LVWRQVHT GNMPPQCREOGKAFGRKEQLTAHLIAH R*KPYGCSGOGKAFSSKSYLVIHRRTHI GERPYCSCSDRAFCKGSKLIHQITHS TBNHYSNCEWITYPRASLKHQKIDL GKKPF/SCNWEQKALK
48	13949	A	51	1	470	RBFNLWEGHRAFAFVDEAGEVLTLDL YADVSELLAIPIVANGTKTDKDLAGGD YTATISAFICASGRAIQGTSHLGQNF SAMSEIVLEDPETPGENGAYANSGVLT TRTIWMTIGHGDNML/LTTRVA*VQ /MVIIPOGIPKAFLEKQKT
49	13950	A	52	26	448	SPOTEREYRIGQSVTVGVTSVDDNSYX RIRGKATVCEBGTPIK*GQPIRLTHVN TGRNLHSHFTSPLYGN/QVAL*GDIVI IL*RRKQRLRGFTREGIKLRFKEVSAPG DEBGGDYLDWTVLCNGPYVRDGEVRF NT
50	13951	A	53	3	495	AMEVIAFAETHIRGFTLDAANSRLIIT QVRHYLKEAATTKIVLDHQHTPSRLA VVRVIGALAMKGV/DNT*VFHEGLNGL EDSGLSMDFFIMLALAQ*WNLNDAS V*HTRNK*TS*NNVIEPOYFGSAYLFRQ VLEBQLEPTVEKISIMAEKAPLO
51	13952	A	55	1	428	ORGTGKHEMDRTLEE*TKBQILKEE KL*ALQREKHQLFLQKLVLEBERRRR KEQSD/LTTLTS/AAVQSLTVHTGTHLS VQSGPGGHNRPGLTMAADRAGMYPGPV LTTRRYVGLAAAFAGTPEHQFQGRPGG VYG
52	13953	A	56	2	453	EDGDLDAFSSDEGLTMAASYLDDIFRI YITETQRCRRYHRPPCAQAPCNMVHP I VICYCYGPEVGRTYTCVCPDYDLSS CKGKGLHNGHTKLAFFSPFGLHSBGFSS SRWLRNVKGLLRWS*WRNGPPGNWSPR TSCA/GEARLGP
53	13954	A	57	3	435	EINTSIFSRPIELGLTFLVLTDSNL VI/NRIGIV/PSVTEKEYTDPSSDGTYA WKLPSHETITRAQILKFLSYDIAYNNP WLAIPHYKSPKCPSTILHEDLYL/NGL *CASAMVMIAIVTYNALLATHRWGL TYMD
54	13955	A	59	409	1	LCCEHROKTCVCPROKFTTNASTNKR



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						SKISVLSFRIMKLRLEYVK* K* EKEKI NWRIRISKINWAKS/WPI*SKITE* TIR MINHOKRENIOITDFRNRTELPDSDTD IKKAIKRY* K* FYNPINFYNPESMNK
55	13956	A	60	1	393	GVNSCGDHFCES* LCPVDPK/VMS*GI* VPERACTQCIQGEDGVHIIQFLESWVDPHQ PCHI CTSLNGRKDNCTITQTCPTGKASTC GI,CELARLRQNAQCCPNECVCPDPEC DLPPVFN* ERGI.QSTLTINP
56	13957	A	61	250	1	REIX*RRVLYKDKVSTACAGPCSV* SCI KAASTFO\ VNHFSLQSS/VVVRHAPPGLA NFFHFLORQVLTTPPGVLNSWVIAI
57	13958	A	62	365	3	IKKKLIWRLFTFPFSGWKKRTKGI PFP *GPKKIPGI KFPQGI KKAIFRGNR* TLGK GN* KKKKKKCGPGGDIPCS* IG/RNI VKILIPKATYSFNTIHKIPKTFETI ETTLIKPL* NH
58	13959	A	63	245	558	FLPTQVVISYVRRLAEGAI* QSGGVDK LSLPARNQAGYFMLPETEITDIDKDSCCM TEELFGWTCVPPDSSSDVIERANNVK YGLARVW/SGNVARV
59	13960	A	64	106	532	BRACCSOTSCQGVPRALGAPR/E/DA FPGAVYIYHGAGGIVPQYSNHPFA*SL YPSGQ/SVAERGNLSGDSFNCHN*GLQG LILASSV*RPVMLNDPILITTKN/ISG PKCHE
60	13961	A	65	2	548	VQKYPOQRNRCVPPVAENAVPQSSRLKY RQLFNSHDKIMSGHLTGQPARTIMQSS LPQACLASIWNLSDDIDQDGKLTAEFIL AMHLIDVAMSGQLPPVLPPEYI PPSF/ RRVSCSGISVISSTSVQRLPEZPFVR DEQQLEKKLPOTFEUKKRNIS* RGNLS LEKRRQALLEQQRQG
61	13962	A	66	72	952	SSRTYTTSLPFLKKEVTRKIRKYFIQNN N*NTTTHMLDLTKVVFSGKLLP*RSR* BYRCKIADLCFYIQHLS/QRVTRKPV SRKINKESPT*SGKTNWSPFLKQK LWNNNINIP* LML* RKXGHCIEYR H* KDKGYIYANFNINLDQDKFERYV TKMD/QSQIVSINLPIADENNA* LNNFP SSSSSSSSSSSS
62	13963	A	67	139	422	VHNGNEPEFL* KQISGHEHRRQPHNGRP KNKGGAKNQ*ASLGMKTPAPAHSDKPR RRQHAAYSS*AMPFLGICISFSQCNL/C PPKLN
63	13964	A	68	274	1	NLRNKAIVITKTA*H*QKNTDQWNRIKNP EIN\HPFYGLIFDKDAKNTM/WKE/DS NFNK*CWEN* ILTCKRWQLIP/SLTINT KLNSOMIKDL
64	13965	A	69	22	419	KTIGEDGDT/PLSENAYSQRQIFSKDLV KLDSITNQVDI IDIYKLHP/KWTVYTF FSSH*GTFSDIHLILDKTYFNNL*RTG IMQHMLSDIKVFKLSTSRKVTESK*HT MSLCNKTLEHPSGGHEDASVYK
65	13966	A	70	57	423	KDKRQSVTSISGQGGK KENLNSWADT R/CL/WIGRWLVLSLPKLLPIPTW PKIKRTQPFMKINPKVLFKTY*TKRTRI AKSLLKK/RQKGISPNRRTYKAYS

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66	13967	A	71	394	1	<p>                     TLESTIGASMFSTLDLG                      KHFRMLQSDCRILLNWFSESTGSPCAV                      SPRITCSKLTIVHSKLGLSSDPASLS                      *VACTTGVIHHQTP*GL/CNT*GSGERR                      SEKQWIKKKNVSEAKRRRT*NE*SV*                      KGDYMKDQGLRLGTVAHAYN                 </p>
67	13968	A	72	485	1707	<p>                     SALGLSQPRFPFGASDAAPDSTPAGV*TA                      SSSAPAGEKQADONMEARRDPGLHQAA                      PAPH*SHLVRDKRAQERLRKTSRGP PHS                      HRSQGVDSLPRSSHSRSTP VHGPYTRS                      APDPRGAPAFRGP IATRCR/RPRAPRA                      TASHVPLGSSSWKEPEENTAPRF*ASAC                      MKWRLEAGCGPHRGVMPGPPSRRLFMWA                      TATGEKSTPSPPTGVWRFGVEACT*AGS                      PTAHQHSQRTWQVPPPCCTNGSRSPWTS                      SYPKNOSKVGTVPKRGWACQPIPETAVR                      QATISQ*ARKGAARPHHQARQVHSTQ/                      ORPQSDSGKDDQSLCEASTLQPERPE                      VQKIKCKFRV/GERRTASPMASVPEKR                      TRTQTMWSTAFIGCSGKRWYSVR/R/                      SSPRIPPPQVGSS\PLKTPPPP                      QDHRKSSSHNRKPSLASSLSNFQRA                      AKPLQVNMKKKLYSTPLLATPTCMGFGV                      HQDKYRFLVPLSLGRSLQALDVSPKHV                      LTKRSVLKACRLNALKSSLSLMSMVVG                      RVT*KYLL*P/YRTNRRGLL*SMGFAPR                      YLPHGONPAHLERGN                 </p>
68	13969	A	73	1	462	
69	13970	A	74	307	436	<p>                     LP*VGCITEGIFEQDMVRGRIKLLRQK                      TRLIGNPCGVINPGBCKIGIMPGLHK                      KRGIGIASRSGTLTYBAVHQTTQVGLGQ                      SLCVGIGGDPFNGTETIDCLEIFVNDISA                      TEGIILIGENGA/NAEDNAECL                 </p>
70	13971	A	75	1	455	<p>                     EISDSKAQAAVALI IDTWRMFCPSE*                      NHEPLRTHCALAASKLLKPD\QAB\RE                      HLCTSL\WSGTNDKNGEELHGGRVME                      RLKAL IAHQMDPSLQVRVFIETLNR                      YLYFYKSNDAVTIQVLAQLIQKILEDL                      PNLESK                 </p>
71	13972	A	76	58	366	<p>                     EFPDLVKDMNLIHQACTENKYNKRL                      MNPHRII/RLNNTTKRKILKAAQK*N                      I/T/IRGSSICMMDFSEITEDRRKWH                      SI*KILK/EKTQNCPLRVCPVKI                 </p>
72	13973	A	77	1	445	<p>                     YHETGCFLWGAIVDTLTFNTYVHFQGR                      MKGFSLLADPQEFVNDSTMSAPMLSG                      NGTFQHWSDIH\DNLSVTHVPFTDSACL                      LI IQPHYAFDLKVRGLTFQNSLNWKK                      KLSRRTIHLTWPQALQGSYDL*DLIDQ                      A*LSDLTLP                 </p>
73	13974	A	78	53	444	<p>                     ERGGYGAGPVAQPLVPSTAPMLQSPPL                      GFADHITPPVPADAN*ADCPPLPYAA*RT                      TGPBHLIAHLUTTGTLGUTPHPSSEASPP                      STPWLPAFPCPLPTWD/RPFCPLPLLS                      SLPTPLDPLCFLLPAP                 </p>
74	13975	A	79	1	353	<p>                     HRTSLDYGLTVVITYSDPT*EADYVY                      IMVT*NVKQLMWTDRTATHSQDVRH                      HLLCIRLMKQPKHIAV*/VLGHYAFV                      SR/SFKHALQVQVQAPRTHDSELYSFC                      IGLTFIHM                 </p>

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75	13976	A	80	1	350	LYFYALLFLSSG/CVAVATRDNCIILD ERFGSYCPTTCGLAYFLSTYHKVDRDL QLEEDILHQVEKTS*FKQLIKAIQLTY NPDDSLKPNMIDAATLKSHKML*IMTY RAS ILIT
76	13977	A	81	76	386	PAYPQVRCFACSTPASCTPNAVLDTT PRGKSVAAHVSVPSSAHRGVTSVIKLWS AKRLH*YGA\KVRPN\GCTP
77	13978	A	82	1	360	ESTLQEDTTLNVAQNNRASYMKG/M LVELQRQIDESIICEDNFTLISEMDS RPFKISKDIVGINTIN*LDIIDIYRL* PTTAEKTFSSSRGAFT*MDHILCYETH IYFKLHE
78	13979	A	83	39	344	WGILEGGYITWVGGSGLSRASGGLSQ PPRQDDSRPLVLPVCHLPHWIGPTD LGHKQW/WGPGAVHVCNPNSTLGG*GE WIT*GREFETSLAMVWKC
79	13980	A	84	1	427	QQAHLAGHRIHTGERP*KCEACDQVYR GKSSL/MK/HKRIHTGERAYKCECHV YSR/N/SQTVEKRIHTGEKP*KCK\VC DKAFQEDSHLAGHRIHTGEKP*YQCNCG GKAFQSTLTVYRQATHGVKLY*GNDG HKVESNAT
80	13981	A	85	88	307	TWTCRAKLVIRIGWALLFPFPPSGSKP PP*TPDALPDCVP/DQSSPWTTPQDPAP DSREVSQDWTQMRSPKEN
81	13982	A	86	5	375	NSLLNTHSRGPGASHCTFWLHERASSRD LTGAESYGCICRLRLISLSIVFSKSIHG LACISILFLFLFLFFVKIGSNKCCPG WPQAPELRQSSLLSLSSWNYRR*PPHQ LIF\DFFCRN
82	13983	A	87	2	342	VIKNEHDYIMIRCLY*QEDQTLNLHSE NKTNINIKPHMTNLQAVDKITITV* CGTSLSTIAVRLKLVKL/VEDLSNIIIN KLDM/DNITKLHLNIRDYTLFKHTWN IYKN
83	13984	A	88	1	338	CNEPRSHHCTPAWQSKETPSKKKKQKKK LTTS/CIFASMSRVQSLR/CHAGVNG *QGVMLEFK/REFTLSLNSKSHS RRVPCIGLKKKKKKKKKKKKKKKK KKFP
84	13985	A	89	931	2	VASINIALPE*LLPVSCHTDLERWGVAR LQPHITELTACRARMESRDTCPGVTLH P*PPSPSSSSPSGGPRTRILTHQAGL EGSQGPLQSONPSAA/PLGACRGWNEP QGGSGS*GG*IMLESLRE/WQEAVAL PTPG*PS*ESORLPPSSASOPTPGSP/ SP*PTQQLGCHPSGLCATAGPQDGS GPTPTPH/PVQPSCRDSGPGQRLSPTPS LTSWNTSPSPPTPGPGPOGRATW/PG S/PSPGRESPSPLPQCTPGSFAGHPCP AP\AAPSSVACLP/PDGFPAPASSGI TTAPSPGDP
85	13986	A	90	66	464	LWVSSYFRLPLRSQASPSFGDILWPL TLFSSPSPLA/CHSLSTPCRPRPS PRFSLCWRPHPSKPPD*VXDDCCPS DVRLSVSENPAGPR/VFLRPP
86	13987	A	91	197	2	NAETIPAQKVGPTIKIWINTFPPPPP



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100	14001	A	105	139	361	ISSKL KHTRAF*MPICARYY\LFGLNLQICATFE KTPVSDRKTCKCTESLVNRRPCPSALFV DETYYPKELNABTFTTHAK
101	14002	A	106	3	350	ELEMIMLSERVMLKAKIKRQKLGILL/QPV S*VVMAKEKFLKEIKSATPVNTQMI\RN SLIAD/MEVVMDDQTSNVLQSGLIQ S/K\ALTLPSSMKAEERGESEARKEKLEGS RSGWTFPKER
102	14003	A	107	225	1	QSLMHTVETYYGKGEPPRCWKCKLVAL L*K*KT*KKLLRKKI*YDPAVPLIDTHP KEIKSIYQRDSCISMPTA
103	14004	A	108	390	2	LGYSGVRAPLEAEVCRFSLKLRAGRT TLFKADRGQHLGLRPLLTFDSLCP/AP RGGVYRGQASLSLCSGLHPVGSASWPRCL PTQASAMAGAPAAASLPPCSLISDCCAS NE*GSVSVGPESEPGTGHN
104	14005	A	109	304	33	KWGERVWYQKMTQVQWDRTESPQLD N*SLTKETQWRKDSLPNK*GNNWAPF SS/RSLNLRKDLTA/TKIKSKWVTDLNV EKHCTIKLL
105	14006	A	110	135	1	KQAILWPGAVAH/KSCNFTSLGGPGQ IT*GQEFKSLTNMVKP
106	14007	A	111	140	338	IMSTLLYGSICYCYWMLD*LIILRWTL ACVAQAGVQWRGLSLQPLP/PCLSLSS SWDTRPP
107	14008	A	112	26	361	RSPFWFFFRKSLGIGPGKKGPPIN* LEPLAEGFGPSGLNPLENGNGPQPC RQDRGF*KKTFPP*\GPGGVKTNPGE TP/RPKPKGVGPPGTGPGPGENLYQ WK
108	14009	A	113	11	330	ASTNLHITFLPLSYFLKGPRTVAQGLN LLGSTGPI\SASRAAGTTGALHCTQI*TY LILLPEHGKAVFF\QETLLRSTHFFFLK HVYPTTYELLVWDRDSLSPR
109	14010	A	114	350	2	GCCPCLLFGPSPTVFGSLYSIRLVAFVR AVP*PVWKA*VPG*PPVIM*FFHLFLYFL KQ/VSLWHPGWS*LAQSQVSRFFPSRLP SNWDYRAPPRLTLFFFFFQSQSGIEAN VLAL
110	14011	A	115	3	341	RMVVIS*PRDFPAPASQAGITGVSHRA RPVYSFLLLSNV*VMDVQDIYFPLVDG YLSLPLVCCV*V*VLLCYPTFPGLKRS SCLSLSPSWDYRHSPLKPA/SCCVLLSS G
111	14012	A	116	1	384	PSYQDLTKIMDEGGYPPQIFSLDDET FYWKQMPSTRITLTAKSIS/GE*ASXNK LTFLEANVAGDFKAKFVPTYHALPNR TICKYATSTLPVICKNNKA*VT/AHVF TTWTFEYFKLSVETCCSE
112	14013	A	117	43	347	CAAGFGL*TPPET*TRKPRDRNGTYKPI SLMNNAKILKK/ILANRIGQHIKTK\L LQSDQVQFI
113	14014	A	118	351	23	PNK*CHNNIFTCRGNLEPYFTWTKI NAIKATQLEENKEVNIC*IGLGNGP/S RI\PKAQMAKETIDKLDFTKLGALCS\N TIKKVKKSELEKIFNNHIGTSIQNI
114	14015	A	119	123	340	AADSSTHSLTKPAYERQNTFFPQWBYC

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						LIPLARGPWPNLA*MQPPPTGPKQSSCL SLPSTWD*/R/HWSPRLAN
115	14016	A	120	1	371	PSYP*DLTEINDEGGYPNQQTFSIHDTT FYWKMPSTTFLITEKIS/GP*ASRNN LTFL*ANVAGDFKLKPVPTFYHALGNPR TUTKYATSTLPLVCKNNKA*VT/ARVY TWTLEYFKLSVET
116	14017	A	121	82	367	YKRSNTIVAGD/FIPLSALDSSSRRI MKKTSWCTIDPMDVIGIYTPRTVSTY TFPSSANGPESKIDHLLGYKTSIKTF* T KLK*HQ/CIPSDEN
117	14018	A	122	27	253	NRTENTLGEITGEVFGVKGLDMSPKA *TIKEKNDKLFPIKVNFSYSKHTI*KI KNQATVMO/KLLTVHSDR
118	14019	A	123	3	305	GTRQGCPLSL*FNTVLRLVLR*ISQNK *INKT/SLTADP/MVLHLENPKGSIK*V LELINEFSQVAGYKINN/QKTVAFLYN N*LSKKEIKKTIQFIASKRT
119	14020	A	124	1	327	QVIFCLGCPKCDYREKPT/RMPGLRGAD FPSLI*ILWEHMF*VMCILPHPCGDPA MLNF*ERGMFF/CLKRKSDIVSQA/G PQTPRFKFRSRLITLLSSDHRHAPPHLA K
120	14021	A	125	74	334	IFEGVLKVTICLSVSSHEVGKICPFFF FFENGV*PCCPGLQGYNGS*LIVLELLK QSSCLSL*CTQDHRCLPPCLANFNILNS SIH
121	14022	A	126	381	60	TVSQVLAMFCSPSYLKAKAGGSLEPGSC YPCGSEL*SCHCTPAWIT/SQTPSL*KI H*KKIIVKRAIVECVCVVVTYIKLIL KFSDSIPFAQTGFEHKEFPYNQC
122	14023	A	127	323	2	RGFLGLSDEVSGQQLFSLSEIENQFN NLEGCGGSL/SIPKMDYRCQPSRLAY A*LI FVFLWE/TINTGFRHVQAQLELL TSSDLP\ALASQNAWLTOISHAEPY
123	14024	A	128	2	354	ENCQINNLEPHLRKPKSEVTPKTSASR K*IVNIRIEKNGLIQK/TIEKINELKSW LFENINKIDSHSGKMWGEE*CVFVVC VRERQSDRERETRLIKI*NERGDIADL TEIK*LLITQKLNKY
124	14025	A	129	74	327	GELAMPLRLIINS*PCNPAA\SASLVT GTDTPLYPAHYYY\IIIIIIISBSHF SVQAAMQWCDLQSLPLPPGFRFPS CLSL
125	14026	A	130	83	382	YEFHASDGGSLSSQGFRRPRMDYLSL EYSGQPGQSHETPLSLSLSF/CPLNE SCSIAQGVVQNPYLQSLPLPRFRF *CLSLCKWNYGHRPQL
126	14027	A	131	749	2	RQSIALSPLRCSSTTSAHNFCLQSS DSPASASVAGITGVCHAKLI FVFLVE TRF\THVGQ\AGLELLTSSDLPALASQ SGITGMSHHVQARCVI/CGPTIGNOM KY*KKKEKNQSTPLEHLQOENRHAH TLRHHTAS/LKSSEFLFAIRTSFLIS*K RSGTGMF*YN/WTIONGVEDRFVLOPP FGI.GVQVYHHSI.LQPOSGLKQSSLFSL PSS*DYRHVPTPSFLKFLRRWGLAILLR L

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127	14028	A	132	371	1	KRNGLNLT*VKINTNIMDTIKYKI IT*KKQEKVGNLQKKEPSDLTPK*SI KGN/TD K*DV*KPFSL*KPM*GNRYQATD *KMSAKHVSNNYP\LSRIYKINDKARN KPIRKWAKQMN
128	14029	A	133	2	318	NHKIILKDAKKAPDRN*HPFIMKILNK* GIRQYAT/DIILKAMCDRPTADIIILNGEK LSAFPQLSGERPLLA\FH*IM*VLAKTVR PRKRNKSGQEWMLALPTLGG
129	14030	A	134	3	362	WSRLSSDSSPFAIASQTAGITDWHRYAQ PGTDF/STSVYPTLPTQRL*ALKKK*VL L/EPK*IPAST*QPAKCSGSRNFLPAQ PYHWHFFPNEETEAQNGNSLLWAC/LRE DWIPTD
130	14031	A	135	12	398	KCSTIVIRISIVKTRREIYHYPTPKMAR IKKPDNAKC/WSGCGATKTLICH*NN\ SLEIWLFIAMKFNICLPCDFRIVPLDLYL REMKYIHENTYTKVSIAPLFR\QPKSP STGESINCSIIIPMBECII
131	14032	A	136	309	1	QSEAPSQNKTKQKTKVGGTTS*PQYH NATVIRKTVH/N/YIGIDIDOWNSIQSP EINFHIHGK/LISNKAARTNEMWGNLSL NR*HEDNRIFTCKRMKVDSPHI
132	14033	A	137	2	251	QCGKAFRAASVLRMHGRTHPEDKPYECK Q*GKAFRASASHL*MHGRTHGRK/P/H CKEGKPFPSAQNLRIQ*RTQAHIRHNS G
133	14034	A	138	396	3	LELLTS*SACILQPKNDYRRFPFPHAK MIL*S KSS\LPPLKSKCINTIWAALLLL CSLVLPL/LPLKRFYAAH*SPDSLKYV LQKLSKLEMLVLHETVQRKEQTLTSLYK PIFGFLVGYSPFLFCYKTS
134	14035	A	139	3	384	LDFIKMKNCCSKELCGRYEKP*T/NEK MFAKHSNK*FIPRI*K*LSKLTTKK*A KDILNRYSLKEDIQWANKM/KKCSI*LV IREKQTKNTMYRY*NGLS*RS/GQTK* QWGGTGPLIHCWNEYPMI
135	14036	A	140	63	388	FMFLIY*LER/CLTLAQTRVQWCDHSS LQPOTPGLKH\PPASASGVATTIMPG* FLFFP*KRGPCHWARTT/WNLNGSF
136	14037	A	141	370	3	GGHFFALFPKPGPLGPVVPFIIIPALLE G*GGGFPQF/RGSGPRGQPCFFLKFQMF PQFV\GAPVVPQFPGNLGRGTALNPEAG GSILKGPFLQPGGKTLFPQKKKKY QHFGTQLILCF
137	14038	A	142	363	2	REKATEENFATS*DWLWPKKSGSHFST KVLGTPSADVSTVSCPEDLAKIMED GYTKIPNVGET\PSRTLIRKEKSVPG FKASKLQRIG*LLGVNNAQDFKIQSVL MDYSENHAE
138	14039	A	143	99	375	KNKQNISPPDLVRYTLLSPLLPFIINS PPPPFPSP/CFF*KKSRFEKVAPOGNN LS*LNPRPKSGSKESCLSLQSTWITGGP PPHWADEFD
139	14040	A	144	39	399	LQITNYNYIWIYIWIYIWNLSKIYKLL QINNKKTKNKGQKT*IDVSNNNMYNG* *LHEKIHDIIVIR*MRIKTIVTYHVMSTR MVIKETENKYN*GYGEKLLIYCWEN





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154	14055	A	159	78	340	GPQPLICPRPGRTHSLXSPWRP VVPHKQAGILLAEYPSGAGHSIEPK TITLFFLGKIVLLCPGMSAVA*S*STV ASN\FGPK*LLCLSPSSSDRYARPHM ANFK
155	14056	A	160	2	362	HLSPSTIPQNRHCHGPPFSVSCWAHLED GVVAGQRSSSLP/M*GRPGGAFSPPR GSGGGLT.PHPLSGGQWPGRTT\ES C*GRPGGAFSPPGGQWPGGGLTPPPP SQTGRLAGRR
156	14057	A	161	293	2	PHLATRPPTVYKSAIYKMDPRTYK RQKMDPGKSSKDR\TIFLAGAAANT KLKPMILD\HSKTKLKNYKSLLPVL CKMR\HKA*MSDHLF
157	14058	A	162	2	136	LIVPILAMAPLRLTERKILGYIQLRTG PNVWTPPTGATYRLLS/P*QP**LFTE P\LEPVTCTITLYITDPTALTIALVL* TPLPILPNVGNLNLGLFILATCSLAVY SIL*SNRNGIPKTYRTKNSRLVTTTHRP QRLEDAAYWCYVQTDIA
158	14059	A	163	1	464	RQGL/DSVTQAGVQRNLSS\LQPL/PP GLK*SSRFSVSNSMDYRCAPPHLANFFN LFFVQRG\FTMLPKL\TRS\GPGD
159	14060	A	164	1	353	FNYSLLGRKSETPPQKKKKKKGRGPG BNPPTPTPGAKGSGNPGLIKLKTTPK GMPCKKKK*PIRGRP/HNPNYRG GPGKINFWPGGGSGK*KSPIKPPPG KKGDFP
160	14061	A	165	45	389	FFVCTFCRRSLLCRSSWSGTFOLK*PS CLSLPKFSDYRHKWPCSARNFLPACPA CLPPLSLPSPFFPS/SPSSSPRQVTVIQ VRVQWRDYGSLQ*PPKTKRSTFLAFQD LGPO
161	14062	A	166	330	2	WDYRCAPPHFVLYLKK/STFNIFFL*RG VTMLSLVSSDPPISASQVARIIDVSHW AQL*RSV/CYVFETGSGSLTQAGVQRN HGSVQPGHSLRS*SSHPLSNRYPPPPC
162	14063	A	167	2	396	YSNVILGYTPKRLTVHMFICV*NTC IWMFITALFAL\ES*CSSVGE*IGKTY IPTMKYYSVMKRNALSSHEKTRILKCI LPSESRCDRLQTV
163	14064	A	168	486	2	LPFGKIYKINASSKIDNRKGRQTQIILG MKDILMTYVQGTSSKYIARFTNLEEM DQLEFKHRR/LIHQYSGHEILGDMTN EFELINVKTPIQNSPGWDDFIGEYCMF EFELSENKTGELL*S*YSLTNSFYEA SITY*PKPDQ*KKQSGPLSM
164	14065	A	169	200	3	GRVCLPPTQSRPGRPPSPDGVQAPRP SIVRNCGILTRGSPGD\PSPLSS*AQL CGSPPPPSFS
165	14066	A	170	2	327	PGGIGGGLR*HICTPTCATERDSV/WN KIIHYIIMLASPNELILPLNLCLLIL* AGPLTAICISMFMATLFTLAQMGKPK CPSTNEWIRKMYIHINEYLYHFMK
166	14067	A	171	2	343	PGWSQTPDFR*STCLGLPKCWDYER/AA TVPLGLFLFITALC
167	14068	A	172	367	3	FIRDVQFISALRYLLTPPERA/MIKSK NNRYRCGGCK/RG/TLLHCH*KKCLVQ?

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion
						L**SVWRFLKRLPLNSVPLGLIYFK/D KEVIYEKDSCLVPIAVQFAIA/RNIHP TYCPINR*IKRMWYIY
168	14069	A	173	102	345	YQLQNI PRWVYSKIQNLISFAFVLL*RRR VFLCHIGWSSLL/QLKRSFHLYLASSND YRQVT PRPAN*ILFRD/RGLALLPR
169	14070	A	174	22	401	STRGLGPRCWDYRCSSCPATYLPF*HS IPLFLSLQKVQVHRRVYLPFLSLMLPL LSKNSV*TY*KSTFLS/HPSRLVLCFPL PCFVTGFESVQARVQWNEHSSLPQPPS LK*SIHLSLSPS*DCR
170	14071	A	175	2	388	SDLQLRAGRTTALFAVHQHLLTQRFL LSF/V*LCPAPRG GAYRGRQASLSCGGL HPGAYRLSCLPKQANWAGVAPTPASLS SCSLISDCCASNHRDSVGVGPFEPGAGC NLTHSRFLSPSGAVVSC
171	14072	A	176	334	1	RLRLRLIN*FNKVAVYKINTQNLQCYTL IRITQKGLSLKTILLTAPKRIKYGLI/Q /LTKGKVLHSHSYTLLEKIK*DINK*K DIPCS*MGWVPFGVCLFVYCPCEMAPRS
172	14073	A	177	339	2	KNSPYNPFGRGNPGNL*SLKSRIT/CWG STFAHIGELFFFMGKKFPAL/RPFFFF EDRVLLCRPGCGSVVRSMIAAST/CLG WYRCPTPCLANPL*ROGLTMLPRLISN SSIO
173	14074	A	178	3	303	DLRRAACLLTLPKWDYRVHVP PRADNSG FLHLII*VCLPILLCHQVLVEFPFIETG FCHVWAGLKLFLGSSSP/LTLA/PSKWD YR
174	14075	A	179	342	1	INRLNIFTMALFSTLYIRFNTIPKIPPA GFVEMDKLILKLVNFKFAHGLGKTTLLK NRVFNKAYYNATVSKT\YWNEDRNINQ WN*IDNLKINPCVCGQLIFNKDAKTNEE R
175	14076	A	180	2	323	STSTPTTGSAPL*PQNVDAEATNS*HI NNVNLRLKIKILLERNTKNDHDLGLAT DIY/SVTPKA*ATTTKIDKLELIKINFP CTSKDIT*KVKRQLIGNSCKSPH
176	14077	A	181	326	3	RRKKKRRREPRPKDBERLRYGKDIYK KRRKDTM/DWEKILQKGVQRMCY*KI* RQVQLKQANP IRRGNNLNKLVHQRIM AWKMKCPKQAVIRLKI*ITFENRYH
177	14078	A	182	5	326	TKTTEKAN*DRSRKQTKFPPETQIR KTTKIDNSKSCFYKDKDKTDKLVKLI KKKTKKLIITDKRKHHTI*DCETSVKGM TECYEQVYANKFONS\ESQDNFLER
178	14079	A	183	3	378	TVLSCTFVWGLDFEG*THFTYS*VFCYK WNCVHNFLRFPPSAYI*YLLIFVY*S*I MHLCLICY*ILL/CSCIEFNI FYMLNFS FWL/CFWYFYVILCPPIFF/CIFCLL FFVYLLFLIFFIFFLFL
179	14080	A	184	365	3	MQLKCIKMSISVQAGVQWNEHFGSQQPP PW/LHHFPASASLVGTIWARHQGRVIF /IFFFFLMRRSL/DSVDQAGAQWHDGGS LQPLLPGFK*FA/PCWDDRRAPQCPAN FVFLA/RHGFTILAR
180	14081	A	185	51	293	PYVNRASVLNTPYQAS/I*KKSNYRP ISLNNIDAKILNKQQLKLNKYNDSRQT

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181	14082	A	186	326	3	GRDQIKPKYCTVSDGGRMRDYPPLTFSS TKIQWILNLGKKRPFQPKKKKIKCPN KRRLANGIKK*DPPTGCIQDICTPRSKD AQRLQIKGWKKIPQKGTGIR/GVAVLTS DNIEFKIKIVTRDRVANYIKGSIHQ
182	14083	A	187	17	330	KDNEM*IKRTMRCYYTSPMAKINLRIN NIKC*QG*GTGTG/L/LYC*WGHKIVQP FSKEV*QFLMRSNKILRYNPAILLLGIY SN*VKI/C*KYIMRMFIVFLITKDWIQP NYSS
183	14084	A	188	124	357	SLWGGDLBGGGKKRGRNPGQKKPKPK KKKGGNGLGARG/VFKKGRPPQKEPKPK KGEKGP*GAGI*GGGNGVKKK
184	14085	A	189	333	124	RLRQENRLNP/GSRGCRFPSPRHCTPGW ATE*DSVSKINKIKYKSI IARDCHARNIS IVSFLSKRGCVFLF
185	14086	A	190	1	327	KSWILGDNLPSSQSLTQKKGVNPSFKSM KADRGKEAABEKSEASRWFMEKERSH LHN/IK*VQGGKASYPEDLASIIDEGGY TRQ*IFNEDY/MWKKI*FRSFLTREKL
186	14087	A	191	53	400	VNIIIGPPLHFPFTVQNALSPNTYIMHML TSLGFLHMSLQTGFPPKPSYLFQPSPH SVFVGF/IPGMQR*PSIHKSVNVIYHVI RMNDISHMIISKDT*KAFDKIQHGSILF PALSI
187	14088	A	192	65	321	RPRTIYLHLTLLGVYASSTKCTGPTDC N*MTTAPTLVKWT*PKSLISGERIN KL/WILICTYMEYYSALKSVLTHLTWV NEH
188	14089	A	193	127	241	ITHDSSRRICNLTEKLEPKKINS/WPGA VAHACNPSTLGG*GGSRITYNESRNKG EQTQNNK
189	14090	A	194	1	337	DLPASASQSACIIG*ESIRN*NKLVKKT LKCSQDKPKEDLNK/WKDIVCSWLGRLS LTKVSILPKLIYKFAKIPTKLYYD*KKN RPGAVAAQYNSSTIGRGGQI
190	14091	A	195	2	333	NFNSLFFVFYSEKLLKPLINCK/VARR ILORINKVGR/LVLRNPNDYKATVITKIA WH*HKDTHMDQRNRTSTKINTYKGAKT I*WRKNSLFNK*CNDR/WTTCRKKVD P
191	14092	A	196	299	2	PHFORDVOPSPPSICRIFSPSSIGIQ SWFNIQKSNVFPYHIVINTQHRSSSSS SSSSSSSSSY*LVKIF/LNKLIGBQNF LILLKATIGKIPVNH
192	14093	A	197	2	199	LALSPKLECGAITAYCSLELLGSDNPP TLASKVF/GITVM*AAQPVVFLILYY FIFFPSSSVL
193	14094	A	198	226	2	KKFFFFNPNNKNPFLGRVFF/CSGP*KF FAPLGFVFLSV/LRQKVPHLGSPOKTFPF FFFFGDRVWTCPCWSAVA
194	14095	A	199	338	93	PQHNGSCL*SQLFERLEADPILNLRVQG CNEL*LYLCTPSWNPVSEKKSIQENNA NLDPREY/RDKRRNWTVC*NSIRBSSE
195	14096	A	200	1	361	PRSHLSQRLVRLSQ/IKRQKTIQKQPR ATG/MGKKF*GRTLEVPPIRGKVQNKPF LKLKSLPRLPKKKTETL*TLGKIPKRWK KFFATYPSIRE*ISKCRDLNHFQKKI

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196	14097	A	201	2	358	ITIPFORAKGL BNKTTMYRH* IPIRMAEN*VLAVGL/L QPWWEYKRV* PLWKINSLAVITLLNINLP CNPTILLGVYPRERKTYVTVACTQMF LTVLFTVAPNWRQSQGPSTGE* KKK*WH THMGHYS
197	14098	A	202	110	357	TWFTICSHLLPEKTSPTFCFPQCIDYS *KTFVHSVLEFFKDRVLLCHPQMSAVA Q**PTAASD/POESSCFSLPGSNVYKRM
198	14099	A	203	2	374	TLRLHAFMAETPGACKTFCDLRQVFF IFIYLF/MRLSLTLVAQGVQNRNLGSL QPPPPGQKRF*GRCLPYFKDGLVCPGLA GS*TGQIGKGIITLSPDCLSGDGPCKG PKS/ASASQGHVG
199	14100	A	204	375	3	LSSILIRGSFNLSLTITQEH*LLLP MPLAII*FISPLAETNRTFPDHTGES ELVSGFNIEYAAGPFAILFIATYNTII INTLTTTITIGTITDALSHELYTTFVT KTIPLTSPALMS
200	14101	A	205	393	3	SARLGFLKPCNDYER/ASTVGL/SIMLL LKSIVSRMKKCE*LVKPLEAKL*DCCKE L*VGNLIMPSTYDQENRVDSSLTWC VLLELLCLLLLPWRQSPALVARQMRN RLASL*PLPPGQFQSC
201	14102	A	206	2	377	FRALQGRWSLQKFLLPQCPAPRGG VVM*RGRS/SLSCGLRFPVRSWLLCLP TQASAMVHAPPARILLPRISIDCYTSS EQGSVMGPAEPGVGYDLLVCLCLRPLE KHSIWVRVSCFSRY
202	14103	A	207	327	1	ILTGNFKQIRMLIYHSVNPRLKNYAKS TLFVNVIKNNKA*MTAHLFIANPGCFK PTVEPYCKKKK\IPFKVLLIDNAPGH PRALMKPEEISTVMPANPASIL
203	14104	A	208	310	2	FCWNAFGKQFPLGEGWLLGPGSPFFLK EGFPVGQGPQPKRNLGK*PPGAHWKG F/IFFFADRVSLLCHPCNSAVASQLTAN PASVQAILLPQPDYIR
204	14105	A	209	374	3	GVRDF/LEEVCF*DKGVARRT/SLP FKAVRQGLSLQRFLLFPVNLCPAPRGG VCRGTQASLSCGLHFPVRSWPLCLPTQ ASNMVQAPSRLPPGSIIDCCASNR GSVGMHSITDGY
205	14106	A	210	3	196	LENLKE/LDK/LEVINATLNQESTSL NRPMTSKI*SVIKTLARMAHAYNPST LGGKRRLL
206	14107	A	211	34	339	ITKSRINYSCHLYPHNIDNFFPFET VRSVI/KLKCYGAPVHTCTNLNPGSTN LSTASQVSGAINRGVPGQF/IGLEK*F LVKTGFCHVA*AGLEPLGG
207	14108	A	212	200	312	HYGQHVLCFLF*MSHSVTV/QAG/VO NP/SLALQTPPGFKQFCCLVSSNDY
208	14109	A	213	300	124	NHIFFFQTHRVCCV/CVCCVCLCV/CV YRYTCVSPN/RN**SL*KECLSLVLLT PTC
209	14110	A	214	1	337	QVDHSDRKANLMP*KIKVIQTHPSDY NGVKSRRNRKTKGLTNIOKLNT/L*I SNETNEKPOIRKYFVNINENTYQDL NDEVSIQAQINPSTLEAAGRLLEPRS

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210	14111	A	215	360	1	LRSAWTFTE LTIETVYCSB\KKTFFKILLFIDNLGHP RALMEM*KEMNVPMPAKTTSIMLPLI\S SPNSYYLRLRIHRTFVVVAQSNLQCPTT AISDIQIGPVAMGILLIPSAPVLWLSI QQVSKLKH
211	14112	A	216	3	347	SSRSPADGLFFYYCK*QTLN*HLWYKT QKEKKTKMKKKORINRA\GDKLPEB EAVCGKPNPANPVQRILVGLDASGSP PHQAMGSHHNLTGTATLINEQWLLTTG KNLL
212	14113	A	217	75	347	PPIFKRTARGKVTPGWEYPAKS\CGGT LGNRGLFPNPGFSGPPPKQVWEGALCA PG*KVCTLK*FI\SLAIPNGSGKNFFT LFEGSPSIL
213	14114	A	218	3	397	GGQGYSGTGHGGIWHKVEH*R*PLPPK KKKKKKKKKKKKKKKKKKKKKKKKKK GGQNLKGGGKEKPPQKGVKKTLGSGRI IKKDGREKHTRGELWKCTFIW\EGEKIG EKPPKKI*DHEGKKVKVLGKG
214	14115	A	219	3	401	KSQWTLHONTMK*SAAVL*ALGLV\FGP TVSGPTGIVLSNS*LDELADTYVVVAH PHYVLISIGAVFAIIGGLIH*IPLSGYIT LDQYAKTHETTLIGVNLTFPPQHFL LGSWRRISDYPDAYT*HLL
215	14116	A	220	162	3	KPADRL*SNPEKEDNLLKNGS\WFG TVAHACNPSLTGGQKQIIRSQV*EQP
216	14117	A	221	374	2	WCRDERERERATERERERERERQTRDQ TORRREEA\BGMAAMAIN*GRAPGTSL AALESCSCPRPPDAPPEQGPFPPTTAR GQPRPPKLLQPEAPSQTRPHGV*WPLRV LPQSGPEVVRPRE
217	14118	A	222	3	264	DHMRPKVRGCSL*SCHCTPAAAT\SES LQKKKKKKKKKKKKKKKKKKKKKKKK PPFFFKKKMNLKSPVGLGVAJNRWIL KHKG
218	14119	A	223	2	410	ATSPITEELIT*HDAHLINLLM*FLGL HALFVALTTTLTNINI*HABETQT*TI LPATILLVLRLPSLR\ILYISDEVNDPS TTESMGHWY*TYEY\TDYSGLLNLY TLPLFLSPGDLRLLDGDDQVALT
219	14120	A	224	399	3	GVGKPFQFWAKGVALPPYSKGYTK*VON LLKVLKLLKNGPGBSLAATGWLP PKARAPKLLRN\DSPKGKBPASKKK EKQPTWEKIFAMHSDKELTSRYKEL QQ*SKQPIFLPIYIHAFKG
220	14121	A	225	360	71	NRTTWVPFKTPPLVYHNTKKK*HTGRK KHKTAKKAKKKTGNK\EKENPHQ RPOKRRK\EQKPKRGKKKKKKKKPK EYSYL*K\YIHTNLQ
221	14122	A	226	3	386	PSTHVSINLNGIFL*ADAVITGHSKI KDALAHFLPOQTPTPLIPILAIETISL LIQPIALSVRITANITAGHLLMLIGST TLTVSTINLSSTLITITILLTL*IA VALIQAY\VCPLLVGAY
222	14123	A	227	3	372	YSLDSPSLTRFTPTHPLPFTSAALAL HLFLHETGSRNPGLGTSRSDKSTPHY YTRDALGLGLFLLSLMTLLFSPDGLG



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237	14138	A	242	3	339	LRL RKDSRRERERANKKKRQKRGKRRKKTSM TVHFSKKTMAK/ARRQ*NPVFRMLRE* KN\FPPRILYSRIIFQGRSQIKKFSGD GNPKQSPPELFFLRIPMEVFNLEAYLR KS
238	14139	A	243	216	3	NETGTQTQSQKFMLSLVKKLISPTYL*D GVLLFAQDGVKMDLGLSQPPPP/GPTL FQKFSCLSLPSS*GGRIL
239	14140	A	244	408	2	VLTS*STLST/VWGLTQ/LQL/KLLA YSS/I*THIG/WMPPLQYHHTITLLNLT IYILITLNA/FLVLPNNSISGTTLLSRT *NEIT*LPSLIPSTLLSGGLPPLTGFL PKWALIIEFTKINSLIIPITLITITLLN LY
240	14141	A	245	3	243	IIMLGQGMVTFPNEVDWVAYKHIDRYS TSLVNN*MQIKITMGVHYAPITVAKILL N/SNTRYWP*RG/CSRTHCWKRKR
241	14142	A	246	2	337	FLIMDLQKYINPKIKEQGETINRKTVSF MINDAKILNKLIVQI*F*FKKONNSKF G/FIP*/SQGCFNINQCTSLDERKXYMI ISKNIEKAFNKIQHSPMIKTNNRKLPL EL
242	14143	A	247	347	1	HYTF*RMRTKQMTDNKICW*GGGPP/GT LLHCW*ECKMVQAL/ML*TVNQLETKLN LLLPTNPITFFGIYNBGRTHVHTKCT LIFILALFI IARTQKQ/PRCSSVDWMI NGLNYTQ
243	14144	A	248	319	2	KKILPLTICTERVFLCCQPMSSQTPRLKQ SSSLGLPKC*DYRESS/POLNVLL*CL KFHLRVAMLFFVFEV*IVIFFLRQSL /DSVTRAGVQWYNLSSQLPPPGFK
244	14145	A	249	329	3	KFFFFHTGKAKNYAVFVINKRIKKQHT HIIYNYGGHQAECCKRIEAVHVCMSYK MMQ/SL*KTAW*FLKK*TMELPYDPVIL LLRIYSKELKAGTRTOVCTSMCSFLPL
245	14146	A	250	316	3	KTKRTMGVNHIPNERTIDST*LEKSNIR AITIKLL/KNNRVSLHDRLIGHGLDMT PRAQAAKKKIKR*IDEFTIKYF/CASKO NIKRV/NRQHK*DTMFANHS
246	14147	A	251	152	364	QLTSLNIIINQIKYK*TRHS/VHHHHHH HHHHHHHQ*KRLPE*SYKSKQEHYTY GMDITGPKNRLTIPL
247	14148	A	252	230	1	PCWICEFTVSSFCWFVLETGSCYVAHA RYWCMSRL*PQVGLKRRSCLFSFRSG WQ*RH/VPIAN*TLRGVIL
248	14149	A	253	3	345	DVGLAGLELLTSGDFENASQIAGITGV SHHSWPLLEFFFFF/CFFGGPFVFLP V*SQGDI/GSRSPNPGPKGISRLRFPN EGKIGDQPLAPDMFCFDFKTLWSTVVG WFH
249	14150	A	254	194	1	GRVDTKWANTHERFSKCS/TTVD*WIFK SWYLCMEYSTINKKILLSFVTWML EDIMLSVS
250	14151	A	255	327	3	VKTAEFVNKWKQNSTKLINSSQAQIDKK IVNQINDLRQTEIWMGDIMNLESRIQM QCDWNTSDFCVTPQ/YNETER*WKKVKR HLGGRBNLTL*IVK/KQDQFSAQ





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266	14167	A	271	1	318	QMCKH LKLLTSGNLPAASQTAGITGINHRAQP HLSPSL*LNWNET/CVPG
267	14168	A	272	108	322	DSHVI FLQGNLTVPVCLFLRAGL/DSI THPGVQWHEHNSL*P*TPGLK*SYHLSL SSI*MYKRTPLRLAFL
268	14169	A	273	341	3	GFFFFPPFFRQGFLLAQVK/VPMGNFR SLQPLPGVGVKPK/KQPSCLNLPK/WGSLKQ FFKKKCHFP*+*FTHGKKDLKFSI FTNPFFFFFETESCSVVQAVQ*HDL/S TRP
269	14170	A	274	41	328	PALLTPQCTERERESKTBRESBERERA GEAERGRGTGIDSLYSLKLYSKTTHLK ILEYI/LATYFKRLPYNNEL*TWAK/TRI IEKPSVRHQQQGRS
270	14171	A	275	3	322	EAQSL/LDPGSGGCSLRSHTSAAWAT KAKLRFKKKKKKKCPGRYLGNIIVLQ*FN ITAKDKYHIVKLI F/CFSSAVTASTQK LIQSDRTVTHRKIKCTROYVYLLD
271	14172	A	276	175	313	STLISYPRDRVLLCYPDWASVGGSQFTA A*NEW/VK*SSLSL/PSNW
272	14173	A	277	254	3	RPRRQFGTGGFLAQITNIYKSKTANVI LYVDRINAPSLISGTRQCPPLSRPLPNI VL*LPVHIIRQ/EKVI*GMQIVKEELNL SL
273	14174	A	278	186	1	PSIMQARQ*SEIFKVLKKN/LQHRIL YPRKLSPOSERIKTF/QLKKPITTSRP ALQRMKGE
274	14175	A	279	288	3	GRKGGKGFNPEGNSKPEFKPLPSQLQ AKTQPVFKKKKKKKTRNPIKK/WAKDP NRYLTKAEL*MASRHMKRCSTSCVIREL *IKTTMRDYVLL
275	14176	A	280	3	329	LKSSRLSLCSWDHRFALPMLSGLVW NSCPQ/CDPSASLSLIGTGMSHHTWL *WLF/C*ETGSHPVTAQGNQWYDPSLH PTKGVYLT/RRFRLGSPSAW
276	14177	A	281	233	3	YITDRDREHFMTEKSTHQGGITATNIC VPYNRGS*KK*KLTKLNGENR*/HSII IAGDFNTFTSIMDRAIRKSAKNG
277	14178	A	282	32	309	LPDITPRDHLSPQIMDFIQBTGCSKWR GGTTPVCC*WBECK/VIVQSLSRVWRF LKLLKIGQVRWLMFVISALMDVEVGSP EARSRRPAPW
278	14179	A	283	1	302	CRNNKAWTVHLFTAKLSYFTPTVET YCS*KTIPTTL/LDDNAPGQPGVLVE MHQMNVAFRPANTASTLQWNGQGGIT FNSYLYRATFPKAIVALIS
279	14180	A	284	155	1	PKRFFFFF*DRVLLCHG*SIAT*SLC TTKSASQV/RQFSCLRPPSWDY
280	14181	A	285	131	15	DRSNGRFLATNSSSLYSRPREIRPSQ APPVNDPI*AT
281	14182	A	286	1	359	FFFFFFSVFWCFSPFFFKKGGAPGSG GPPPKKPTLPSPOKNEFLQKK*PGKG FKGPGLPPNPGPG/RNGPLKPGDZHP PDFTPRNLFKPDF*KRGSPPFPDPGFP KNLFLKVP
282	14183	A	287	52	419	LEBRAGTSWPKENKQHFQCMKKKKKK KKKKKKKKKKKKFFKGAQIFS*GVV

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						NI/H/SQPGPVLTGGGGRRSPPPPPSP PSSILFFPSSSLPLSLPLSLPLSPSS PPLLSS/CPPLPSS
283	14184	A	288	236	325	LNIRTPGSWLXAVAHACNPSTILGGRRI IT
284	14185	A	289	218	409	KVRGNKADLIRSSANGS*/N/VKGVLCQY LEKSPCLETBFHSCLPQLVWRPDLGLLQ PMPPGIARF
285	14186	A	290	3	426	HSEGTSPRLCESSMITAHCSLDLPKLK* SSHLGLGS/RHVPCLATPL
286	14187	A	291	382	1	ANFVTVLVQVGGPFLKLSRRDA*PCDHP TNAQSAGITGVSHHAMPKMSITLGVY SPGESVPSIFKPYFLETGSSFLPOAGA **CNHSSLVP*TPGLKQSPHLLSTSV YRYLPPCPLCPVLV
287	14188	A	292	3	309	HEVYPPTLNQOLEMILKLSKGL/VKAGG \ISQIVNAKEKFLKEIKSVIPVNTRMK QNSLIA\ETQEVSLVMLEDQTSNIPLS *YLQSKFLTLFNSPKALM
288	14189	A	293	2	415	ARDQYRKSTK*ARDLYRHFPNEAL/HM ASNYK/KRCSIS*VIRKIEIKSSMTSCY THLQN/ALKLESDNFKC*OKCTAMGILL SHWECNLVQSLMTW\CNLLMLNTHKPY* SAI/PTSGLYPTEMYRNTEQASLRMFWA WRGG
289	14190	A	294	335	108	LPYFK*PSSPPLHTPYTTIPKP/RPPP P*HPPHHPPPPLTP\PLPTHTLPTPT PTNLPHIPPLYSIPSSSKIS
290	14191	A	295	266	2	GFPKVFPSPFGPPKLGFPFISVFS/LFT FENPGLCI.KPFOFPFSAFLPQFSPFF FFFFFFFFFF*DRAVLCHPGWAVVRWMLT ATLV
291	14192	A	296	347	1	DSLQP*TRGLN*FFHLSPLTRWEYRCAP QCPANFC/VFL*RWGFAMLPKLVSOLDP ALASQAGITGVSHHAMPKMSITLGVY HPSKASETPWAGNQSQTSPSEYPATYNFK IYSC
292	14193	A	297	284	2	CROGFVLCRLVSNSCDQVLCVLCV*VL GLQACAT*LGAGVSIEPSPHKGRCGL CRHRS/HSMFSAWC*PHTHHTHTHTH HTHPSMQLV
293	14194	A	298	1	96	GTRLCIGATITLFAAVCALTKQDLTKIV DFST*SQLGLLIVTIGINQPHLSPLHC THALPKALSMCYTITDILNDQDSQT IRLJANTWHNLS\LTIDLS*L/GKP FLN/STY*QKDLTKVDFST
294	14195	A	299	3	134	HEGRD*PKNQDTLGLKIQKAGSSGV CLIKRLKMCENHNP
295	14196	A	300	2	333	GVGRGGGRKRGKESGNGGIRRRSGV KREEGKRYRDEVDPRKRGKESGGRER GRGWEKEKGAS*/C/EEGRVK
296	14197	A	301	354	1	TENELLSIYKNTQIN/RYSKMSKK *RK*QAI/TTETLQTNKHLKCSISLI IRELQTKR*ILYT*LVKKLKTNGLYC WECCRELGC
297	14198	A	302	1	282	GTROMVAGAYNLGPPSSDWR*/CLPFC LANFFVSLVERGPTRLTTLVLLS*LYDS PASRSETAGIPLINTSCVYVSLRNAD

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
298	14199	A	303	361	3	IAILCKQAV LPKWDYRHEPLCLATFFFF*AFFPVPL CMYVPPN/RVYAFFPSLSGF*ICCTFTL YIFPOLMDG*AVSSFLFLQPVGVKPKK FFLSFFK\KRSLGMLPRLILNSWAQVI HPPWPRPA
299	14200	A	304	2	352	ARMVS*PCDFPA*ASQSAEITGMSH AQPIIIS*TIAYVPSFLSSLT*ISSVR SFTKSMQLLYFYFVSL/PSW
300	14201	A	305	334	1	KNSFFPFFKASIGLAQI*VQWSDPFT LQPLPKVK\LSRLMLKKD*RGSG LGKFW/LPI*RGSPQLQNVLEFFF/ CPFTSSRSVAQVQWHDLCSLQAPFP SSC
301	14202	A	306	270	2	DWAGGGGDDGVPRQVIFVLVETGKWR VGQAGPQLLASSYLPALA/FPKCDPRH *PPHSALKALFFT*DGVSILLPRELNG ASSPA
302	14203	A	307	306	2	HIFQVCVCVCVCVCVCVCVCVCVCV KLIVISQT*LSPLCSGP*A/CTFFSVVCV VCVCVCVCV/CVCVCVCVCVSDLTNL SLCSGP*A*HFFSVVCVSC
303	14204	A	308	117	332	SPFVILRCSLSVQNGKTRPLK*LK MEL*FHSALPLGIPKGRPLYQKDT/ CHSIFITALFIK
304	14205	A	309	1	351	GTRKTN*KNADLSRHSKEDIRNQ* V/HMRCASLIRIM*ISITV/RYNL TCIM
305	14206	A	310	1	352	PSPPHSPFLSPSPQPPYPFPFPRP PRSL*YTPAPFYW/PSFLTPSP/PS DPPEPRSRP
306	14207	A	311	1	405	FKPSF*PLTALLGLNTSGLAM*FHL SIT/LLLLC/LNT/LTIYQ*WRDTR ERTYQGHHTPPDKGLRGILFITSEV FFFAGYF*AFYHSSLAPTQLGGHWPPT GMTPIANPLEVLLNTSVILAS*VSI
307	14208	A	312	3	176	HEILSSNF/CQSTQVSHCPG*STREL QSSHLNLPCKHRLA*TVVGLTTIFH LGKPKHVR
308	14209	A	313	298	327	SLTSLPRL*KIKK*RRK*NCXQGCET GAFTHCWGCKMVQLNKS*W*LPKKVK *KLSYDPAIPLV
309	14210	A	314	344	3	HSTSLVIRM*IKRMTYPTTTTGAII *KNRS*/WLGCKTGLSLHSM*KC*HVQ SLWMTGQPFILKI*ELTIPLLDLVRE MITYDHTKCI*MFIVALFLAQNVMS LV
310	14211	A	315	18	321	WALFVYCLKKEFGQPPPLACPFWDRV SLCLPGWRAVMGSHV/VRPKILAFI*S SHLSLPSWYDLPLPPCKADSCSNR VSTVGDGDKKVERGKGD
311	14212	A	316	289	52	ETSCDVPKGLHFGERTHIMPCKWAK GMR*YFH/KEDK*MAHTHKRC*TSLVI MKMQIKSSTPYHFIPLRLTKPLKSANT CW*TCIAWLYLSSNMKLSHALCPFFNH DVCISLTVONAPTGHITRRFS
312	14213	A	317	57	324	YCVTFFFFGKQSFVLSPLNCKGPFVW CSLSLSTWYGLVPGIQPFF/LPLVQR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, - = possible nucleotide deletion, v = possible nucleotide insertion)
						GPHTVAQVGLKLLTSODLLP*GSRGAGF TGLTHC
313	14214	A	318	65	341	QWLLKRSRSCYFFFL*DRSWAVAQA*VQW R/NPPPPPGFKQF/SCVSLSSWDYRCLP PHLADFWIFSRQDFQHSQTSSLKKKK KREIPNLFGLG
314	14215	A	319	2	182	ARGDYRIMPFTY\H*LETGSCFVQIAGL ELLOSSHPPALTSQCWDCTCEQPSWSAP CYSI
315	14216	A	320	345	3	MPFQAMF\VPFISGPHVAAGLELL GSINPPPSASWDERQAGAVUTVGS HHAQLGTITSYHLLFLKKGRNAC*SQ HDPTTCLHVNCLCSLLAISRPPTTNL PRA
316	14217	A	321	122	466	QSFPTVC*KNWTL/CPLKSIDSLVAPY TKIDSKWIIDLVNKPRTIKLLGQNMEN LCHMLSKDSSDVTQKA*SEKQINKFN SHGGTRLRSQPLKRAEVGRVRLSGGRS YSDL
317	14218	A	322	3	345	HEDAVSAPCNLHLPSSNCPASASRVAE MTPVA\PCPANFFFFFLEREPGCPG /CK*K*VFQKKPKGKKRIGKKGVWG PKLKERERKKRKEERKKRKEVTE MNGG
318	14219	A	323	206	446	GNLHQCIFYKWIHLAKMCEQDSIC*IL KECYQKPLLEKSHLQAQVDEKPADW/ PLLAGTYVWD
319	14220	A	324	62	327	VERLLADLEHICRPPDQSEAPWCFILR PGMRAPCYQIRRCTDDY/PQGEAQQW LQSRAGSLEPDRGEVSA*W/SARTHR
320	14221	A	325	441	1	RKIK*ILQGL/EPRLEHVASPHRDHY WPRQCKLFSECKNKATMTVLYPEE/S SKKLGRS*GSE/CISVFRITLSVGVVA YTGAPVSI SERPSAALYHRMNK*HQHR RHLLGFSEQEPVQGVPLQGSQGPKEP QPSPNPAPRA
321	14222	A	326	2	358	ARARTLRIMVNLNAXSLTPVLCRGNK VVWTHLFTASFASYFKPAVETYLEKI FFKILQLIGDAPCHRPRLMDMKVNVF VPAKTSIQPMD\ISPFSY*EITFQA GCCGSL
322	14223	A	327	1	430	ARENMPGHLHRCIIEQDRIHMLIPRLN TQMIKIV*YWKDRYVDE/YNNTESTE VHLGYIGELIPRSRAKILQWNGKRIVLN KRCWD/NNL/SCKSH*HDSYLTCT* K ITPNIINPTGRAKTRLL/EKTOVSFC DFG
323	14224	A	328	146	374	KCLMLKFPYINRLTP/KLR*/CQDTF P*SYVA*TGTAVRTWGLPVIPALWEAE AGSRQGEMLTILANTKPRL
324	14225	A	329	2	322	ARASRTFIVRKTQCLASKDTLTVRG* C SCDFOLKSMILIDYSEPRALK/NMLYKR NNAWMTLGLFTANST*KTPTVETCSQ *\KITLKIWL
325	14226	A	330	350	47	ENGLFHAGAGLELLTSGDPPFASAFQSA GTGVSHRAPAN*KKKF/CLKT/RVFL CCPGWS*TPGLK*SCFGLSSHWYRHE PPRPAQFLLLIDPYLRHYRES

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end-nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, ° = possible nucleotide insertion)
326	14227	A	331	753	458	FFFV*GVL/HVAQAGLKL/TSRLPTS AS*VARTSTTHHRA/LHLFNFSKYFCKE QILLCCPGWSRTPAIKRYSHLCLPNSWD YRHEHCNEPEEISLI
327	14228	A	332	256	3	TLVLMSLCLSLSSNDYKHPPF/*LSNT FNLPMGLSGHNPIINGISVSLDRVVVL FLFC/LCFETOSHSVAQROVQWIDHGLSL HSC
328	14229	A	333	25	358	TFDLR*STCLSLPKNDYKHVPHEHANI FT*QLFF/LSQQAANLW*EGGTFT *A*RPHEHSYLRKQTLIPIYLF/LR WSL/NSVAQAGVQ/WHNIGSLQSLPPEF K
329	14230	A	334	3	329	HEDVVSPPWPGNSQTPDLR*SAQLGLPK CWDYREPPHIALNAPLT*NIPNL*W/C LSGSNPIIRISICIRFLGKG*LLPIFIF VNFILQSLNHSVTQAMQMDHGLSLQ
330	14231	A	335	26	330	SQQLGRPQENHNTGSGSST/CKITL VCFWGLHLLPWNFR/ILYLE/CVUSLG FNFCSLVL/CWFLCFCFCAFMCFLFY* WFLVCHFLFFFLFYFFVWMLFF
331	14232	A	336	3	348	DEVFKS/YH*HFMCLK*GDYSLLFHGSS DLTQTQLTHPSTTAMYEVHYQSP*IL YGTIDT*PPVYHRNPHTRTYPYCLQAS TAINLQLSHMNCNSATPHSLGYHQYTP PLTV
332	14233	A	337	2	329	ABAPAAARVTOIAWYHLIGKGLSPFFF HALLFL*GL/NSVTLARVWNTKSSM* A*PPGLRCMSLCPA/NFLYFLVE/IGTA T/PRLQAICLGSSDLPTSTGASAITGV S
333	14234	A	338	60	354	NGKECKKLIYLSIYLSIYLSIYLSIYHL C*YL/SLCL*I*LSN*LAVYIYLSVCLSVS VCL/VASCL*ISIYLSIHLFSYSDRLI AHCHVPTCSLPHATH
334	14235	A	339	1	351	RDADVMLQLIVIFQALAGVQTEGMAG VTHDRVLVNWVFPQCL/HRV*SNGT/ P*VGTSASERPGLKQSSHPSLPSNDYR CEPPCPVNF/CFFV
335	14236	A	340	190	358	EGSNLVFFF/CFLFSDSRFAP*AEQGPP NFG*INPPPPGLRGFGLSLPGTGDYGP V
336	14237	A	341	306	119	LRWENHLSIGN*GCSEF*FRHCTPTWIT E*DSVSKQKQKNHLEKKPGSS/CVVF LPECLFT
337	14238	A	342	1	122	GRRCGEFPRSRCTLA/*QSKTPSKKK KKKKKKKQPPFF
338	14239	A	343	92	316	VCWIDFHKKSRITCLLP/LVILF/FTK ICSSPSP*KGCM/NLGAHVHACNPSTIG GQSGWIT*GHE/FTSLA
339	14240	A	344	83	329	ATAPAPCYFILLCTCMVCVCNHTSVCT /CVILCMCMGLCHIL*TCVA/CTCLGMR FLIPAHITICVRKFLCMGSGNSGSLCL
340	14241	A	345	127	357	YGVLSRGVLPCWPG*SRSTGF/SSPEA NSWPCLANILYLVETOPCHVACAGLEL LDSHPPTASQASAITSMN/HRA
341	14242	A	346	312	1	LNMLNRSVALLTRGVCKHAFSTTSL LIGALK**QSKSLDGLSLSGVKHLND

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						TYRSLRQSEEDTS\KWKDIPCS*TGTF NIVRMSILTKAIYRFNASC
342	14243	A	347	350	243	FHRVGGQDGLNLLT*ST/PC/LGLPKWD YRCEPPRIAY
343	14244	A	348	165	338	HTLDPASHEGPTFLFLS/PVEQCLK*LT LKVATIVLFCFCF*DRVILCHPGHSAVN QSQ
344	14245	A	349	328	2	SVCPHGSINLSPAETTGACH/RLLA*NI DSRV*AKTFKGR*TNCSYNNNNNNNN NNKPFLLRLLAGDRPQ/C/PFRCH FNGATPAGP/PC/LRRSHSSAVSC
345	14246	A	350	3	338	HEIEELTYFHDAALYGHITIGSLVLA FITLTTKLNTNINLHAKSIDTVRTILPA IILILIA/LPSRLRLYTDEGNDPSLTI KSIQHOMY*TYEYTDYGLIFNSYILPP
346	14247	A	351	124	382	NTFKS*NSNRTKNAIT*AKDTQKHPG EDIQANKHMRCLIPLGR/SINQEI S PRVRINKIRPGMVAHICNPNTILGWGRQ IT
347	14248	A	352	3	368	RDRASLFCPGWS*HPELK*SSCLGLPK WDYRR/AATAPGLCL
348	14249	A	353	390	161	FSRDRISPRWSGWSP/DRLSP/CLSLP KWDYR/R*ATMPGT*FHFNLKQDARN QITPCNLTKYTYMSSFLVHS
349	14250	A	354	123	345	LAPQHFASLRARF/PAGPCCRPLAPP RPS*FSPAPLPGADRSVPLSPVPP*S LPPPAGAPPR/PPPPRDSRR
350	14251	A	355	37	393	TKHFVSTCYVPEF IAGTHQKRRIRISVL ANVQKQITLLVETATTSYENLHVL LVFVCFSPPKQGL/DSAFQAGVWREH NSL*P*TPGLKSSSHDLQSSWDYRRVP /RMSSYP
351	14252	A	356	2	335	ARETSKDELTLGLGAGGDF/KLKPVL LVHSENPRPLKNYAWST/LPVL*KNKA *MT*HVFTENLAEYFKPTVQTYCLEN/K FSILLINNPI.SHPRALMDRFKETIGVLM PA
352	14253	A	357	199	377	VGSSCFLKVCQ/C*AVCCVCVCVCVCV CVCLRCV/CVCL/CV/CVGGFFFLVLOG CGCVCVC
353	14254	A	358	1	335	GTRITCMYHVPFRSANT*LVLERWGLPM LPLRVANSPQPTILLQPTVLPNPRT SALY/YRPLDLSPTSISPRIPSSPLTS SLSPAPPFRSHLAPPPRPDPHPPIRPS A
354	14255	A	359	3	369	KPSP*PLTGALSALLMTSGLA/M*PGPH STVLLGLSLTLLTLCY*WRDVRVRSST YQHHTPPVQKGLRYGILLFTSVSVFF AGFF*AFYHSSLAFTPL*GHLPLIVIE LINSI*FPTLY
355	14256	A	361	337	121	LWSQILGLRLQSDCLSPRSQGNK*CH CTPANVTE*DSVSKKKVYTIENKSSSL KKK\NSCHMQQFGGT
356	14257	A	362	256	375	EKKTIVQYPIHYGIN*KNLPAKKTGPG DGFIDKLYNTFRGITTSPHILFH*PKE VAVLINS*SK/AASITLTPKPNKIMRK ENYSPISSYIWNQCSFFLEQIFPLSRKL NCPGLIIPH

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
370	14271	A	376	11	324	DKPLEHPPPLVTVQNAVGRGSPLRCLSL PTSLFI*DRVLICSPAMSAVAQTWPTAT ASWAQ*SSNHSPSD*R/PHTTTGHFFCR DKVL/TMLERLVSNSTQAI
371	14272	A	377	85	364	YQHNYSPFCISQIVYRLEFFFT*TFKKK GWFF*RLNFQGGNG/SME2*PP*IRQP FCLNPLN/SPDRGPPRGANF*IFLKKK GPQVPSLSKI?
372	14273	A	378	1	382	GTGTSYSTTFNGTLTALSSH*FFT*V GLEINMLAIPVLHQYTP*YTHAALM HPLTDSGA/SVLNIEILLVSNST*GB*S SIIELOLISITLSEMLVFNKPGAAYS IHALCLDRPOLLHLILI
373	14274	A	379	24	323	IFGLERSRLGLLCKDNR*DNFQWCL KNFNMAAYFVCKICCAVDPHGCSLKV SFFLSF/CFFFTKSRTPVQAEVQGGDLG *LEPLPGMLPPSGLSL
374	14275	A	380	2	317	AGWPTPDLR*SPCLSLPKC*DFRG*PP CQKLFPLCIKIF*TRIK/CYLNLT*QSL PLMHFKKNVITYPILYKALPFFFLRSL /HSVAQGVQVHDLG/S/LQTSPSGFK
375	14276	A	381	1	323	VKRQPTBWKIPA/TLYPSGKGLITRY KGLKLEBGN/KSNILIKNAKEDIQTA NXYMHCSTSLIIEI/VQIKTTRTHL TVMSAFLIK*/GNH*SYSEKRTLI
376	14277	A	382	2	248	TDPLLCCLPPASLYRFS*YKIKQWVF P*EKKSLKGIQHLKGP*IKTLIKK KKVDGKTSPDPFTWYKATVLIKIVSHYO
377	14278	A	383	178	1	HNPELAI*SPCFFFFFFFLRGGL/NSFAQ AIVKQVDRDLQ*PLGLKRFSHLSLS SNDH
378	14279	A	384	312	26	FLRGVFFFFFLRRL/DSVAQAGVQNP FGSLQAPPFGMPFSCFSL/SFFFFFL VE/MGF*MLARKVSI*PFGPPASAMP VEITGMSHCLANMF
379	14280	A	385	1	849	FFFFKQTRFKLSKYNTIKS/SAPLY ISNYLKNKFKKIPST*L*FEVNLKLLK ELTFYSKERYTN*VTHKNNLT*HS*GTI FNS*IFVLHGMICRYNATSIKIPVTYFI DIF/BKAYLKPIWYKTP*IAKALKTK GI/LPDPFELHYKTVTKTVWHNLNCRDI GGNSRRKRGQISVFTAN*F*IQVTF FKGNISIFN*CLNFMSTCR/KKK*DP HLTPYKLNK*ISHLNVRKTKGLLH QKIE*KPBNIIGLSKKFFDL*ISQDTG R*SQSDHF
380	14281	A	386	3	318	DREMNALSLGNRTQVHETTSLSLCK AFB*TLNKKDK/KGRI*KNE*RLQFWD CVK*PDLRTIGVPEEGKSKYLENMFEE TIEQNFPLARDLDIQIQAOR
381	14282	A	387	1	382	FTPTRTAVVK/SDNWCNRGCSGLR HCSWECKMAQLLW*TV/WTFRKTRQPS DVCCDMVIGLPYDPAVLLGICPREMK YVHTADMSVITSVSLVII*ADSENNLNV PSADEWINEMWYIHTVDY
382	14283	A	388	1	341	HKLENLENIVKPL*TH/PLRLNQRKIQ TLNRSITSSKIGSLIKNTPTKREKKAN DGPFGPREFFRA/KKGVPITLGNPQ



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						KFRERGSTLNYFYKPGILPRIPKLGKKNR GKXX
383	14284	A	389	168	1	KKFFFFSFFF*GDRVLICHGPMNAVMT RLTRAS\TPGLKQSSHFTLPSTAGYTG
384	14285	A	390	337	1	TGITPLNPLEV\PLINTSVLLASGVST *AHHSVIESIGNLI IQALLITILLGLYF TLVQASE*FESFPTISDCIYGST*LVAT GFHGLRVIIGSTFLTITCSIRQLIHFT
385	14286	A	391	1	235	LNFSYSSMYPALFTIVP\WVFLNP*KF FPM*LIHLCTVL*YFLM\FVCLLWFM VCF*FFFFF*FF*FF*FF*FF*FF
386	14287	A	392	1	258	SCDRLFANHLNKKELVSRKYIYF*RSQ DSTIRKQTDKK*AQELNRRFSTKDLQMG NIKHMKRCS*PLAI/REMQIKTMLRHC IPIG
387	14288	A	393	2	317	LAYCNLCFLPGSSDPTTSSSRVAGNYRG\ HHDVSF*RAEDINMHEIQFISFLFIARD EVSLCCTGWS*TPGLKRASCLDLKCNW NYRHEPLCLAFFNNGSWFQCQI
388	14289	A	394	91	408	LGAEFDVRAVLTSCRLTPGVFPFLTGFY SKDHII\ETANISYTN*ALSITLIATS LTSAYSTRIILLTLTGQRPPTLTLINE DNPTLNLNPKRIAGSLPAGFL
389	14290	A	395	3	165	RNKKLKNRHRWGC*SECTLIHCWCCK LVQPLNAKAV*VLR*/LKTSLPFPAPAI P
390	14291	A	396	661	1	LCPLSFYRKCALLGFWFVCLPFVFIIRV SLCCPRWLQTPGLKSSSHLSPLISWDIR HLPRLALGANVFLI FVLMTCLR*FNDP ISLSF*QQRN*LIHLISL*NYDICTL OFTKWIFL*PKNS**LKRQCKLEKITEL /PKNRQIYPTD*MSI PRSLSFYLVL FVCL*MESCFVT/TMAVQMDLGS/L QPLPPGFKRFSCLSLRSMWYRRPSPC
391	14292	A	397	320	1	PDSKQQIFN\DETVC/KRKMPSRTFLA REEKSMPGLKASKDRILLVQANPAGGF KLKPVLTYH/SENPAIKNYAKS\TVL* KWNSKVMITGLLFTALNLSRPLAL
392	14293	A	398	1	158	CIGFMWENRILTGGRGCSL*SCHCTPA NAT\SKTISQKCKK*NMKVMICQ
393	14294	A	399	264	1	LINEFSQVAGYKINKQKSLVFLYTKY\Y SKLSEK*IKKAIPTTIPAKKEIKYLG I NLTKVDKDLNRYNYILAKIRDT\KWA DTFC
394	14295	A	400	3	343	HEQKRQSKVREVR*LSQGLNMDRKRNSQ DLNPGCRTVALSPYHTRIGALNCGRQW FVCWTFP*KKI*F*FKFWDRVLLCHLG WNAVVP*SLTALISW\VK*SFRLQLLS W
395	14296	A	401	1	345	CTRKNTDHTKCR*VCEGVFPIHCWGY KMVYPLGLKVHIFLKKVSIHLPGYTSAL LSLMIKELTFPI/CHTKCTQM/PIVULP PIVKKKQPKCLPVGELANKLMIYSHT IYSAI
396	14297	A	402	102	355	DRVIRLANFCIFGRDRVSPCCPSWARTP GLKRSTSLSPKCDHT*ATAPG/LRAI LLYFDYRCLSPDLVNFACCHFSVELWA FF
397	14298	A	403	156	3	NNKNGFP*SMLPQPSNGLVSI*NL\PLK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
						*QKWFSPFFFERVSLFHPGWSAVV*SWL TACSIDLPAQVILPPLSLNSSC
398	14299	A	404	1	364	GTRSRVITYKLIQTPWVI*HMRIRLLIQ ACGAR*MMWIL/MIILIGI/TCRITTYC* WRDVTRESTYQGHHTPPVQKGLRGYIML /FITS*VVPLSCVI\WVFF
399	14300	A	405	3	365	HQTSKNIPLSQSPIT*SKILMLNMQA ERGSEAAEKKLASRGWFMRFKGRSHVH SAKVCGBAAKADVETASYPEDLVKRTID EDGDTYKQIFVWVKTAFCWKNPERSIS TAREKKQCLP
400	14301	A	406	3	356	HRSQDTYAN/KLDNLDKSKPT/RYVK LQKLTOKELQNTNRPTTR/ISIKKKKK KKKKKKKNFSPGGFTGSIPTTFKQKPK IFKKFFKNLGGKTLPI*IYGAG/IKLL PKIKK/DPSKKK
401	14302	A	407	116	362	YKYSLTQKLYNHSYIKNNHNKNNRNH STTTITTKQPPPGFKRYSCLSFPLS*DY RCTPSCPWNLF/CVFLVETGFHVG
402	14303	A	408	3	360	HEVRINDAFERNRGGGRNRRKVDWILNY RMWFHLIF*ARCYSICRIHAYYSCLIGP VILLLLFVLIILLPCCL/SFFDYF/VWVF FIFFYSSFFLLSLFFSLFL/CFIFLYF FIF/CFYLYFFFF
403	14304	A	409	388	1	ALLKFPFVKVLKPP*GSFPP*GF*LLS /LIFPPIKRETLFFFF*KKVFLCPDPM SSMARSVPAGSVFVKARSLSLSLSV PPOVOVNGFLTFFFFPSW*RGCLPLLP RMVWNSWAQALLDNDPS
404	14305	A	410	1	386	VFNARESAV/YWETMPQRKPTR/BERQA P*FQREIS*YCANAVVPTIRTHHCKP ANPQALKKKKKKHQITVFWLYTKK* TMRITFLDNFCQCFVPKVRKYLASKTLPL KVLILILDNAPGHLKPHFN
405	14306	A	411	2	417	AHHIFTARIDVDAIYFTVITTIIDIPT GDEPFS*LATLR*INMK*SGAVL*ALRL IFLFTVRGLTGIALPDL*LDIVLHDTYY VGAFHYGLSVGAVFALLGGFID*WPLF \SCYTLDRPYAKIHFTIIFIG/VDLAFF P
406	14307	A	412	295	397	WQWPGTVAHACNPRTLGS*GGRV/TLRS GVRDOP
407	14308	A	413	437	3	PGFOSLIGNLIPASGNRKSXSCVVCV CVYKVKKCT*SLCEHFTCLDQICVR IGLMW/CPQNCWCVCBGLDRESVCV RLCYCAWAWWMSGSG*VCGCSCWC ICVGPLLDSLECLVC/LIAGSKDCGL RCRLPAWCV
408	14309	A	414	2	392	HLQFIFFWLLKIPHYL/FLWPFYLTSK ALFYLO*QKRNMYEVFNRGLFF/SCGE GVSGSPASSSSPSCSSSTGGGAVGG GLGFVCFLLFWGFWVFLFCNFWCVG WVWCWVWVFFLLGV/CNCFE
409	14310	A	415	376	1	GFOASKDEL/LDLG/ATAAGDLCKKPL IYNKNPVLKKNFAKCTLPVLYR* NYANWTAHLLKSWFTDVKSTIQ*KISF EMILLINNVGHPRTDWMYKELANF\N PANTSIP*PMDQGIVL





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						KYGERGLFLANGPYEPGLTLIPKFGKNGG
435	14336	A	441	320	1	WGNNWLPSP*EKKGRPFLL\SHPKINSK WIKDLNVKGI*KFLBGGQIG*YLMIFGV EKGLFRGGPKYLYKRY*NRLLLFKR YFSLTEKSPARICHIKKLAKK
436	14337	A	442	8	391	ERLRIDQVGLIPGM/QSWRT*ESVDE I/QSV/NQLPKTHITLTSVSGAROKF NTYS*FLGKTEKERNFTAWIKSTCTSP AASLTLEQKESPP\PRSGTRKD/CLL* P/LGSGMVLALGTAERTTRKEK
437	14338	A	443	363	2	HHVQACLELLTSGDPSNLASQARITG MSYRAQLSIVTFSAAYPLVV*KLSHARGL ML*QSIII/HVLHFHQVQGAHV/S/PEN SQPLHNVPEFDKIF*EHQRKTVPPIHTA RKLQDLEPLV
438	14339	A	444	1	900	DSSAGIT/GICHAQIT/LFVFWETGF HHVQAGLELLTSGDPPASASHTGGDYR HEPPLIASLSFLNKLCTWPERRRKPIF SLPKLDPNKRKPSFP*LP/IGS*TLIN SLFCFRNVCTQLADPTKSIAYQSSLMKP FQKSLICFGSEKFPDKVYLFSSDRJAKE QVLVVVVVVEY*I*DSACQ*ALGF CY CLSIN/VELPKEFELACSLPSRNDL ILSLKXKQSNSEFFVCFEFKXSNFVP QABGQPLFG*LKLP/LPGFRNISCLNLP GSC\QTGAVPPPPVNMFGPKKNRVS P
439	14340	A	445	3	346	QIGRVKELNK*VPEHPSKGL\FLBASS LILCNHNSPFLSRIVTNDENWILYDNN* QPAQLLD*EAPKPNLHOKKKKKGLAP FWGAPSRGNFPYFFNPQCKLHF*KFSSQ KRG
440	14341	A	446	2	246	FRGKTRALMHWBEGKMLQL\RKVWQ LLAMNMLPREPAAPLIS PRER/S TTAKTCA*MCILATVCTVKKHRLGL
441	14342	A	447	38	393	VILHRQGLSL/VTCARVQWYDZNSLP* TPGLKQSSCLSPKSYCHG*LPVVVVVF KMM/GFTMLGLILNSWQ/CNPFVAVDA QIAGIRGFHS/VGQAGVQWHDLSLQPL PPGFQPSHLS
442	14343	A	448	54	540	RTPFHAAGFLQSSHQKHCLLHPLSQ VSSDQ\FRKGLSRQSGSLYKAFLL HDCFKRQSDPSCPNERYLLYREWHF RSIY*KQPLDLIMKYGKIGIYFAWLG YVTOMLLAAVGVGACPLGYGLNQDNCI WSIEVCHPDIGGMIISAQDRDL
443	14344	A	449	2	310	FFFLRQSL/DSVAGVQWDRDLGSLQPP PPOFK*FSCSLPSSWYRHAPARPANF FLYP**RQGVIMLRNVLIS*PRDLPS ASQAGITGVSHHAWAKISL
444	14345	A	450	2	466	KQRLFSVDRTAFYWKNNKSTFHS*REG TASKLFTNG*ILLGPNAGDLGLKPVFG DDSGNLRALKNYAESPLPVLYKWNKAW MTAHLPTAWFTEYFKPSLRS\FRKISWK I*LFMDNGPHIPRALMEMCKE/NAVMP ANTTSLQPMQGVILI
445	14346	A	451	670	212	SSSSP*GS*YQNRNTIPSPKKKCTKK\ KNNHYS LP*DAELISN\LANAQQS I

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						KRFTIRHSQGLGFTILAVLGHVNIQTPTNAT CYTNRLLKKNHMTILINARVLYKIQPSV I*KLFPDLRGAP
446	14347	A	452	407	219	PLISLRNRNHLGPGVQGCSEP*LCICTP AAMTE*YPIPSQNKTKO\HTRQKQH KNKCVKN
447	14348	A	453	2	395	WFLMFRRESHLH/RVQNERAASADVEAAA SYEDLAKLIDAG\AQIVSVBETAFAHH KKVPSRTETREKTTTSALG/RCLSLSV DNAAGHF*VEA\MLIYHSDNPRTL/N/ VAESTLEVLVYKNNKAMTACLETTS
448	14349	A	454	424	38	EBTEPL/HRPISSAZVEVLVINKLPL/KH KSPRDPDGPIAEFYKQKE*LVPIILLKLC QKIKEBGLL\NSFYEASISLQ\NSGRD TV/RKENFRPIPFPMNIFAKILNKLANC IQQHINKLIHHYQVLPSSLSHR
449	14350	A	455	2	309	PRVRSOTPGHKRSTCLGLFRCWDYRHP LHPATASFLVAAPGM/FADPP/CNNHLL NE*MNE*MGGDASEILSFMRSHSVTQ TGGQWCSSHPQPGPPK
450	14351	A	456	3	441	DAGLVLDRERPFIFPFFFFLGNQGYF RGPGGRPGGEGPMPBTSVSVPKILLRGP QGQGGKARKPHPLGPRGPNHKTG*KR AYPTGSEVLTETPKPTGPGNGPETPV IGKAGAGKPLNPG\MOGSRNPKWAHCP* TGGKKK
451	14352	A	457	1	234	PTRNHLLGLQDRCREPRSSHCTPAMAT ERDMVSKKTKG/EKF*KGRTK*MS*VE QGGSGGKGLPTLAISNPLPFF
452	14353	A	458	42	470	KRTPOLKESPLPLGHPGKAVGKINFPF PRERPKNEF*KKKTLTKTPPKQKFLRKKS PFKKPHFLYSKATKKQKRGKKGRAPP KKKKKKENPKIVIFRTBITVASPVLSWA VKPIIHHFFPREKKDHA/KPPPF
453	14354	A	459	2	393	DRPIEQWNKRERPRINLYIDGMIFSKG TTAFS/WK*NLCKYVNAWIC\NRKN PYLTSSRKINLR*IIDIKVR/PKALIKLP EQNTRCSL*VLGVGRDFLENMNYTRKK\ IGKLDIFI KISQLGMVADTSNFI
454	14355	A	460	338	33	GBEKTERSPFFPISSLCFVF/AYL*QQI RLLIPTNRSRLFIY/CLFLFMGSHFVT QGVQVCHHTLQFRPLGLGQSSHLSSL SSWYRHLPLVLKWTBNCV
455	14356	A	461	77	435	AKVVESSLTARETSLQGGGQGGQGG KHKH*PRIAKAI\LS*KEHTTLP/ELQL CYRAMITKTAWY*HNRHIDQNNRND KYNHITYSLIFDGGPKSI\SLPNK*CN EYMIPICTR
456	14357	A	462	157	3	NGRVDLKIQKJARCGGALQSQL/ROBN HLNPGEGKCSBS*LHHTPD*VTKQ
457	14358	A	463	363	3	PSVAQAGVQVCHHTLQGGGQGGQGG ABA/SQ*LGQQQATALYIHKYILFPCN VLISPIFPFFFLMRSHSV/SQARVQMH DGSPPQPPPELKRFSWEZLAVSRDRAT ALQPRQ
458	14359	A	464	3	396	LKEIARKVKRIKFKQQLRL*MKRTINR YLKEN/LNOLLEIKGTLRELQNAVSSFN NRL*QIERGISKLEDKAF*WTSQKIRK

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						INK*TK*TDVYKEPNRIIDVPGGEKA KSLKRLFEVILERNFPGLAR
459	14360	A	465	399	1	PPGVILNGPPFFFFFLLGLGPGWVFGQPL KTPILVFPFNQYHIPPCKIRIF/LPTR PPQVPPICP*PFSSPWGLKVPFILLSF FFFL*DRVSLCHPGWNAVM*SQLTAASN TW\VK*SSHLSLLSS*DYRCVLS
460	14361	A	466	279	1	TNIFNPREVVGSTDAGPLNNKKEKENV KRRQATQWEKIVAKDTSDEGLLSKIYEE LLKLNKNTNK*/ILCLKWSKGNRYFA KEYIQMANK
461	14362	A	467	2	436	RGELPRLQDKLKK*TAIILANGREL/R/A CPLRSRTOGQCSLSPLL*KKFPPPKSHI ESLLFFNIILEVLVSAYQENIEIKIVEI GKEEMKMYLPTDGNHLKNSERIRN/Y8 KVAGYKVN*TIITIFYISREQVEFIK KTLSMNRFF
462	14363	A	468	2	420	RTIALP*AVRQGLSLQRIILLSP/CLC PAARGSAYIG\ROASMSRGLQAQASC LLCLPQAWAMGAPPSASILLPCSLID RCASSQPSDVGVPSEAGVGNLVVRGL LSRSEKR\NIRLGVTFRSVC/LSPSL TRR
463	14364	A	469	1	416	PSP*PTGALSALLKTUGLAN*FHFSI TGILCLLITNTLTLYQ*WRDVRSTYQ GHT\QAVQK\LYGLLLETTSBSPP AGLV*APYDSRLPTQLRSHWPSITIT PLN\HLQVAVLGEPPVLLAS*V8IT*ADH
464	14365	A	470	211	398	IFFPPKGGGGLSTILCWRKRRHFKK*K* STCLGLPKQWMEYRCPP/VPGQKQKFRP *KTKSKPPPLVSGGASASNIKL*IALPP FLEKKKFKKQGFDPFFLPFTQNPQGG NFFPGKI*YCPPIFFFLLRRSFTLWAQA GVQWHDGLSLQPPPTGFRF
465	14366	A	471	62	424	TLMHGKWKQWVHLLKTVLNLLIKIN/ RTLANH*PCNPAILLGVSLREMITVH KKPCP*MFIVALPMVTKNSKHLKSLTC KWTNKLMSLYTMKYIATRKELNLNHR SCRNYSDDMS
466	14367	A	472	427	20	LGLRLFPYQBEKNPYTLPAPSPPPPP MSLYNSPIYPGKGFLLPSKNNKIPPLN FLRMSHL*/FALLGNKDFHLLGLGSP IGIMGNMATTSCMFSSVCLFP/CFE TGSISVQAQGVQWCHNSLLGLPRLK
467	14368	A	473	424	98	NNLYLYTYTYTHLE*RGGL/D8AQAGV QNHHCISLQPRRHLKQILPPQLATSN NYRHKPPRLSPYVQAQGL*LLGSSDLPD SVSQSAGIIGNPLHLASL*FLFAPP
468	14369	A	474	415	75	NHPLKFFPOTQANGPGGNKFFFLKTRF CFFPPGKRPWAYKSLQPPNSGGQO\8 APTP*IKGAPKGGPTRVKFFFFFLP/L KWSLRVQAQGVQWHDGLSLQAPPPGFM PFS
469	14370	A	475	3	413	PVQKGLRYGI\ILCITSEV\LFAGFF* AFYHSSLAPTPQLGGHNPPTSITPLDPL RGPLLITSVLLASGVIT*AHSHLIEN/ NRDQIIQALLITILGLYLTLLQA*EYF ESPTTISDGYGSSFFVATGPIGLHYI

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470	14371	A	476	1	440	ITLTDRSLSY*ANRL*LAYTITFTV* IPLYGLHL*L\PKAINVAPLAGSIVLAA VLLKLOGFGVIRLTILNPLTRHIAIYPL LVLSL*GIITSSICLRHDLKSLIAYS SSSHIALVVTAILLIQT*SPFGAVILII AKHITSS
471	14372	A	477	2	397	LFVVRHIDGATLYLAGA*IGVLTGELS LLIRASIGHGPNLGNHIIYVIVTRA FVILLPIELPIIIGGPO*NLVPLIIGA TDMANPRINNLS*LLPPYLLLLASAI AEDGAGTGTGYPLTGNY
472	14373	A	478	442	44	SSSSPTTPPRGKFFFKKTPRKKFPS/SP GNKGFFSPDSP*KFFFFNPPFFPGGFF PNFPPPKKNFFPKNSGGFFFPPLKJKKI FFPPPPINAFAPPKVFEKSPPPFFFFF FFFFFFFFFFLRGHGWRGSI
473	14374	A	479	1	439	PTRSRTPRLVLDREPRPPFFFKKGGPP SVPPAGGGGANLG*GNPPPL/GVKKFFG FKPKKIGR*RPVPPPGGQPCSPFLKKN GLPHGGQGR*N\PPPPR
474	14375	A	480	420	0	YSPPSPPK/YRAPGKKFF*KKPRKEKF* KKKILGFFPLSLPKFFFPKAFKFFGG VGHCCPPPKRFFSKNSGGF IKPPLKGG KNFTFPAVKGPPRGGFFGPPGFFFF NKT*WTSILKSTK*SSSSSSSSSSSS SSSSSSSSSPVK*IKKCTSLTISSS SSSSSSSSSP*IAKKIKIDS*PKWQGC REIGLTV/LVQPLMWQFLKLSMQII*D SANMILSMHARG
476	14377	A	482	3	335	HASGRDHTDORNRIKNPEITD*ITYSTF *QKC/RLI*WRKDSLVNKC*SNMA/SP MKKIKLDLSSSSSSSSSSSSSSSV*NV KILQNNVOGNLQYRGLVHTVDVKAHI
477	14378	A	483	1	418	GVR*FSPINPFSRWGPKHSPNLL/LNFF FFFFVFLVETRFHPVQAGILELLOSRA PASA/FPK
478	14379	A	484	1	356	FCANAVRSMIKTLVLDKATKP/RAMKON YKHLVPFNCKGRT/DSGNPTNMFYQC FVPEIRKYLARVGLFPN/VLIDNAPGK PEHHEFNTSGFRVFLTPMPLIQPLEQ GVLTALTA*VQCFVPIRKLRLVGLFP NVPLILDMAGIHSFSTSGFRVVL TDMPLIQPLEQGVLTALTA
479	14380	A	485	166	406	PIFWSVSSSSAEGGNSV/SSTLRVIVR PDETVDVT*HLLKK*CRCAVAHACNPS TLGGRGRL/TLRSGVQDQPSQHG
480	14381	A	486	107	429	FWVYTFPGFFMLNPPGGELMPPPCPG NFGGNFKKGQFLLPGGVTPGPGIT PPGPFPGK*RGPP/SPGPGFLGKXG GGP
481	14382	A	487	399	2	GSTAPGLPKWGFPGGPPGPKFVFFKL PKGGFPGAELI FLEFFQRGKGLGP:FP PVFLKCTEGGTL/NSFFKGRVFLVFKP KAGPKKKKKINYPILYNNITDKFFNN MLANRI*QCIKEVMQDTRG
482	14383	A	488	419	2	PPPPPPPRKGGLYPNKILGKSPFP RNPKDS*KPRVLPFGPKPKPKKFK* FGPWGKPGDG*RNKPFK/PPFFFFF



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						*DGVLLCRPGWIAQAQSRPLQEWNSIS KKRGGPCVLGLSGSEKVPANADANADAN
483	14384	A	489	629	0	SSSSR*SLICKCFRN*GEKIRNPFRWA KVMHRLFTKRCINI*QDVRSTSLMVRT *ITTTLRVHPSIRLSKT*KLNRILYG* DOGETGIFHOMNECKMF*VL*RE/VWQ YLILKL/LHIPVDTA
484	14385	A	490	2	351	KRPEDHGM*GY*VNDGGDTTYQQNE ELRS/WCNDNRRLAKVLJLYFP*PHIT ELNSKWT*DLNLTSPFLVLENN/I* F*HVGIGKHYI/T*LT*HE*K*INLH ENIMYCL
485	14386	A	491	42	507	NLAK*IQ**IQTIMHDDVFPQIQGN LNILKSNINIYYTNR*DKHTITISIDA EKAFDKI*YLFMKGK\KPLSQLGBGN/ YLKLIKGIIH
486	14387	A	492	18	417	REGKESR/VHFNIRKGRVMSTGR*KIQL /SHSNAHSNQAQISESQPHLHDFKXK KKKKKKKKKKKKRGRKKKKRGRKKKK KKRGGGGDP*KGVRALPCTFFMRKKFFF VGGGGGKPLGCLQADPLMGA
487	14388	A	493	413	82	FFSSPPPLPFFPHLFPDPNFFFFFS PPPPPPP/PPP*KTFFPPPPD*FPDPPP LFFVSPPPPPFWWWSPPPPPPPPPFF FFPPPPPPPPPPPPPPPPPPPPPPPP FFPPPPPPPPPPPPPPPPPPPPPPPP
488	14389	A	494	1	413	PTPTPTPTPTPTPTPTPTPTPTPTPT KKKKKKKKKKKKKKKKKKKKKKKKKK GAKKKG/EKKKKKFT*KKKKKKPPGK GKKKKINGGKRAKTPQKKTP*GKKKI LKGSGGKKNPKPRGGKKFFGGKKKKK
489	14390	A	495	274	1	TYRIDCAVKKVSEKSTISLPHKMLE N/QLNPK*/RRREIKIGAEINEENRK *IREKINRTESYF*WKISKDLAKLKKEKT QITINTRRAY
490	14391	A	496	336	1	VFOYTTINKVLSMFTYCFPL*RNGLTVLL RLVNSNG/PQD/LPSSAS*VAGTDAHR HTQLCFITLSDLEPYFHLGSPFISLL* FFFLNTRSHSVVQGV*WNLGSLQPLP
491	14392	A	497	445	382	PRVLI*FLFTPRGPPPPPPPNKVFPPPP PPQNFPPPPPPPSWGGFAPK/PPPPPK SFFPPKPPPPVPSPPPKKFSPPPPPH FAPPVFFF*PPPG
492	14393	A	498	430	2	SPPPKPTM*VKVTPGR*KKGGGGGGG PILSPILGSKGVVPA*VKGR/PLPG*A GKPPFFLKGPDPYRAGGGGKCPDLSGL QKKWGTPEWLLI*PKSFPSSSLVDR RTYCLAKMLLYTSWMLLPASCLNLYT FPIV
493	14394	A	499	363	3	KKLVTPAKVIGDIPENRFTLMPQOREN FLCQVWMTKPTTIFVKTCKGKWLILSL KRFCPAKKKT/IKILVNRVNRQPPWEK IFANYASDKGLIGSLYKDLQVYIRKNN PITK*VKGMY
494	14395	A	500	145	435	VFMCSINSLFLFIPWYETITWVPVTCRR T*MFIALALFVLRNWH*SRCPSTGNW/L KLWYIHTME
495	14396	A	501	162	1	FYNVTIIPYIPIPIFLRNL/DSVVHT GV*WRHLGSLQLPLPKFPDPLSLP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
496	14397	A	502	343	2	IKKFRMGPKPPLKEPPGV/SDEPFL/N FGNPGVPVKDFKPNFPKCKKMGGRAP PVVPTTPGG*MGRRFP*PPAFGVPRGGDG SPPEGAPKEGSLSKKKKKKKKKKKKK KSARL
497	14398	A	503	23	405	KGRNYLWSEKKKQMLVRGKIGGGPPPRI PKF*KVIFKTPDGGPPPPGPDLPNFFFF KTDAPLFF*NHDPKSKIMALAPPKKKIF LNPKKPPPPPPPPHFFKKNFPRAFFNF AFSPRGASPPF
498	14399	A	504	418	247	PPKNGPVPKPRGGFFPPPKGKKKFFFP PDG*EGPDGFF*RDPLHFFFFFFFFFF
499	14400	A	505	26	426	GCTGLLH*MYAKIVCCDTHSET*VLSF APISRISYSPTHPQLLFF*IFFFLVLE TESCHIAQAGLK/LPASLSL/VNASQA
500	14401	A	506	337	2	IPNLKESA/CPNLKPGMGFKD*PPPPSQ ISLIFKYPKLKFBI*KKKPLKGLFW WV*KKKAPVGF*Q/ENALGKFFFFFFFF FFFFFFFPFRRSFAPVAGAGVQRDLG S
501	14402	A	507	454	2	TSKTGQPGRRGSPFPT*WAGQKRSSPP RRGSRAEALLTSOTGNPGRDTHPFDG RPRGAPLFPDGAAGQRSSLPGRG/VP GRGAP/QSQMGQCLGRGAPHFPDGVAGQ RCFPFPRMGSOVEALPTSQMGQPDGRPT HTPCGVAGQGR
502	14403	A	508	390	13	RIPPKSRWKGQPF*VS*NPBQL*KN FLPPDP/K/YGDPGPPDPPIKFLPLKK KGAPPICPGCFEIPAFRESPLAPPKS* NSRGNPPPPPPFKKKNPLPWGKTKLKL IFFFFFFEAGSCYVA
503	14404	A	509	2	282	WQFLTKLNLTPVEPVMELCIYPNESKT* IYTKTYA*ILLAAFLIMAKTWKQGVLLK V\TDKVNHIHMTY
504	14405	A	510	400	250	LLSVTAQGVQWHDHSLLOPQ*PLK/HP PTSAS*VAGTIGAYHAWIIFFF\ITY CRDAVLVYWLGNFPGKLLKWDYWC/P/ RMSGLLVFVWSDLGFRSEVS*ILLSWDYR CVPCPLDNFFF
505	14406	A	511	99	242	VTREKGGHFRIRK*LIHQETTTNTNGV PNNRTLECKQKLTKEKEI
506	14407	A	512	139	374	SLWGRITFFFAGDPHPVPQAGGA\WGN HG*LQPTPVGLKKSSLLTFPIGWYRLG TPPPANFKIFCRGVKPKCCACF
507	14408	A	513	23	401	SYCLRLPKCDYRSEPLFALCNFL* MKGVVWMPFTLFFFLFLHKT*LLQEN FVYVCLKKNTKLA*TSQKNGTGN* ILVDNLVLS*KKWCKLWGSILFF/NF LRQSL/NSVAGAGVQV
508	14409	A	514	7	386	FFVFSTHITLLFLIFLFFFLFPRPPGPF LAGEKNTPPAPPEKPPPP\PPKKRGDP FFFFGPPQKKGPNPSPRGGRGPPPPRPP KMEKGGPPPPREIPPPPEFF*PPKTIPP PPGGGGGCKKTPPER
509	14410	A	515	370	2	FVFFQVVLPS*NSFLSPFF*KGLC*RD LAFKFFPPPPNNKKLWPSL*GFLKNS*K FNFLSKSLVPPFF\CFPKFFPI*AFP RFFFFFPDP*RG*IFFF\*DGVLLCHP



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
523	14424	A	529	57	485	RHSSLGNKSETSQSMKKKKREKKKKEL SFDPAISLSI * PKENKSLQKD/TCICM FITALFIIAKTQNPCKPSTDE * INKRV \IYIYIYIYIYIMKHYSPIKKNEIM/SF AATWMBLEAIIISETMQQKAKYCLFSC I
524	14425	A	530	399	3	FFFFFFFWENPPPPPK/WRGGKKQAP FFKFFKIKK * LFFF * GGGGGHQKKKK KSSSFFFFFFF * FFFFFFFF * FFFFFFFF FFFFFFF * FFFFFFFF * FFFFFFFF * FFFFFFFF P * FKGLLCTTHASAHASAHAS
525	14426	A	531	491	4	SKNIKDIANETK/TKKFBET * VKLPM LGLGNDLSMTPKA/LKIDKSDMTKIKN /PCSSD/TKIVKQITWVKIPTSYYI FDKSTSRCTCKEL/RQQONKPIQCKSK VLNRFF * FREDIQLSNKLMKGCSTSLNH
526	14427	A	532	184	309	PQWPAHSFLPALGSSSGIPY * VVKQTFD SKDKESSQ/WSHETSDRPKADHRRSR PSLATSP \ PRLPHPSPLPNHISGLPISSL LPWGAVALAPTHFSALAW * RPLPCNSQ GEKFFFWPGFF \ BRSHISATQAGVLGID LGS LKPPPWGSGKGFPCPSYSG/NNQKN HLSP
527	14428	A	533	401	3	VIREMQIKPLHIQ/PGLW * SKSVKYY * Q GGGS/NVLHI/MLAT * IMGPPFKIWM QFLKLPYGVITLLSGIILWMBKKPP KCTQIFLAAPFIQ * PSESNYNINHQ KNQ * DUHMYHTMYVYLALMBIH
528	14429	A	534	419	93	SLATKQ * YKIPFYTRVAK/TEKSHT KYWKRGHATGTLHOMWECMA * S * KIW * FLIKSNINLPFNPVILL * GIYPREMKT CLYKD \ CM * MPMVAFPIBONGKQPKCL
529	14430	A	535	414	2	NFLARGYINCGPQFFFFP * PRELNKGV LSNTFPKL * KGGIPGDGPVK/KINFTFF FLFFFF * KKKP * CSPLKAK/WKIFGL PKPP * PGLKKPSFLTPKKGDKRGPPRR GNF * FFFFLVFLVKTFFHYVQAGLK
530	14431	A	536	32	435	DRATLQIG * KSETSSYKKKKKKKKKK DGGAPLKKNPGGAKKPGKKKNTPSKR GGKKNPPGNF * KICTNPGGKNGAKPQK KIT/AWGKKKLNKGRGGK/PKTLGAKK FPPEG * KKKKKPAAKPGKSS
531	14432	A	537	348	1	EYIKSTHMGKNTPLKNTVSSGQ/VWLS PVISAPLAKSSQKPKCKRHWKGL WCV/WCVVCVVCVVCVCMYHSAKNE LMAFAT * MRLETI * IISVETQWNTKTR NPSL
532	14433	A	538	523	66	TDQTSHTNPLSOSLQSEVPTLFSVKA E * CEEA/AEHKFEASRGWPTLKERSL RNMSV/GEAAGSPEDPATV/INGGRTO PQIFSVABATLNKKTCP * PFI * GREKSM PGFRASKDSLTLGRDFKTLCLVPHYWN AKHVQVYILLKVTAKI
533	14434	A	539	413	2	RDV * PCRSWSQTPREL * STRLCPLKC * DYR/R * APAPGP * FL * VHRHVS * I * FKS PLSCRCSNFQD/HDSIKPSFTI * QYAH NKPOL * T * PDTLIF * FLKNSFTFVAQTGVQ WHNLSLQLLP * PGFKRS * DAWADAWADAW

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
534	14435	A	540	385	2	MASKHIKT/CARQLAIREVQLKTTQYHV I PTRMAVKKT/DNECWGSC*NTLINCW WDCRMVQLLWKK/SVWSSRGKMTVQLP CTPAT PLLGIYTELKTCSEHN/T/CT* T FIAALLVIAEKWK/KCPGABEW
535	14436	A	541	44	398	RPPFFFFPKRPLWKKQGFPPPA* RGE IPSAKK/VPLGPVSGGNPPGP* KP/PQ NPPPLGGSPFGKKPPLDLPFGGPIGKK KMGSPPLAGGATTGN/PPPGGNFWGGK APPFPQKF
536	14437	A	542	370	10	FFLRTRVSLFPFVQ/KVQQLIAAPPS WQCVIPLQSP*LRQKDPFSPGG* GCS EPCSCPLPAWMTEDPNSVKS* KXKKRKK ERN* KKKKFIINTTGIRPRIH
537	14438	A	543	1	370	FLLRHTLLCHPGFCSVATYCSRDPGS D/PLPQAPLPDQ* PRLQA/WHRLAPPH SANFF** RQGFTVLARMVISQPCDP PH WASQATATKADDYQK
538	14439	A	544	50	395	TPGLTRQMLDPCSPSTPPYT/P* VQP STPONSSSPKTHNQKGLPMP LSPTPKP STAWKRAILEHTSSSSSSSSSTCRNR NGYTYTVPEHRPARGHTASQTRKQV LAA THKP
539	14440	A	545	1	370	LCSVTQAGVQRRLNSVQPPFFPRKQVS CLSLFFFFF* KRVPTLEPRLSGRGLI FMSPTLR* GDPV* ASKLRTKGS PH OQQLINLP/CLGATGPTYGAQGGFKSPG LRRWAPLGPPRA
540	14441	A	546	178	365	YKKTDAITXNOK* DSTRLKGSFSTVRBT INKGNR/QPTWEKIPASHTSDMGLISQ ICKELKQ
541	14442	A	547	11	236	RGITELVVKLSDFKSYFCAIVIKTVNR/ WHKYK/HIDQMRKIQNPINPHIYQMI FKKRAKNKQWKDGLHKR* WSNDFQET COBOTMEKGRSQEKAM
542	14443	A	548	355	3	IRIKNLGRIRFCFQBEKTP* TKRKKP LENPGGVFPNPGFPPFFKAKIPEGPF FG V/SFF* RGGFKGYPPPLFFFFFLL* DGV SLCHPGCSAVAQSRLTASSASQVHALL RHVDEGR
543	14444	A	549	1	373	CFLICRHTSHMRWIFQTTAINQIQW*K BSQRVVSQ/LYI* KLHLVSVQ* HFV*K YTO* LLENADTK* AJAVGKVLIDLLK ALSLIPRL* KMK* NLGNWPGHVAHACN PSTLGGQGMILTS
544	14445	A	550	446	2	NIDKAPTVLGKRVSTPSSRSPPGP PC CWCHRRRPPRPAYFGI* ILFLTPP* NPL NNSPQHLGGKLSGIFSDPSLSVTFSSFF FAPDPKKFMLCF* PFFFFF* DRVSLCH FGWGAVERSWLTAPISQ/IR* SPLSL LSSWDHREA
545	14446	A	551	342	26	WAPFIFFPPPYKRSPOKFFPPPGENSR GF* LPG/RGGFFKXGLSQFFFFPLK KV FFFS PGGEPQGYFPPPYASFLKRIFFPP PP PIKKGDPGRGSPPRGNINPPF
546	14447	A	552	3	167	QPHLQDCL* QONPVAVG* AFSSHP RDSL NNPW/WPGA VAHACN PSTLGGRRGRII
547	14448	A	553	3	413	TLTALSSH* FFT* VGLINMLAIFVL

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						TKKINPRSTAAIKYPLTQATASILLI AILFNILSGQ*TIITNTNOYSSLITIM AIAIKLGIAPFHP*VPEVTQOTPLTSL LLLT*OKL/APISFVVOISPSLKKK
548	14449	A	554	441	1	SSPPPOARGEIPFF*INPGEISQHNKK EVPPPPPP*KFFFSPKAFIF/RGGGGPK RPPPKKKFFPKKTPRVFIKPPQKKKKFF FPFVKPVPRIPIFKSPPLFFFF*FFFF FFFF*FFFFFRRGCDRWGKFNIL RGGF
549	14450	A	555	3	455	NTNSMYVCIYVFLRQSL/DSVTQGV QNRDLSSLQPLPP/GSDWHRHLAQ*YL FNVLLELV\FVYBERGTIMVPI*DCNVN CRVFGTRSLGVYCVMGIFYRC/HIESML CDRCIFDFDIGSHSVTQGVHNCNLGL/ MKPLPPG*RNFSGLN
550	14451	A	556	1	299	RRMRQENRWNPQGTGCSEPSHHCTLAW ATRHDSVSKKKKKIRSLGKKT*FYHNI LKAMG/CITGIHKGPEGAWQREGHPTTP QQPKIAPORGOTYDPD
551	14452	A	557	3	391	PWWNSFEASGWLIGPQRSCICINIKV QGETASASVAGVSYPEDLAKITDEOGY IKQIIFNVDKTI/TY*KKISSRTFIVRE KSMGPKASDRLH*PLGNDASNP*LK PLLCSEKIPWFFSRKKS
552	14453	A	558	337	1	TRPFFETAGSPKSPFTRVDPPLL/RE RKIFPLDEVEVGQFPALCFPGFLFN PSKRGPPGFWLPGPF/CTPKFLPKPFL GFFPSRRGQFFFFFETVSLQPS*SAVV Q
553	14454	A	559	117	419	IPPLLLGVGLFFFFIRKRGVFSPPNR GGGNSFGLLETPPLGIDPFGLTPPKSW ELRAPPPPIKF*KFFLKGQGF*WVSPG GLEISALLVFA/SASQ
554	14455	A	560	347	1	TYRKLQCLRRKSNLYLTKWAKNPNRHF SEEIOMNRQMKRCS/TTPIIREMLIK TTLEVPASPVKMAFI*DR**MF/WQR CEKGT/H/CWCEKSVQPL*RAVRFLK KLKILFL
555	14456	A	561	2	375	IPPLQAGEKIFMI*TOAEKAPYKIPF PPPIK/TLNKVGIKGNFPHIIRAL*EKP PAYFKGBASFPVRSGRLCP*LLULLP HEVLEVLVRAICPLN/H/TKG*QCKGE ASGSKKKKVPFTRGSDPLGNVPLPL BGGKGF*P/RWQGPDKLFPQKQGN PFFFFFLGPKGQGFPPQGEKGVGFP PKRSQRPF*GEKGVPPP*REKDPFF PFFFFSETVILLPKLECS
557	14458	A	563	384	3	ISDSGVHPLGPKRITLCQLSYHWD*P KCFC/PHLCLPMTLPOPP*GLSPVCAPS QOEHEGCFPIVARQEC*PLFPKILDT* HFVGNLKPFFFF*DGVSIGHPGWSAI LTHCNLCIPGSSNSLPQ
558	14459	A	564	522	120	SLFLPTLCEGNTISARYNLEHLSGSDCP ASASIVAGITGNCNLCPLSSIDPSTAS *VAIDLRK**GARGNCPS/VLRKQWPE AEMRGESASWMDPLGRPGVAKICRR HCCPVQGPQVSWPSPGASPN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
559	14460	A	565	73	264	KDRHIDQWNRIESPQIKSMTHLSWPDF FLQGY* * KDRHIDQWNRIESPQI\NL*L YIYGHLI FFYKGT/IQWRKKTLSKKNF WDNHI FKCKQ
560	14461	A	566	413	1	EKKKKVPSQVLTTPKPVIGNFPFSEEQ *LSLV PVSSLLPQLSLGKNQGP*ARRVA LCPGKSPGSGQIWF/RLP/EDIVTVVQA SVSKRLFLSLDFQVLRREGAVNSA NLSLAEN
561	14462	A	567	397	1	FLGQSLTVAMARVQWCSHSLKPLPLGL KGSRSATG/SASPYLVMPPLSNLFVHV YIL*LYKTMGI*MEM*PTSPCMYSVV RDV*IFPSFTEACPVAGLQWNSLGL PQPPPPGPKRFSCLSLLSND
562	14463	A	568	437	1	KFSEDPAKLIGEDGYSKQVLAN/ETA LYWNMLSTFLARKSTSMPSKLQGTG* LLLGANAAGDPQLKSMLTCHFKPRALK NYATSPLPLVHKWNNAWMTVHMTALL TEYFKPTIKTYTHNTTGSLLTPHSAH ASAHAS
563	14464	A	569	234	1	FPFPFPFKASSPPQGTSSSRGVF/PEFF PPPKKGFPFKIPGSSSSPPFF*EKTYFR FPFPFLAPPGVFFR
564	14465	A	570	2	396	FS*AFHFGALATPQLGSD/SPAGITQV ESLQVFW/VNLSLLASSEEIT*ADENV IQNNPRIRIGALLITVLGLYFTLQAS ENFKIPTTISDGIYSTFFBCAGLHSLH VIIGSALLTICFIPQLTDFC
565	14466	A	571	3	403	HASGLPSSWDYRPPFRDANFFVPLVEM GFHHLNKAIKSPACNEIQPLSAVSVAG LVGCV*VCKLFPVL*Q*LPQ*/S/HS IANNMRENPIRLSLF*LIC*GERMSGFA TQSRDDPCSLGFLYQVLSLAKFR
566	14467	A	572	100	371	YKSNDFYVYGILHPLTTI/VFFFFFKK KFPVPVQVGGQGNLS*LNLPLFLGLKF SCLKLPRSWNNRGAPPPPNPGFSPKNG VSPCNFG
567	14468	A	573	371	1	REGARES/TWSSSHTPVQGLRYGILLF ITSEVFFFAGFF*AFYHSSLAPTQLGG HWPTGITPLNPLVPLNNTSVLGSVG SIT*AHSLTEN
568	14469	A	574	333	103	SLQQLPQLN*SSHLSLLSSWIYRHKFP CFANRFPVFPFCRDGVLLVAQGLRA/S ASQSAGITGVSHLQVNLNPLLYFSRNG D
569	14470	A	575	1	206	FCIKKIGTIPGK*GWPNISQVPSLTN RIKEKIHISMVAPITISITKXVDFKIQ HPLILOKPPGQK*RYKFLN.IKGICEN /PIPIIYNGEILKOGCLSPFLTNIVL EDIVIQSVKIKSINIEQELR*SLNIR IKEKIHISMVAPITISITKXVDFKIQH DLILOKPPGQK
570	14471	A	576	157	255	YISPTPPFPFDDLPF*NYLENPKLISAP NFOIY
571	14472	A	577	365	3	DPHDSVFFF*KSPDDDDP.FFFPDPPFL FRGGPLYYSPP/SPPLFFSRRGKDTNPP PYGSLVAGQTPPPPPRTPLVSPDPP PPFFP*RGGMKNAKQITTFKSDGT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						PMRVHPSITLLLLRLTNTLTITQRRL DVSRESTYQGHHTPPGQKGLPYGIMLFI TSKGFFFAEPL*APYH\SSLTPTPQLGG HWPPTQMTPLNTLKDPLNLTCTVLASG/ VSIT*AHHSLLBNNNRIEALIMTIV
586	14487	A	592	175	2	FFFFFLLRHSLTLAQAGVQCDCSLCQ PPSPGFKRFSRLSLP/H*PGMVANFCLF SK
587	14488	A	593	107	733	AAAAASKULM*REGQLPGATGTGGVGA *APGSVA/AEGASVGGPGQDTAPRGQ LSFTRSHQGGAGRAS/SSQGGPGRG DGASEVNSGAL/SPQGGDGASASVPRG PYAAEAKGGMALRGLGVAAPGPSRAG QAPSGS/YTGPNARPAWPIPGQQGLR RDQAG*VSSMTGSTGTGAHTARAPGHG GKGSGQQPHQPGQQLPT
588	14489	A	594	10	435	FRWLKSHATCFWTR*SYCDNVCPVSL NAHHIGIRTIPEIFFFLSKFLCTSIPIHF TYRRQLRLIQGST*EA*EDKLEQK*AL GAAQFTLPGMDVFCVFCF/CLFEMRS HSVT*ARVQMDLQSLQLPLPGFKQPSCL LGL
589	14490	A	595	437	3	DEPKKWKTI PCSWIERINI/VLKNATLP KALIRINA/VPKLGPTSPFFTVGTFSGN *KTLIKFRWQ/KRA*IAKATQSKK ASSIT/DOVASNYKTVTKTARETNRR HYDQWNTENTETIKLHTYSQ*ILSKAGT SKQMGKEHV
590	14491	A	596	2	498	FFPFLGKTKPTTLEFFPPPPPPFFFPFK IFFGPLEKKKNPKK/PFFYKRPSPFPKGF FFFSPPPPFFNPLESKAPPFFFFFPFKKI FFFPFPPLFKKSPPKTLP*ILGFFPSFP FFFPGFPFFSLF*GGVSLCHPSNPFVVL SRPSSKLASAFRMPVEG/SPFPFSP
591	14492	A	597	1	311	RRVSSESRWRSLESRSLETYQDERP RCQRFRENSCVAPRHCKPGGKGLQALF *VPVAQLGEPAQLDGPAGHGEATVPEV QGE/PAALLPGTAK\PGEGSGPGFIPPR HCRGTGEGSGPGFTQGHETSQAQRTGC FLRCROCLCLSVSGDS
592	14493	A	598	302	2	FLRPFHKKETKALNRHRSKDILLSS NHRKCGNSLVTRD/MLKLT/MKIQFI PTRMA/IHKTRVYQGV/CEKLT*TFIH CH*NEKRVQPSNKA\QCLRK
593	14494	A	599	3	386	HTWPPPPPSPTAPPARTQFPSLQALPA PQPGKKKALRNEKG*NGSKKG/RGQPR PPPLRGPNRTRSPAGICKGGGCGPGV SKAQGAPRPGQRETVPVPGFGRPPPLPR GPGPPGVLTWRHCPRLR
594	14495	A	600	374	53	EGFFFFFPRWVGQRALEWSPHFPDGV KIFFPPPPPGWGLRGLPPPPPPPPFFFL KKKGFSPPCFVPSQLPPAGVPPPPPPPP/ TGLDLRG*PPGPPPPPPPPPPPP
595	14496	A	601	393	1	VSPPKGCVSENKIPPPGYFAKTFVHV KLFGVAPLFQLIL?*GPPLTSIRGLL\ WIPYSQY\TLTLIAPRHLRTIIPV RSVLPKTYLGLSGMPRRYSYDPDAYTT* NIGAFRIARES VVGRKLDL



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						DGGGALKKNPQGAQKNRGEKKKFFFF*G G\KKKTPGGFWKKN*FLGGGNFADPPK KKKPLEKKNNF*GORGEXPSPLPCGKEK FSHKKK
611	14512	A	617	3	429	GLLSITTYKELLQINKISNLVGKWKDK/ NQFLKKKEIHLAK\YMKRYSTSLVITIE M*LKTRYFYHPLNKLKHDNNIHC**GYK EYGLLEILLLEA*IGKFPWKAITVTVLNA PVFCL*PCFMEFHS CCPSLKCRCAPTSF IGAS
612	14513	A	618	427	6	WGGPPPPPPPIFFPPPPPP\PYFFPFFFLQ ALFS*RVFFFLTPPPPKNFPP*GPDP PPPPPPPCV\FFPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP SC
613	14514	A	619	68	434	YSKD*PINTKKKKKKKKKKKKRGGAFFK KPGGGKNGKGGKKKNFF*KGGGKNKPRG NFGKKTFLGGGKNGEPPQKKKSLEGGK KI*RGKGGKT*NP/CGGKFFSPGGFF* KKFPGGGGKY
614	14515	A	620	454	90	NFFTPEKFGPPQGNL*KAPPPFF*KG PFFPFG*KORGKSPKQPPPOQKTI FR PBP PKGGGPGPPPPPGKLIFFLEF\KK KGGPFG*DRFFFPGGKPPPPPPKPKAG IQGSTPRGP
615	14516	A	621	432	2	PEAFLSSLLHAPGKFFPLKKTPESEKFL TAKKYRVFLPPPPKIFFFP/LRALFL GRFAQIFPPQKGGFFPKIPRGVFCPP* KKKQFFFLSG*IFAPPGIFFKGA PPPFF FFFFFLDRVWLCYPGNSAVARSITS
616	14517	A	622	422	2	GGGPPIPPPPRGGLPPP**KA/VGGKK PPPPAPL*NP PPPKKKIGGGGGGQNP PPLACFFPFFFLPPPPPSFWGGEKFF FLSGGPPPPQKKKKKKKKKKKKKKKK KNKKNQTKKKKKKKRAARDPRVRPRV
617	14518	A	623	176	401	KFSMFIILWRAYTILCVGV/CVGV/CVC VCVINYLFISSQ/RLCLFLGEGKICIS LTVLRGRSVCV*SQDLVPC
618	14519	A	624	1	355	HSSGLDNLTAHSHLCGV/CLCLFLVL VCVGV/CVGV/CVCLVCVCL/CVLPQV PK*SYNSTSCLLPHFTSARTICR/CC/ CVFPCCFPA/CYQVCL*ILTSL/AIC TASGVCL*ANKSY
619	14520	A	625	2	400	HTRLFCRDGVLLCCPQNLQTPELKSL FSFGPISLFFFLERDPGSHGP/VGGG PNLG*WKFWPLG*KQPSFLTLNRGNT/ RGPPPPPPGLVFWF*KKIGFCFVAQAGL EQRPPGDOPVWASQAGITGV2
620	14521	A	626	307	3	VFFRLPIATQPGIACFCPPPPPCRFPS FFGNSPFPF/L*KLNFMAFEPFPPFF PPFFFSILPKDRVLLCHGWNNAV*S* P*TPGLN*SSLLTLPGRV
621	14522	A	627	1	391	NPPPLGAKGGPPPKRGSNPPYPYNT PPFF*NP KIPGGGHPVIPSFGG*GR KFPLREGGVPL/RPNFP
622	14523	A	628	191	375	LILIPKTIFFNFIILNFP*SGGATQAGG QGRNLG*LQPPPPHKLKPSCLLLSSW\

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
623	14524	A	629	3	382	DYRGWP HHQIRITLITASSVLCFVLFVFFET GPCSVTEAGVQ*CN/HQPLSPG/PPTS AA*VANTADVHHANLFCVLLI*DGWS VTQAGVQ*RDPSVQPPTPGLK*ASC\PA FQKCLDYR
624	14525	A	630	396	2	CRIENVLKKKLEMSNLSEELGMKKNIG QKSLILAPQOVVNAKESLLKEIRSLPL NTQWIRWQSLASADIEDL/VVNI/DP TNFNIPLQSTIQSNA/L/LTFPMPK* RGEAAA*EKDTAIG*FTTKERS
625	14526	A	631	47	392	LHSFFPLFLGKRTPTGGGGGQKDPF* NDPPPG*RNFFLPD*KTWNGPADPPR KTFQFLKKGFPLGNL/SIGTPPPRGT PPPLPDRGGCYGGGPPPPPIFFRTFK NFSN
626	14527	A	632	39	382	LFSSPPFFFNFFFFFGRFFFWGVAPIF PDPKKIFFSQP/LQVEFFSP*KKKFF FFPD*IFADPKTFFSIDPPFFSFFFF FFFFF
627	14528	A	633	2	213	LDPKPGKHSKISSLOKI/INGVCLQS*LL GWLQEDCLSEGS*GCSEL*FYRCTTAN ATK*DPVSKKKKGLK
628	14529	A	634	2	206	QENGMNPGGRACS*PKIARYCTSSNATER DVSCKNE/TNKTLLREI*HFVGDPNG KKULLKTYGGIT
629	14530	A	635	205	2	KESLGLAQ*/VOWGDFKTLQPLPGV KQISRLNLLKNDY*RGPSLGLKFW/IF L*KQGFQFVRUVFN
630	14531	A	636	3	399	QVQQTASCPLSDSEEDQLDAMSN TFPKKKKKKKKKKKKRGAP*KKTRGG PKK/IRGKKK
631	14532	A	637	122	373	VSNILNTQSLFFFFFLKGSFLVPQDQ QGGLDLG*TKFPPRGLKEFSCLTRISG NYGLAPP/HG*FCFFIKGVFPCCGN F
632	14533	A	638	390	3	LLVLFLPQDQSPFAFHQKLPSPK ANAMLPVQAPK*AHPTFFFY*PSPFR FFFAWG*SS\YFVNLTKSELKGP NDMREVFVFFIRLLILFFGDRVLQGP GWSSVVO*L*LIASA
633	14534	A	639	392	42	PSGPGKGGKTFLRKPPFQACRQGFY PLFPKPLKNPKAPQNRNIGP1CPPPK P/QGPLRISFQNSQSGSL*GPNIGNCFP A*TWGPPGAP*RGPPKGGPFFFEKIME AMGLA
634	14535	A	640	390	1	LSFSEEGMSTARAQKLGPLCQ/TQVLI NAKETFLKEIKSVIPVNIQMIKK*NSFI ADKEKIIIVV*TDQSPH/IPL/SQCLI QSNVILTFSSKKAEAGEAAREKFINFS *RIKKAASADREAAESYPEDL
635	14536	A	641	368	3	KGGYGVPPFSPPPGFLGGSLPDKI KVQKTL/SWPPPPPPGGKKTPTFFKKK RKNFLTGFFFF*KGPPFFFF*CPVV* KFWGGGFKPIFFFFF/RDRLSLCCGN SAVV*SQPTPRV
636	14537	A	642	134	413	QKQRRRIESEL/IR/PEHTNLI.FDKG VTGQYQKDSL.FNKWCWN*RE/ITQNL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						SLDPAITTNVNLKWTICLKARE/VKTLVRNMGRLRD
637	14538	A	643	2	436	GRVESINLPIGCRILFKKRDNIKCGVGRGGSLIHGW*EC/EVUQPLMKRQQFLIKLINIHLPRDSTILALDIDLGGHPKTSALFIITHMCCFIHNP*LEQPKCPSTDVWMEKFWPIHSMHYSALSAVWDFNKGILL
638	14539	A	644	446	75	LDLITS*SACIAGLPCWYRSEPPPAFNF*/STIK*SLMSSHQDYICRLISYTTATQKFTSLITTY*SHLKT*NAQMDRLYLQSLILGISIP*KSNLPR*PQCAAXAENH*SDLYCQIMLFSGFM
639	14540	A	645	318	1	KGVRKCKRNSYGVPPSGPPPIK*LLFF*IF*DRISLCSGPNWAVFES*LPV/T*TTGVKKMWPLSLINI*GYKGVPRPGIFFFFFDFRDR/SLTWLRLRLVWVQVIFQ
640	14541	A	646	3	348	QFSSFFVLLYPLFPWVSFCF/WCFSNLVLCRIIFFLIFYVYSILNISFFCYCLLVLFLSKLSFF/C*YINITVFCSMTSFF*RII/CCLNFKTSPNPL*FGWVLESCFFFFFWP
641	14542	A	647	2	553	AILIPDKIDLEK\VTGDRE*NVTMIKGSIHQEDVTINITYASNSR/APKYMCKLIKSGEKKQISIP*K/VVGLFNTPFSI/DRAPRQKIQMSIEDLNIHQIDLDKLYTTFHTSEYIFPSSAYET/PSKIGHKLKKTSLNKYK*TEIMQSMPSD/HKMGLENNE/NVGKL/DNMKSDTLVSDWLGVAWAHA
642	14543	A	648	388	1	OPPR*SDPPFGKPGAVPG/GGGGLKPPGQENPPFFFKPKPIIAGQWGP/RNPPPLGG*KGKIP*/PPGGGSKNPNFSPSGFPGKQKQNFPSQKKKKKKKKKKKPPS*CFQTSQPQVTDGQALNAGISS
643	14544	A	649	387	25	FGMRGGFFPFFLGNFFPPPGP*/VSGGGGGPNGGPPKKGFFPKNPVGVFSPPKKKKIFPSPPPNLGPDRDPLKQPLPFFFLQKNPGVFFRAGQGNPQKLAKIFPLPPGGGGGAVRHI
644	14545	A	650	918	2	LGLGLTIYKILHSTIADHTFSSSHGTFAMTDHIHGKIHILSTFSKE*EIIPTSPSPQ/HHSRRLN*K*INNYNNKIPK\FWRLAKTLANT*TKS/GLKGRNLLS*TRNTTYQILWDAGKAVLRGKTYLVT*IEKSERSK*TSFPIRKRNKGLINIRTEINEIENRSEKILN\TKSNPFPEKKSKIKSLKTLARIANKRKESTQIPKHOK*RRGITTGNMANKIKRNIHEOPTTHKLGHLNDIQQFLEKRYLPLKQGEI*SGWAYIN/SKEMESIINTLPKKAQDLKMPQSSE*YQTFKEKK
645	14546	A	651	282	265	GVFFLKKRPVTF*KKKI*IGPHFLKGPFGVFO/HFPI*NFGISRGDLFFFFFFFVFFFLFLRGOQVSVAQTGAQWINGGSLQPPGLK*FS
646	14547	A	652	6	223	LYAHKPNILDEMDQLOREINTPKLQRE/HRLTVIK*IKSIVINLPKQKA*GPDGFSGEMYQLKKEIITNYP



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						SEFMKVTEYKLNQY/SQLYLYMPKRN *RV/ILEKHPL*PQITKYFGEILKKDVL NLTYDKYKISLREVBKGQKNKNNVSS
662	14563	A	668	405	566	IHCQWECKTBQILNKTVMWFFTKLNL PGDSAIMLGLIYPKELKMYHTETCT
663	14564	A	669	218	2	LLMLESIMFVPPFPFPERWKL*TY/CH GAHANFLSPFFSPFFSLSFFFFYNRV FLCCPWSAUVRSGLZ
664	14565	A	670	2	210	NFGQRENSRNSLCSYLLENLEKGEQTP KASRRKEIIK*AEI*KVQSRNRNK* KKWFFKINKIKDKPIARI*KKWKT*ITI VRKETGTITKDPADTKRIMKEY/YKLLY MHSP*NLGRNLKRYREVIKINERSGSL KRSIKLTNL
665	14566	A	671	200	3	SLCHLPHVASKATLET/OLVSHM*DPF CFFETESHCAQSGVQMCNGLSLQLPP RFKLFSCLSL
666	14567	A	672	94	374	PKFRPQRTTQTSQFLQINCKRGRKQ KRTYRLGRIKQSQPMATFELYLD/H*F *LAKETL*LGAVARTCNSTLGGQAGWI TRSGVQDQPGQ
667	14568	A	673	312	3	WRMQLPGRPQLPQLSQEKILSINS PKKKKL**NILEPKKRPDCFTWKFYQ TKSEILFP/L/HKLT*EFERKEILLKS FYBESV*AKLKAIDINKTTH
668	14569	A	674	34	438	QUT*ED*HFIKSTQCKTFSSSTHVF AKLGHNLVAKNLMKFKM/QVSNRFL DRDIRALKINNK/PSSPLKYLQTHLL NDPRIKESKREIKDFALNDNAT*NL WCL*NGTLRKVYTTKCLERKEGDM
669	14570	A	675	3	349	QKDKSVRFPSS*NPPLAVERITPY/LKQN PERFNGPAFFKIAHOLTSSLVFCANSN YERTHSRIILSQGLQTGFAIKTFKLL ASLANLALPPTINLGLS I
670	14571	A	676	346	1	KWRL*NIWRLK/GLTGVPHGSATF PFFIPFPKEMETNVHKTCTWAFPAF FPMKKKKQSQNNPTDS*IQKK/W*TH IIDYSAIKRNLTHATSCNITLSKRS QTKK
671	14572	A	677	357	6	AAGDSLKPMPFIYCPKMPML*IMLKST LLVLYRWNHKAMTACLTANFTE/HCK PKLETYPSEKRFSLNIT*LMKASGHPA LHEMYKENNVFKSNTYCTLHPMDQEV ISTENSY
672	14573	A	678	401	155	YYSVAGNVQVQWDRSLAQDPPOPE*FS CAPASNDYKHKLITSGDLPASASQSGI TGVSHCAOPLSLFVFFLINQRFVAAIS
673	14574	A	679	292	395	Q*KTSPEMLITINNVGHPRTPMENYKE LNFF/MPANTSIP*PMQGLVLT*FKSY A/ENVFCKIAIV/DSDFDGFQSGKLET FWKGTI*DVIKINDDL/WRGVKIPILT GVWEKILPTLINNFVFKASLEEI
674	14575	A	680	275	3	WPROQASLALNT*SIHTYITHTDRTHAHT YIFOMKSVTQAGVQWNGSLEP*SPGL RRSSHPSLPTSGRHRTPPR/LADFIHC L*R*GFMTL
675	14576	A	681	330	507	GSV*PVNLIRNCPFVQSGCA/SLHSHQ EWYMCSPHPRHYLVASVIFILALFF

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						LRRSL
676	14577	A	682	390	43	HLPLRYICLSISSILCLSPIMVLS / IYLSIYLSIYLSIYLCOROQIPLVFLCLLLS*LS*IILILNFSCTFFVQRTIVLS
677	14578	A	683	396	63	ADPTEIQRITISDYDQRIHKNLGNL*KN DKFLKTYNLPRLN*EEVETILRPIANHEIALI IKSLPIKRSPLVGGSGVG*HIDKEELTPVLGLFQKIKKESILANSFYER
678	14579	A	684	1	396	EETLPLALDMLIYIKKQKFKATTESEKRY*N*WVFGKRYKRYNTCKSLN*QYTI*VKVIGAS\FSSSPQONKIGINLTKEIQNVSYSENYKTLKEIKDLNK*ESIPCSQIRRFNIVKMTVLLKLIYR
679	14580	A	685	283	3	NCVSSNTILWEPQKPLSVSLTDVCPMLSAALFAIA\RSYTLTPRSSIDE*IKKMWYIHTMEYSAFKKGRIMFLMPRME LKIFRVNKKIR
680	14581	A	686	53	324	HCFCDRIAAFCFYLLDCFFSISTHKL I*IFFFFFLERESIFVPGVGGGPNPGSLNPLPFLRRRFSCLTLRGGDYGLGPPCPT/NFCVF
681	14582	A	687	39	208	NIFFCRBGFAMLARLVNSN*NMGPKVTHIHNP/STLGLGGRITQTEFETSLVDAGA
682	14583	A	688	47	341	SSGRVFLVLCFFETGSHS/VLFLRAYSGGISAYCSCHLLSSGDSPIASATR/GITGMCSSAQLGFCVVCVC/FIVF*VKIGFC HVACGLLELDSSNPPTS
683	14584	A	689	229	1	GRVCGRITACQEFKARLASQSAQITGVSHRAQPPFCFC/LLFVVTMGSHSVTDQAGVQCAPGSLQPLPLRFK*FSC
684	14585	A	690	339	1	KKGPPGGPTKPEGGRFFRPGPPGGGKRVFPFPFPGGKGGKRGADPPFFFLKGGKSGKGG\N*FFPPGGGKGGKGGKRVFPFKKKKKKKKALSLSLSLSLSLSLSLG
685	14586	A	691	372	0	YDLYIKKL\N/LREKIDKFLDTYNLSRLNQBEIENLNPITSNKIEVTVKSPPT\KQKSPGGE
686	14587	A	692	117	297	APLLESSASLYHFSN*DLQMAH/KATKRCSTSLAFREM*IKTKRRHHFPTTQATSKRHT
687	14588	A	693	122	322	EQTNSWSIDFFQRCNSNAGEKNCLFNKN*WNYVAI\AKRGLSLFLKPYIKTINSK/WIEDLNIRAKT
688	14589	A	694	21	342	RSHFRHLNEYATQGNSDVHPLLIHNSISTAIHWLQGRERRRKKLEKVENNEKALKEIFLQNWILLCHLQSGSPVGS*FIVTIN\VHIGQSSHSI\PSWSWYRVP
689	14590	A	695	2	343	KVPLHSILGKRSQKTLSCRRKKKGGVFLANAKVQWNNHG*QGP*TLGLQSSCLSL*GGWVKI / PGRHRHAGFHHVKVGLLELLTSDDAPSSASQKGLITGMSHTAPGK NLV
690	14591	A	696	336	3	IPPVKSPPKFPILLKKKKFSLFCFSGAPFPCYSPDRAQKGGW*KIFSPPPK/QKKKGALFFSPKPAFPFPFPFKKKKKKKAKBCHYLMIKGLIQQEKIILNIVASNIGARRRG
691	14592	A	697	374	2	APY*KKMVSRTFLARKSSMRPFKASKDR





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						TPQQAQRKRN/WDFPTKYLKPCA*EDSI ERV/N/RRSTEWETIFANHQ*GN*NIQ RLLLKSL*ARLKWARDL
704	14605	A	710	382	30	PATGTHHHHTLTFVF/GRASATITCWL VWNS*ACSACLSLKPCND*EPOIDP/RV SPNTRSGIF/LISTNPSLSLAFSPGQFV FLDPHPFASHPETALAE/PLQTFPSLSP GPPTFAS
705	14606	A	711	1	377	LLVIGQMKITIVRCN*TLNKLATIERK TAKCC*HYGGLKTLHWCCKSNMVGPLC KTV*QF*KKLINQLLYLLK*KKAYIHS NCTQMP/LA/ALFSLVLAENKQSAAY
706	14607	A	712	1	390	LKYIKMPLGMAAWCANPNYSGGSPGNTA* TW*AYMALTRLEPGRGDHTAALQPGRQS TTP*KKKAVP/PRA/RPVKMRERET*KP FSPE/RTYSQAQEGPGRTPGSAQDLBA GGRGHHGMAVQKEPHRLIG
707	14608	A	713	2	393	KVRQILINVDTATDSIGIKWIKWYAY* LKYAKPNYLAEMDPTVVERYKLP/KEIDV MNSLWPAKSLITVVKLLITKTFPHIEPT NBVYOTFKKDY/VNVLKGLPKKIEDIRFT LSSPCEAGINLISICKRPF
708	14609	A	714	219	1	PRKGAVAHACNPSLTGGQGRH*TGSS IKACCLILHDLAQTKMT/WPGAFAEA CNFSTLTGGQGRITRSGARDPVSQHSKT PSLKLQKKLASVAGACNPQYFENYIQ KLLRPGPT
709	14610	A	715	381	126	ITAGGQGYCT*SQLFKRLRQEDHLSPQV RGYKEI*SYPCITLAWVTE*DPVF*KKNY /TLNTPSPKETNKK*GVRCKITKGLVLFV AAG
710	14611	A	716	417	1	CYCCWAGATNKILLTDNASGRQIVLMDM YKNNVVFVVPNTRSFVQLMDQGITLNF KSYLRN/TF/HKCIAVINSNS*ESGGS KLKALWKGFTVLIACINICDSGVQKMF LTET/WKEVILPLMGDFVRNRTSEKQNY KLS
711	14612	A	717	406	122	WFSRIAVSLCCLGWS*PELKLSSSLST PKCNDVGRPEPCSAAXDP*IRER/HSC RNIIRNSDAMOR*TTLVSYDENP*FES PPNPSPLCPAA
712	14613	A	718	535	1	HNLANKIV/NLHVENVKLVYDQDKT*ISC LWVRR/LVKIPVLKLFYSVIVPDIRSL VRYPIEVCITFTLKCIKPEKDLQPNRP* KKKKVHLPEFIKVVY/KLQ/YIATVIRK VMY/W/YSKIDKAKWYKTEGAEV*PHEIY DQILIAEVQINH/NLPNKCY*SN*TTIG KIMMLNLSSTST
713	14614	A	719	255	1	GKIQPHRGLISTIY/NL*KLVRKSNPEK KWAKCMNR*ITKGIQIAFRHMKRCSRP PFKAMHILITWS/HFSSSKRKTIRIQLIL KIVANNTIKSLDLEINNTLYIKKLL/ DEBETACASBVLKIKAKILBELT PIKTDNDSPMPLAKIKHQQ/PFKLDL QKKKGVRSKVPITKRYENRVITNTNTE /KRIIRREYDII
715	14616	A	721	3	381	IYRWRDITRIGTYQGHAPPGRGK/VC RGIILFITSEGGFFAGFP*PNNKNS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, X=Unknown, * = Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
						PTTQLGGPWPPTGTTPLNPLKVPLLDTS VLLASGESIT*AHHS/LENNRNQLIQIA LLTTLLGLYFTLLQA
716	14617	A	722	56	455	KTILNIKPPALIQYQTPLEPV*SVLITAE \LVLLSLPGLAVGTTILLTDNRNITFEL DPAGGGDPILYQHI.F*FPGHPVEYILLIL PGPGLISHIVAYYSQKCEPFYIGNV*A MISIGFLGFIG*AHHIFTGGIA
717	14618	A	723	398	3	HQLFVFWQYXKGAJNTKPLFVDWIK*CL VEFVSKYPSAGSI*PKKVLMLNDAED/H PTNSMSS/DSKGLIEVILPFWISLT* FLDQGVIRTYR/RHYPOYSMQRSIKPMQ EISNKENIKVKWNSTDDAIVA
718	14619	A	724	318	14	TTPPFLNITPHLLFLFFSPPPFWFLTKS LFPPLLKPKVFGK*SLSKF/CPFFKFN PKPQKGNFFPPPPPPPPPPFFFLRNL/ VCHPANSAJAPSQLTATSAS
719	14620	A	725	2	371	APKCKRFSCLSLPSQNDYKCMPPFNVF F/SIFSRAGGLS*PMMIPPA*A/EPK/ CWDYRHE
720	14621	A	726	430	97	PKKNPPNKRANNGGAQRDVPISLP/SGW AGGSFWGPGF*PPLGPKGGPPFSKKPG GVGPFIMPTTPEGGGKGLA*PWPGFNP FVSIFLPRPPRAGGKKGTPFPKKKKKK
721	14622	A	727	406	1	GGAPPPPPPPPPFFIKKGVPFP*QEGFF PGLKN/LPP*PKKVGXGGSPPGGGF FFKKKVVFFFGSLTRQIKVPSILVG QG*KLIPQVVSQGVKESQQAQLFFF FFFPBESHFPVTAQLQNDIGSP
722	14623	A	728	98	368	KPHENAKCPIRVATVAMENKKN*GVG EMGIT/LHY*WEGNIQPNW/T/VWQLL EKLITELCPDPAIPLIGIYPTLESRDS NRFFIFFTFSF
723	14624	A	729	19	404	VCVISICLATEILFFLHTRPCVCICYCVC VCVCIAVWGTLVCVVCIESCVCVCFLHT GVLC/V*VCVISICLATEILFFLHTRPC VCICYCVCVCIAVWGTLVCVVCIESCVC CVCFLHTGV\VCVCVCIESCVCVCPT CGTVVCVVRPPGVLCVCVCVQQAQAVAV SMCLTP/CPC/VCVCVCVCV
724	14625	A	730	432	12	FFHKPNFPFAKGRLLFFPIYPSCKLISP KAL*F\FGGVGPPFPFPKPGFFPKVPR* CFRPLIRKKQILLPLPLNLAPPGVIT* N/PPPIVFFFFFPRDRVSLYCPGWSAV A*S*L/VAVRTGLK*SSCLSLPKCMWY KCRP
725	14626	A	731	332	7	NKTRKKKFLTRISRF/CFPPFFLRIFF FPLRA*FWGGIQLIFFPPPKVVF/PKI PKVFKNPPLRKKIFFFPLLLGPRV LLKGPPLEFFW*VF*DEALLCHPY
726	14627	A	732	70	294	FLRQVETAINKILATILANF*NFL*ENG \FTMFPRLVSKL*DSSDPTTSVQSQVGI TVVSHHARLNFYQNSRR
727	14628	A	733	1	355	ILLRHILLCHPGFCSVATAYCSRIPGSS D/PLPQAPLPDQ*PRIQA/WHRLAPPH SANFF* *RQGTVTIARVUSISQCDPPH SGPQGA
728	14629	A	734	50	395	IPGLTRQNLDPKASPSTPYT/P*VQP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						STPQNSSPSPICTNCKGLNPLSPPTPKP STAWKKAILEHTSSSSSSSSSTCRNR NGYTTYTPBHRPARGHTASQTRKQVLAAT THKP
729	14630	A	735	451	0	GPSSSPITNIPTPVSNFSK*SSQVAGAT GTCYHAWLIFVFSVERMDFY/HVPA*ASQ SAQLQCYFMIPLGRQGVSLCPGWSAVAN SKLTI/CLCLPGSWHRCALAHANPLY FWR/RSC
730	14631	A	736	2	477	PSHVSNKRLISKTYKELIHLNSKKVSNP I*K*QGSILNRDFSKASVLP*RCQVNN RYIKRCSLSLLIKEQIKTITRGLTPV RLAIMKKSKDNKPSLVNDC*IRVLHLF/ CK/WICQVQL/FWILLNLFVKKQPF/Q LPAPPNSPTLG
731	14632	A	737	3	2344	AAGGPTAQSPAQLAGALRLARMRVAV GACRPGAGSPCSVQGNASELSRPPQTW IGSLKP*TFGAAG*AHRRGGGSAALIN* ATPRPAPGLPASPTSSQALPAPLGAWGH SDHQPRAPP*SPQASTAIRKEKQRAOP GRASVCPASNPFISRRALPVLQHGPPAI SGAGSAVASQAPGSS/GSHAESGSPALA HTP*GS*EPHSLIVESTRKS\ELPSSSQ GRLLLPPLTPVAV/FVTKLPGATAT AGALHOPRLRLSLQGVGANKRQTCGC CLQLPTTGLPQAPGALRLGRLGPAAP GHRHRTSPQQTVPVGGIRQGWEPQRL RAYGTALPPHTPGSSGP/RQAPGCRG SGAGERAGIRDITGGGPRRAPSQASP GRGGWQAQVGCETCRGCRQSS/GGAVQ PGLPRKVPYHS/AR*ENLVVFPFCSPT RAQEPQTOGER/GVEGPGSPCAPGAVR GRGIQLSSRPGKLARQ/PASGDGP*EG TGQRPSQAFSSARHPVSEARMPTDIAIC RNQAQ*LOLTSSQPSMGPOLRKSLEPATP OPNSYWDGNSATLGRTITNTRRHGMSN FGAGDILLGTVP*QPLMRKRKEKRVG GSPVQSHTVCG*\PAGVSRGHLRPLMLP ERWPLSASSGSGRGRLPLSLA/CGP SSSPHRTCS/GLDGLPDAGSTKPPSL VGAGQAGST/GLD/GRGLSLSPKSL LPPSSPATGLSGLGWAQSAF*SLITVA* WLNVPVNGPSDADCTPAQAPTAPAMLE NQANKSDFFEH
732	14633	A	738	37	450	NQKKEPPRESSKPARLEFFFL*QKYLRD P*KTYQGCFTFFPPPKGNPPPKRGGF FFFF*KKXGGGPP/QAKKRGGGGPPQK GGAKINPRGTRVFKGPFKKRGPP
733	14634	A	739	2	426	QSFVLGSAFGCGVGGGRVSSPWGDR KVGGPSNRHWNKGAGPSCPFGPSLAAG LPGRENGSWAPVLW\PGPP*GLAQLPSP LW/PPSPORRRPLPD
734	14635	A	740	21	392	AQRFSSLGNNRPLPYQKKKKKKRGG GA/RPLETQPFPGGGGKGGKKKTSR P/IRGKPPFL*KKQ\CLAWGGPAL*P QFFGGVGEKKTFWPGGGGLGKPKPPPT PTRGMDTPQKKKK
735	14636	A	741	1	408	PSSQGG*RAAG*LRPRESSRANAL*RD

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
						/GSPERKKKKKKKKKKKKGGGPKK TPGAKIKGGGEKKNFPGGGEKKNLGG ILEKKLFFGGGKNGEKPPKKKKGLREKK KF*RGKGKKAEPPGGKKIKFKKKK
736	14637	A	742	394	1	RDPLESAVCPFFSDQLRACRTALFAV RQSHLSLQRLRLVCLCPAPRGAYRS RQSLNRRGGFHPRATLLCLPEQASEM AGAPPA*LPCCSLSDCCSNQ*DSVG /VGPSPGEGYNLAVRRFLS
737	14638	A	743	384	1	FTGPLYKNNGYSTFLYPSPSVLGNQPF PHGRVFP*DNFNQWIFVSL/ISLKL DEPAFSTLYSF*QHFF*ITLYLPP/CF FLIESCSVAQGVQMCNTRGSLQPPPGY KRFSVGLPSSWDYRCV
738	14639	A	744	2	410	TPINPLEVPLNLSVLLASGVSM*ADH SLIENNRNQIQALVITILLGLYPTLLQ ASEYFESPPTISDGIYSTFFVATGFHG LHVIAVSTFLTICFIRQLFHPFTSKHHF GFBAAG*YWHFVN/VRGLLYGSTYN
739	14640	A	745	393	1	PPPPPPRGSGPPPPFSSRGGPGKGPFPF GNFFPPFKRVFP*/CPGGFKS*V*GVP PPPPPKIFKFGGTPFPGLNSPLKSKGS QFVFWPKGGERKKLFP*PPPPFLRPCL SLSPRLSCGASGAREHL
740	14641	A	746	2	290	KMLCRNFKTE*KKLKTWOLCKEYKV *MKIKEN*HDLANFANIKISTLI KVIYKNAIPKIPMTFPA*LK*ILKC V*NYKR*IVKLI
741	14642	A	747	59	364	CRFFTFGLGGGGGGGGPPPP*KNP PNPPKKIPNWGFFPRGPGFAPKKKGPF LGRPPWAGAPLNPFPFGGGAFFPPI FFPRAGGPQKRVG/RPPPPPPPPRPK KKKNIH*LECVEGTEETRPPTP
742	14643	A	748	2	371	SSCLDLPCNDYRHEHLHJHLV/LGIF LLLLFCFVLRW/RSCSVVQTV*NSDLT SLQSLP
743	14644	A	749	339	198	IADMEKV*AF*TEHKHNHSLNQ*IS KVLTLFNSM*ARD*EGPEEKFGASTG FMRQEIISQLYN/IDV*GEAASADGEA ATCAEDPAKIPDEGGSPK*YINVD*AT FIRDLGWIFCTSCSFSISTCCFLHVM L
744	14645	A	750	249	2	KFKKPAFFVSPDFPL*DESSPDEP*1 SGRGVGP/FP*PKGFPKNGPVGFFS PPLKKILLVPPILNLGPPKGLRPP
745	14646	A	751	1	288	VVNHMTDEGLSRIYQPLQ\KRTW PVQNTKCPNRRFSRDEQMRKHQGN PASRAIRGTOSKIMRCHPHTRMARIK KEKTAGGGSL
746	14647	A	752	494	2	ETGSWFQRLLEVQVVMKSSLQ*PPW APVILPPQ/LSSG*DRHVPSRPG*KKK KFEL*RWGLTALPRLLLNPL*IASQNA ATTGVSHCARSAVFLIRQGLWREB/ GAQN*SALSHLP*/LSR*WCQ*PIG* DSGSGSLWRRLAYLPLCALWEVTWCS
747	14648	A	753	1	533	YLSRLECSGGITAHN/LRRPGLK*SS QLSLQ\SSWDCRPAAPRPAARLFFCRF EGRRSHYVAQACLKPGS/SNPPTVA/

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						FFKCGYRCPEPPTGLCS/GLSEFGFCL WNGACSESSHHNPGCGTA/CBAVFLHSV GYASHPSSTRTAFTLGA/VLVFVRDKG LTVFSQAGSTVGVILG
748	14649	A	754	1	346	ELSKSTLPAICCGNDKAMTAAHFAW TDYLFPTVENYW*EKKLRKLVLLIDNA PGHPVALLSMYTSIHVVFMEDTTSIL* PTHQGVISTLKKCYL*NTFHKVQ\CTID SDSS
749	14650	A	755	1	323	EDTSHNNVLSSNLISKALMLFMSMEA E/R/SEEAVEEKPEASRE*PMRLKERS LQNIKVGQGEASADGEPACDPEDLAEI TDEGDCIK*QIFIVDKTAFYSKKMPS
750	14651	A	756	1	344	ARQPGDFPARGSGRGRL/QPRQASFC TGTTLARARHTCEGAGVLRERPADKLASLN *HPSQKKKKKKKKKKKKKKKKKSSSS KKKKSSSYSSSSSSSGSSSSSSSPPPP PPP
751	14652	A	757	119	317	NRYPFLAVKKPVPWGGPFFLR*SLTL LTLVAQAGLQWRNLSLSPPLGPKFPS /PSA/LSEWDYRR
752	14653	A	758	2	363	CILAIVKSAINRIAN*YI*KCSMSITTK RQA/IKRKNKTRRTQLIPVRMTLIKKKK RW*CEEEKGLAHGWF\CKC*ROPL*RT S*PFLKKLKPRTATLALDIYFKQIK SE/CKKH/CALLFIALFTIAK
753	14654	A	759	358	1	KADCFPFPTTSFVKIKTFPFFPKKRG* KGF/LPDPGNCVVF*FKKRGFSPLGG GFYFFPDPGPPDPWPFKLGKGLTDP GPPQKILVFFFFFFFFFFE/DGVLLCRP GWSAVAQS
754	14655	A	760	316	2	KATRSODIRRIQVKLKEIPQKFLQKTN KRSYFF*KH* *NRTLTRVMENKREK/N EIDPIQNHKEDITDPTQIQTIRKYVHK LYARKLKKLBEVDKLLDTNTL
755	14656	A	761	3	321	FFLGLWSLGAPEGAQPLVPPPLSKRV VPCL/DKGRSAVTNTVYSSGSSRVVP PPCM*LYRLCIKGRSSDPEQKKKKKKK KKKKKQAKKKKAPDSSSPKT
756	14657	A	762	315	2	KTRW/VFEKINRQGS*DLTKYQNRN /V/QINKIQNRGGLSTGSTEIQRVIRG FCEPL*AGILLDNLEND*PLQPFILPRQ NKKKKL*KKISFVIELVNL
757	14658	A	763	226	329	NPTFLSGQGGKSGPZF/CSRDVSPC WPGMPTDPLMRSVRLGLPKWDE/RR* APPPLGLNFFRMLSTHGS/CQHPCKF PDSAFQYIYIYIF/SFLRSSTFVAQAV VOMHDLGSPQPPPPGFKO
758	14659	A	764	335	1	QSOERDPSFOVNLTLPRAPSMFLVSPR TELKSP*/PPAFLCPVWPHSTLLSQT LKY*IKYP*STPFPFSFLF*RDVLLF HPGWSLAGS*LTAAASNWAQVTL
759	14660	A	765	100	310	HFGRPKRENCSP*V*QDTLEHTHTHT HTHTHTHSRSRGGMLTTPHLPVRVW\ GTIC
760	14661	A	766	315	3	IFPNPRTIFIQPHFLPGFPFKKKEGE KNNAETPRFSPPLGGKKAFTGPPPPP IGF*GPKFLIKRGF*/PPQHTKIFFF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US95/15,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
761	14662	A	767	1	309	FFFFF*DRVLLCHPG*SAVAW KRPKYKTSI\HNRIKVAQGHLSKKKKITW VSDS*ASCPSKTRGNF IGPSAGSRAPSE KLEAHFHGCGSVNRVHLT/CK*HKRRLPL GVAHLEBVDQKSGRTSLALD
762	14663	A	769	1	316	GRAPFPFPPPPPTPRVHTSSKSESEPER /DGR*EPIKSLERL/LFFASYFCLLEAR QSTSALEPLPLSPESGPTVLLCPSFPL PGRFPNPTKLSERQQTQCTEAR
763	14664	A	770	2	366	AREIILITF*QNTITFNITKGT*SLILA SLIIFIAITN\LGILLVYSFTPTOLFI NLTMAIPL*AGAVVIGFSKIKNALGHF LPGGTPTPLKPLPIETIILLIQIAL AVRLTANITA
764	14665	A	771	2	364	NAPFVISGAWTEYPLSHFQRCRQKE/ LNLQIQKESEIFLFDKAML*IESPKES VQKRLDVIYKFSRIAUCKINIQKSNIVV YVKNITQFENEVKTI*DPQ/DIKHMGILL SQRKKE
765	14666	A	772	3	376	HEPLGRLKLSILLFILATYSLTVYSIL* G*ATNSNYALIGALRAVAQTSISVTLIA IILLSTLLRRGCPNLSTIMTQBL*LL LPS*PLATI*FICITLAETNRTFPDLAER ESSLLSC/PNIEYA
766	14667	A	773	3	350	HEFFFTFKRYLGGQYFICPLFFPLGF HLK/HKSCSVTAQKQVRHLGSMQPPP GEMQFSVAELKDVHNGHQLLYFIRFPI F*F/HFLRHSLLVAQDCVQWRDLGT*Q PLPPPG
767	14668	A	774	1	359	GTRYAAMLSALGFIFLFTARGLTGIVLA NSSLDIVLHDTYVGAHEHYVLSIGAVF ALIP\GFTH*FPLFSGYTLDTQTYAKIH/ FTIIFIGANLITLLPQHFFGLSGMPQYS DYPDAYT*W
768	14669	A	775	2	369	ARGSTCLRQTELRKTVIAYSSIRHGLV TALLIQTP*SLTGAVILLIAHGLYTSLL CCLANSNYERTHS\RIIILSQGLTLLP LITF*LLARLANLALPPTINILGELSV LVITFS*ANIT
769	14670	A	776	2	353	ARGTGA*VDS*LITLHGSNMK*CAA\LL \WTLRCKILFTVRLGTG*AITNSTLDIA LNDITYVVAHPHYVLSIGQFALIRGPI H*FPLFSGYTLDTQTYAKIHFTIIFIGV ITTFPQ
770	14671	A	777	3	353	HRLHL*LPRAHVRTPMRG*TDALDGL RLRGYGIHVTLINLPLRKHILHPLVL SI*GIITTSITCLRQTDLSLNLNYSIS HI\SLVETAILIRTPLA\SFTGADILLIS HGLTCS
771	14672	A	778	367	2	FCPI/CPNQKFGVGVAGPALYFNPFG LGLN/TVAGVILNAGPPG*TPPEPKN PNLGGGPAFFPPLKGLGWKIALTPEAK GSTNPSPALPGGGNCTFSKKKKRKK LMLVYSIELTSA
772	14673	A	779	3	432	HEPLHNLSSCCVACPVCVCVC/CLNLQ VGVO*CNYSWQHEPLH*VHTRVYVVCV LCHSVQAQGVQ*CNYS/CTACNSN
773	14674	A	780	213	466	DDLPLVMNYSISLFFFFENRAFFLPQW

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/555,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
						GAGTQL*LEAAEN*GPQKPSRLTLL*W\DNRHGPPC/LDNFI*FLQKXNLTLLPRLALN
774	14675	A	781	304	373	R*VFFFFFLKKEPHFFQAGGQNG*LEPLDPGAG/R*CLTPPHSWDNGEGPPRPNNFCFFRGKNVSPQCP
775	14676	A	782	389	1	PPPKN*CRVNSRPNVKRTY/QILBGNLQASVDDLBFQDDFLDTIKVQSMKERS/WDFIKIKNVCFACKNVKRGPAINWKKISVKDLNKKLLPKIYEELKLNNTET*RLE*KWSKVLNRQLTRETALA
776	14677	A	783	1	383	GTS*PLTGALSLLNTCOLLA*PHFSITLLILGLARTLTITYPGRGDVSRQSAVQGHHTPPVQKGLXRIILFTTSEAFPTFGFF*SPVHSSLSPTQLGSHWSPTGIALPLNSL*VPLLNTWRLL
777	14678	A	784	1	389	GTSIVIPGVKRVN*LATLHGSNAK*SAABL*ALGFILFPTQSLGTGIVLANSLSLIVLHDTTYGGAHFHYVLSIGAVFAIIGGFH*FPLPFGVTLDDTYAKIHLT\IIFI GVNITFFPQHTFLGLSGNA
778	14679	A	785	374	1	ELNAYNWNVNQNLINWAPLTSMQIFQILIKSQIQNTLVVSISDTGYLPGIDKNWCI*LKILCIVKVTINRAMPVIDWENTFSTYTHDKGLIPRYKELKES\KQTNLIK ENAKGLHSHSRA
779	14680	A	786	1	363	GRIDYHANT*KKLRVAILISEK\TDPTVKILRNKRGHYIMIKRSLLEGITILYVGTPSRRVNYIRKQLIKPGEDISTII LRDNTPLSVIDASTRKIKSNIVESNN IISQLDLD
780	14681	A	787	1	361	GTLPSSERKNPITWVSLNQKLEMYKLIE GMLKATGRHKLRLQ/TSQVVRNAKEF LKEIKSATPVNTRKTRK*DSLADTKGV LVACIED*TSHNVIFS*SLIQSKALTL NCMKPERGE
781	14682	A	788	1	352	GTRNYAKSTSKLYRMYKAWMTAYLFT ANCTEYFKPTVETCYSEGL/S LKLLLL I DNASSH*RALMEMYKQINNVFMLDNRI S LLQPVQ*VILTFKSYLRNTFFHKALAPARDNDSSD
782	14683	A	789	365	128	PIDCHGTPTLLKTKQLARRNGAHLSYQLGLRLRHENLLHPGGRGC/SHCIPANVI B*DCIKNQTKKAPRVVISHSA
783	14684	A	790	217	257	WSGGVAREPVIPATQEAARELSLGRDCELSRCHS/CIPA*VTQAGVO
784	14685	A	791	2	363	LAILGHTVS*FVHAKKFWKDLLKSAI PVAI*MIRNMSLHLLAGTIV*VED QSHLIPLS*SLTQSKALIFFKMKYDR GKGAWE*KFRATRGWVHLKPKCLS/H HIKVOG
785	14686	A	792	2	362	GQKGLLHQTYSKPVNAKGFPMKELAK SATPVDI*MIRNRTS\IJSIMRTV*VV* KEDQTSPLIPR*SLTQSKAVNLFRAK PVRGKGAWE*KYASRGWNPQYKEKSC/ RMCNIIQOG
786	14687	A	793	2	360	ARAGSTWAFRNYAKSTLPVLYRWKKA* MTAHLFAARVITYKVS/YCLNKKTPFKI



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning location corresponding to first amino acid residue of peptide sequence	Predicted end location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						*VFIDIVSHPRALIGLYKR/INVEFPA NTTSTLAHPTDQEVISTFKCYFKNRFX AIQLPYSNSY
787	14688	A	794	2	359	AREKLYLSILTPQLRSLVDFAATELTRL YYILFETTLIPSLAISTR*GD/QPERLN AGTYLLFYTLVGLPLLLIALIYTHNTIG SLGILLTLTGQELSNS*ANNLI*LAYT LAFIVKIP
788	14689	A	795	157	365	GIIEEGYLPQQLFNAKSGMISAHCSF RLPSSSYTSA*TFP*CVQWYDLSSLQ PPPPFKFLPYLSDPSTWYILAP/RPS **FVFVEVMEGRQTPPE
789	14690	A	796	224	372	IFFIFIFITYLFTTRRQSFALVA/QAGVQ WRNLGSI*PTHPPPRVKLISCL
790	14691	A	797	482	1	NSGFFFFLPPKADKHDFSPPPFPFK KLKGFCA*APP*VQKPVFYLKSF/CLKDY MLSPFESKVNFPSPPL/SPSLPTMVG PPLPPEYTFSPFC*DPHSINFLPPLGPF LPHFFFLRNVLCHPG*STAV*SLITA TS/VK*FPHLSLSPSSWVYRCS
791	14692	A	798	1	415	NLGGGGCSELRSYHCPANATE*DSISK QTKTL/NKDHTRAGWERA
792	14693	A	799	2	401	VQTGFHHVQAGL/LLTSGNPPFAS/Q SAGITGMSHRAPQ
793	14694	A	800	73	307	PMALEHHGCGNCLDPLPTFGKSHCFVLR CAEMETRSLFPLSWSAGA*Y/CLLQPPPP RFS*LRPLSRWDYRHLPLCPAN
794	14695	A	801	87	401	SLIEIWTLKSGTCENLYNVLS*HSLRA IVLARS/VESLTHVLLKCLV*MEVFAF S*RLSCLFLKLSRPVVVARVCNPS*TRG *GGHITSRDRDHDPHQEIPIS
795	14696	A	802	3	354	LRHYTP*PG*QSETLFPKKKKKKKKKK KLSPFPDPKPLKKKGLFERNPKKKKKI FFNPDPKKKGFLLVNDPPKKKNPPPL GGGGPPKKIY*KTFFFPKKFENPFF FFSPRF
796	14697	A	803	1	830	VETGFLHVRQAGLKLTLTGDLPL*LAYQS AGITGVSHCAWLEFF**CLAVTQTEVA PS*LTIASN\POLKLSFFTLPFHARLI FKIFSRNEVLLFSR/PSQTNLMSQSL SLPKCNDYRCPLYPASLSF/FKLSC MLKCLEVKCNDVCNLL*NTLKNINEMI EGWIGRLTCVKIEKNVICRI*VMLKAT QPVGTSP*ESRSTNSGEAM*SKONT FVTVSVFVLRQS/LCFVAGAGVQWSHL SSLOPLSPKLS*SSCLSSLSNDLRARA FVWPKGADNFTFVFNWTLKIKPKG FRKKKQLGPKIP**KKKKGAPFLML RQGVFFFFFMEMFHS\DAQGVQWDL SSLQPLPPRFRFSCLSPSSWDTEHAP PRPANF/CVFSRDEVSCH
797	14698	A	804	389	3	RGGGCLQSQR/ERLRHENRIMPGGGGC TEPRSYRCTPANARE*DSVK
798	14699	A	805	161	21	FFLRWTL/DTVTRGQIQCNLGSPOFP PPRFKRFSCLSLSSNDYRPPPCPANF LYF**RRGFTMLRLVLP*PRDPFASA SQSAGITGVGHRANMPFIENRFDL
799	14700	A	806	405	82	
800	14701	A	807	938	2415	KITFWETFWITTVHPIHCKREATAIGIL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LSFGSRGCEI/QQPARQGETLSQTNKQ TNKGRPHQVQLPCEFLINPKETITCLVLR LPGNSW
823	14724	A	830	432	1	GYNNOQIFDVDDQAFY*KKIPSRSTIAR EEKSMIGFQKSKDRILLGAKVAGDFK LKPMLVDPSKTPKELNN*ARCTLPVL/V KSN/KAMMTAYLETV*FIQYFKETVDIY C/KLILLIDNAPGLPKAVMDR*EESNV FMVMTTL
824	14725	A	831	1	233	KRLQIKYKLINLMKVTTHVWISICOKLM KEINEDIKMGKRDVLCMI*RLNNSILH KLIN/RINLQLRLI
825	14726	A	832	3	477	YQCKREDLTQMLKIFQRIKGEIIPNS LYDASINMPSKDKDKTKF/NVPRISL MSIDAKILMKILPQIQIQLKQFIPFPE MKG*FNIRK*INLIHLITMKTKTPTMI SIGTEKVFQDKIKY/PFPIITLTCLKIDG RSLDAIMVARE
826	14727	A	833	3	402	RYOTFLIV*TVLITTAIGLSLIPVLIG GITIPLTDRRLDTTFDPAGGGDPILVH HLF*PPGRPEMHILLPGWGIISHIGTY YSGKKKPPFYIGWR*ALISIAFLIVIV* AHIIYTV*IDRDTRAVILSLN
827	14728	A	834	7	395	DFQRVSCMALSSNSFFFWERKSLFFP GREGRGLWNGTTFPLGKRNSPASFP GGITTKAPKLHPKPKKGGGLEKPE*N QRGGPDI*SPQGGKGFAGG*KQGGKSG GGKKKGRA/DP*AYILK
828	14729	A	835	41	444	DPEVRKKERENLYRSVSIKTESVI*NF PTKKI*GLDGITSEFIQLPKKKPK\IK KERTESNPFDTKNTITLI/SKPTFTTKK EN/VRPVSIMNI/DCKILLKVLNCTL/ HI*REIHEDS/INFIPIATISFNIQKTN
829	14730	A	836	3	415	HAYYIVKTSF/WIPKGLSALLKYGLT M*MQFQSIKDLRLGLLITLTIYQ*WRD VTRKSTYQGRHTFPVQKGL*YGIILFI TSEVFFFAGIF*AFYQSSLAFTPLQGGH PPTGNTPLNLEDPILNTSGLLIGVS
830	14731	A	837	378	0	TPPKGPGGKIFLKK/SPGRKIF*PPGNG /PPFSLPLPKFFPPFKAFNFWGGGPGQ GPPPKGVFSPQNPFPQGRFPQKREKNF FP/PPKMGFPQGF*RAPF
831	14732	A	838	383	38	GGKELFKPKREKLSPPGRKAFPPF SPKLNFFPPQGVFLGSGKGRDPPKK GFQKTPRG*LAPOKKKKRNPFRGRKF GPPQ/RI*KGPPPPPPPPPPPPPPPP WSL
832	14733	A	839	39	418	TRISSKDKQY/TPPGW*MAEISTTFED ABIDIALIFPNLPIMLEHKPDCKSWKS VYCKLK*VVLSISATGLDIINT\LEEM KRVSGTWIATDLAKTFFPI/PDQKEFA FSWYG*KDIF
833	14734	A	840	3	335	IRHLF*INKFNLDKMDIT*KLTYEGLE SLN/RII*MF/PVVKSLGSGSFTSEYS LFKREITAIYKPINRVERGGI/LPTCEA TRITLIPKPETCIMRKNCGPVLPMGNH F
834	14735	A	841	1	38	RRLLLEDHLISLY*KINSKIRELNIR/P

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN (09/515,126)	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ETIKLVKGDKNV\QDIDPGKDFNV/KTT KTKIDKSDYIKLQSFYIANETVNRV/KLQ PIE*GKLFKNYSSGKGLLSMIYNRLKQQ HRNNMLI*KLEDHLSLY
835	14736	A	842	2	424	GRVGSITPLSQSLQSKALTLFSPMKAAT GQRAAASKVRANRGWTFTRPKERSGLCNI KVQ/GAGGDTAASSPADPAKINDEGGHS /KQQIFPSGNETAFY*KKNSSGTSIAREE KSMPIFGASKDRVTLLIGANAAGNF\KL KMPP
836	14737	A	843	281	3	FFFFFFFFFFFPEKTLPLFFGYMPSIFPF LFSISLISFSOSFVFATQFPF*VSR YHYQHFNST*FL\KL*FIT*IFPLISI LFLPHGVNF
837	14738	A	844	409	1	ROGGTCPSVPULRLR*KDHLSLRG*GC SEP*LHEKTPAWATE\DSVSKKNNKKGI SCRQHTVGSFPFHLKGLLGLISFPFL NVIYVVBFKFTLLFLLYSICLSHLF SFPKSNINSKFSFSLVCFNPSFS
838	14739	A	845	63	451	KNQESBETLNNLPKASTITLLPKLDT QK*KKRKKKKRKKK\EN*KPITHRNII AKILNKLIAHQ*QQYIGRIIHHQVGC P/GAPDKIQYRCMR/TLQKMGIEGTHL NIIKATYIRPTDSIENREKP
839	14740	A	846	60	460	RNNBPFDLQIVTFYFKWILYDNR**/PT QMLDREBGPKHLPKNLR/QKKVVVTVW WSASLTHYSFLNP\ETISSENYSQEIDE M*KLQSLQLASVWKKQIPLHNPRLQ VAQPVQKTNELGEVLPHPPTSPR
840	14741	A	847	344	2	NFLKPHKGSETPLQKGVTGYVSDPTP*K FPFSLKPLNPLGRGVPPFPDPKGGFPSK IDQGGLSPLPLRGKVPDPPLNRLGPPR VELKAP/HPEFFFGI\PHGLQPRPMI*K PTRP
841	14742	A	848	439	132	RRVAAPPSKNIFFPDGSYKGGVWPQK SPPPK*GFFPKP\SGVKNPPQIQIKVFF FPHARIVPPGDPKTFPPIFFFCFNSI NPSLRGAQLYVMDPLGSGC
842	14743	A	849	94	470	LNNPLSFFPLSFFPLSFGSLSLSLSP FFFWKSGSPPP*GTK/QKPLCKKKKKK GGGGGQNFFTPGGKKNPPQGGGGGGS PAQKKK/EGGGPPGSKKNPGGGFKK KPKKPRGGGGKPPFP
843	14744	A	850	2	396	FFKKNIQMANKHVKVYTTLLVIREMKI PFSMRVHFTSIRVAKLLKTDNTRC*QEG RTIRLMCLQKQVLL/HKINQFLT KIKITL*VDPFISLLGYRSMKTVH SSFINGSKNNRIGNNLAVNH
844	14745	A	851	369	36	SKGASDILEKPLF*EVLGTFPSDPLGE KMP/FNYKGGPGHGISLITPPKKKFTPP GGHFFPFP/PPFFMORVLCHPGWSAV AVSQLTTSASRL\K*FSCLSYSEG*DG RIS
845	14746	A	852	1	367	PPPKIKSTPSGKPPSKRGSFPAPPRGG KFWFLSQKMGGP*FPPPGVKPE/NIP *PPRGRVFL/HMLAPAPPGPPE/PKP PSP
846	14747	A	853	1	378	AMLATLISNS*PQ/CDDPALAPQSAGIT

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						GMSPCARPTSCSPYP*ILLTVRTPIKTR NFFFFFDTGSNFVAQPGSGHDHG***P QPPGFNKSFNLSLPSRMDYGGAPPCPVI LCIPCKDRVSSCGSG
847	14748	A	854	369	1	SACRGLPKCWDYR/R*ATTSPSLRTIYI ER*EKTTSPHNARFVDVKLHHYDCSVN DF*KAL*NGDDPPVLMKMHMQSLNII\ FVPCFLRQLALSQ/AGVQRHDHGLQP QLPRLQPSSSLHL
848	14749	A	855	380	335	NFGSGSCSELRLCHCIPAMAT/SETLSQ TKIQPKKQV*LL
849	14750	A	856	373	1	LRIKILNKKGLANLYP*RR*KLTHSQVE PIPEMQA*PIIRK/TPSIKPIVIRTKKK KKSQMLISLDTREKIPDKIQLPIAVKPV KLIGBTGPIPIFKSIY/KKSTATTIISG LNASPLRLKTRQDF
850	14751	A	857	369	44	KVONLYPEKLLNKKIVDLNKA/NSLCT RFRKANLANIIMPKLHRYN/SKVKPIPI KIPANCFGEIDKLILKFI*KPKRPQIAK IILKKNKGXILDPDKTYIYVQYHLC
851	14752	A	858	1	348	QWHPAS/LARPPPRPK*FSCLSLPNS WDYRHAPRIANFVLCFVG*GGIHL
852	14753	A	859	1	366	CTSPTFNOKLEMYL/EBGMLKATG*K LCLLQCKV/QVNAKEMFLKEI*SASLV NTTMI/RKQSPFADMEKV*VV*IEYQTS HNIPLSQSLIQSEKALITYSSMKAERGE AAKEE/LRASR
853	14754	A	860	12	366	PSTLGLRASCLSLLSRWD*RRMPHPA N*HNPICRDG/SLTMLLRLVL/NSWPQA THSWPPO
854	14755	A	861	424	78	NRPLEGGTASFSLANNP*TLGKKK/NP FF/SLKNPPPPPPPPKINAAQQCPKPPS FGGLNGGFPLPRVKAPIIHKGAPPPQF PQKKKGPRVFPFKKKKKKKERKEKMT ARCYP
855	14756	A	862	327	3	SHWFFAAV/GREISM*AMAPDQTKKCP RSARDAIKYFLTQATGSILIRAILFN RLSEQ*SIINTINQYSSLIIMATAIKV GMAPPFH*VPEVTQGSPLTSGLLVL
856	14757	A	863	1	341	YDRNKWDTPGS*TERLNTVLSMLPTV IYNFNVILIKIPMFPAITKSIKVPFSR DYE*PKQS*KEQNMETHP*FQ/QPFTA TVIKMWY*NKDRYTY/DQHNRI*SLGI NPCT
857	14758	A	864	32	324	LVPFFFFFFF*KKKFFFFFFF*RGK NFFFFTPPPPGLANLFF/CPHPLKMKER APFFPN*FFFLKKGFFFTQXGLNF PPLSTPPLTPPKGL
858	14759	A	865	350	3	RVKNPDRFWGF*VVLKLSFFSKTNI* LPLKIPSPKIVPWGKILGAL*NPFF CFKPLNFWGF*KL/SFFFPPIYFF*KP LAPLKRKRSFFFFFFF*DGVSICRPQWS AVARSR
859	14760	A	866	342	118	GSVTOARVONCDHSGI/QRT*PGIK*S/H PPTSSYQVGTGVCPLGLAMLSRLVLS SWPQAILSPWPPTVQGLQV
860	14761	A	867	1	354	VKPSF*PLTGASALLMTGLTM*IHFH SITLLILGLISNLTITYQ*WRDVTPE

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						STYHGHTTPVQKGLRYGILFLITSSGV FWAGSV*TFYRSSLSPTPOLGHHMPTG ITPLN
861	14762	A	868	3	344	QINNPENISIC/WIOGATGMFLHCWEC KLQPLWKRTT*HO*SR*AVPLSGMFP/ NRYSSSTCTPASI*KTLFALFMHTPL/C LSRVWILK*SWCNQKL*Y*SVNKRSEF SLANA
862	14763	A	869	345	1	KONGLKNVKTG/EGASVQSR*VS/YL GTIKKITEEGKYLPERVFNAGASAV*G KKLPORTFISK/EEKQAP/GSEVGKDRD TLFLCANMSRFMISTALLYKADLOSILK GKDKHRL
863	14764	A	870	340	45	FCSFORDRVSLLCCLGHSKAFGLK*SSCL SLKCK*DHRC/AA/VPAMFQRCTLEKN QIY*CAERIL*SERPHTRHLDSTVNL PCPLSKVIFWKKKQIY
864	14765	A	871	209	72	KLWDIMTMEYYSYSAIKRKNKPLYTIMND LKDIMLCCKANKRSHTV
865	14766	A	872	3	353	SFFLGPPPPPPPPPPPPPPPLPIFFWRF FCFSPPKKPP/PPFL*GSPPPPP*RG FFFF*KKGGGVVPPPPPPFSPKVSPPP PKKGGG/PPPPPP
866	14767	A	873	3	267	DPTMLARLVNSN/MPGVVAHTCDPSTLG G*GWITRSQVRDQPGGHEI
867	14768	A	874	1	346	PERPPPPFFFLVPIYFKVLYL*DRV LVCHPONSANVPHHSQ*PLRKQSSH LSLSS/MDHRHMLVFSFYRDEVSFC LANFCIFL*RDQFSNLPRQ/VLKAICLP WPPSL
868	14769	A	875	1	172	KLSSGSPASASQAGITGVSHRARG LLNFFC*CAFSVPGCLGYDPTFTH/LC PPSFHQSIVASLDPSCLS*L*MSF
869	14770	A	876	1	348	LLFCNNYSFFHGVKFKIPAFFVFGPGC LPHFFPPIPTAPFFFLDRVLLFPQWRE MGFP*APPTFSPPQ*GVFPDPPQ*LP RGPVPGVGVFFFCIPGRDA/LAILPR L
870	14771	A	877	1	203	GFHYAGQASLEVLT*STCLSLPKSADY RRGP/*GLSYFLYSLRS*FICAMSI HPIFKKKASD
871	14772	A	878	343	102	EWEDCPSFGGRCSEPRSHCTPAWRE TSPKYLFLQP*KLKNTYLSISIP* LEVA*LLKLHFWNPHGVSDFP
872	14773	A	879	2	359	RDITKDMQNETGM*SSSTLSLTSGLVH NSPIRPSXMKNDSTRWGCACRATRLI HCWNR*WVQPPGS*ISSFKKLNAVLS YDERPTRYK*K/P*VHPKICV*WMA AFFLISPNW
873	14774	A	880	205	1	FFRGVTEGL*EDPYVESVI/AGGITARR PLEFFFFFFFFFFFLRWSEFALVAQGVQR DLGSPRPPPPGPK
874	14775	A	881	150	2	CRARVDGVPRNPGSLKPPSP/GSSDP TSASQECGIGTGMHHTLTL*VF
875	14776	A	882	345	1	KGNOPWKTERRALFC/TLKKKIFONS PRGNF*KFFVKKKLPLKKEGFSPTWG KKEFFPKKKKKKKK*AKDLNENFSRS DVQMAKHKMKRSTSLIREM*IKTTIR

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876	14777	A	883	2	355	YHP DRILFSASHLDLGLTYLLPQA*SGVLST SF\SLTLRAELGQ\SGCLL*NDHIYMG ETAHAFVMDLFIVRPIIIGGFGN*LGFP NKKGADWAPF\INNISF*LLPSSLLELL ASAIVEA
877	14778	A	884	262	2	PTCEQSEREIKTKIQPTTESK*IKPVG NLAQAKADLYITETIAYKLLKEIKDTNK *KNIIIV\SWTRRFNNFELGNAQMLMP VTPA
878	14779	A	885	16	318	TLRADCADLFFFFFLGCKKRGCFPRLKG RGETLLN*TLIFR\VKGNF*PKLPKW/ DFGKNPXYL/AENFVFFFLKKGGLTLFG LVLS*IKEFFHMLMPKGV
879	14780	A	886	298	322	KRRTP*YPPGSPHPPPPPPG*KAGAP PPP*PKGFF\PEKCKKPGVMVQGTQKP PKKTKVRVD
880	14781	A	887	353	3	FFFWGFLKTLFGKALWLFKQFFFFAQK FFFLPSLPPPP\LGFLRGLT*FKIFSP LF*KGAPQKGLSHPLFFFLISPKPPPPF FFPFFPFFPFFPFFPFFPFFP\RDVLL YCPGWA
881	14782	A	888	22	341	IPCTCLKLGKGVHDHDSQLWMPKQZEE MRTLENNLAVQSLQLWLDLSPYDRAI ICAREIKTYV\QGNCT*FMALALCITAK KW\QLKCPSTDEWVSRRMWTCTR
882	14783	A	889	51	338	ERSQLQWLPILPSLFFFTGTQFLCCCP GGRAWAIFKIFELPA\PK*QPSCLTLQ TI*VYGLNP\PRKPNFVFLKRGSLFHVG SGRDLPPSGDPP
883	14784	A	890	1	225	GRRLPENNLPNGRAGSLRLCYCTPAN VTERDTIS/RHTHT*NYFY*GST*OLAN SCCCNMANKPNVICILRMC
884	14785	A	891	357	164	GKCSDSRLCHCTPAWAT\TKTLQSKL ILKONKFRS*LDD*INMCTVMPCFHV FLFIRAAPLFSDWLYNK*MRNT
885	14786	A	892	207	302	EPFSGIITINESIHGEIIVLNVTSSNR PSKYMQLTLELKGKVKRSTIIVGD/FY THLLVIDRTSR*KR
886	14787	A	893	86	332	VNRVSCCLRD*ISLCHTNSAVVQS*L TVASNSW\VKOSSFLGLPALWEAELGGS LEVRSLRPWAT*TP\FCKNKL
887	14788	A	894	2	336	FFF*PPQTLFLNKGPGPKREEGEGGS PRQCKGPPGLHLTGFGGQPGG*KNPEP GPGGRAPKGETRGGGGPTRPQIP/QLI NGSGKPKKVTILNGANGTIKIFLITPVG
888	14789	A	895	1	214	ARKSLASFLAPSLPFLGLRFLPSLPL FYFSLPSFLGSGSLPST*VPS*LSDF LLFPSPFLPKLWFLPS/FLPSFLPSLPL SW
889	14790	A	896	131	352	TLHSDSSESVPRDEKISDALAVEDDORS PGTINAAELS/SSVRERKKKEK/KPSPG L*DQSIKESDSYMSGRIQ
890	14791	A	897	3	184	CSVAPAGVQCHDLTSLQSPPP\SSSNPP TSSNPPISAF*VAGTIGMCHAWLIVF LVDA
891	14792	A	898	327	264	NRAVSLMNLDAVL\KLISASQIVYTK



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						KMIH/HNQIRFTIRM*GQFTT*TAINIY HKLIK*GRKHMLPLIYAVKIFBK*YHN IMIKTLHLK*IKRPPGSPFIYSL
892	14793	A	899	3	313	TKAASHSQVRANIQFLVGRTH*HLKSKT ISPGRVGATAAVNSTALLEYLTAEVLEL ARNASKDFTVKHTTPHYLQLAIRGDKEL GSLFKSTIAGKGVIPHILKS
893	14794	A	900	340	1	HLCPHKEHLY/LQITSCPLAIIT*FISTI ABEHTKAPFUMAKVESLWSGPNIEYRAG PEAFLFLAEYTNILINTLIVTIFLGPT YVAJSPKINNTTY*VPRKIVVVRVFIID FV
894	14795	A	901	1	252	LTFFPQHLLGLSGHRRYSIDYPDYAT* NILSSVG/SGPSLPAVILITFIMI*EAPA SKRKLVLIVEDPSINLE*LYGCPSPSPSF
895	14796	A	902	326	1	LGFPPFLKEPFGVFFIFFF*PMNFGV GPFF*KLILGLILIDFPQFFFGVGSQIVP PPF*GKIPPF*KNTPPFF*GLGGSIDHP PLFFFFFPL*DGVLCHLGWSAVA
896	14797	A	903	1	352	KGTFPVNCSG*KGTQKGGISQGGQNV PPGCIHFVKFELGFPQAQLLIS*GRLRI F*KGPKKGLP*TVFG/RRAQFEAPR
897	14798	A	904	325	2	RLERKINDYWNEMKVGKNTYEPLNLVE DIQKRFDQTVWQDACLAKRK*PYGMDQ HLEK*WYWCNNHDSQFRYCM/FKQDPEDM DUVHPNYGKPKKPSKEYTFWSQMP
898	14799	A	905	1	329	IGLATIGARRIVRGQTAKSVAHNVCE QKLIKKKGGPGRBFQNLKVENPKNQGS SF*RGLGPOSNFFYLKQ/RLGTFE*KKP PKI*ILAMEPPNKKIP*KINKKAEFFF
899	14800	A	906	148	2	DVDKLLPLLESLPL*RPYEGSYMIEGT\ TQGPYGTMSRFTLEANNRIR
900	14801	A	907	384	1	ESKRSIFGPNPNPPPGKFGSRHAPLNL RSRSEPHKAGVKGFPFRFRGGS*MPIP* SFLOQLCQRPVGFPSLPPPGAFPIKSL FLRQESRSVTOAGV*VGLQCRPRLK SPSCLSLPNSWDYR
901	14802	A	908	3	297	TRIXSL*INHLTRAKTVLLEENMGINL HDLSSGRQQPFYRDTFO/SMINTAIKX IMKLSFVKMGSPISORTPLRERQLTK* BKIFADVYLIIGRRG
902	14803	A	909	169	373	ASNILSATDISNTRGPPSGSGFSGREAY VEAGTYNTNSCLGQVNVF*YMQQLIVS IVLL*LL*VTQKL*L/GPQKRFV*YVP ABT*ASLPLPKCDPGPKVFEWSVADS/ DV*SLMLALIGSKFKCLVF*SKFLSS AYIYSPLEKKLFIILGCFVMIICFCFPL ERVL
903	14804	A	910	132	368	GRIFLPVGQERGARVSFLPLF*DRVSLC HPGNSAVAQSLTTS/TNTQNNSSHITP F*VAENERCA/PHTPNVLFLC
904	14805	A	911	2	339	NSWAQK*AGITGSCHTQTLTLEF*AHDR QMMFFLFFLKINPTFCPPA*RPWPGGLG TE\PILPGLKHFF/CLTLPNNDKGHL P/HYPYQ/CGFLKNGASLISG
905	14806	A	912	3	381	LNFCDTHTPLTPRPSVQRQCLPLVEAGI RWRALISPOLHPPT/YSLSSWDYKHAA PHPANFFFFFKGSLTMAPRPGGS*IF

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						IYLLIYLERESY/AVAQAGGQGNFNSG QPLSPRFKQFSYLSLLR
906	14807	A	913	394	1	MSKGGKITG*KLS*KFAQKVSQF/NAKEKL LKEIKHFTLMNT*MI*KRNS/LIADLEK ILVVWIKNTGYISIP*TNRIQSKALLI FYSMMTTERGEEA/KKFEARRDYFMRKE RSRLLNNKV*DEAANADGEAA
907	14808	A	914	326	200	HNWLSINKKVKSNCPL/PHPTKINSIKL DIKI/R/LHRIKILQRNVGNHIYKI* RQ KRS*PRHNPLHKNCKCLAVHKTN*NH* KIYL*CI*KTFAPVM
908	14809	A	915	3	334	LIVRVGPKPKFWLHQLGLYC*VISFF INKSKYIVLHRLK*DEKNIP*MYTKKL *NVLK*VLVLPFSSKNL/PQSVAHT FNPSTLGDNRGRI*TOQOEP/QLSLTWNK
909	14810	A	916	14	299	YQKLQPKKSPENAPTDKPYKIFK/LTA ILQ*LFOKI/E/KETPLPK*SNESNAL I*KPDKDIT/SKNVYKPSVSNIAKILN KI*GYGVQOQOLYSK
910	14811	A	917	3	339	SLQPOSCKLKCSCISLGSCHDYCHKP CLA/NFF/VFF*EKGITVIN*NGDYPL GRVTKRDERHG* NAGKVLVGV/ QGF ETQSRVFPQAGGGRNLGSLQALPGLN PPS C
911	14812	A	918	2	321	GLISGIYRELSPKMTDSSTKK/KDLNR NPTKEYVQMAKHMKCSASLVIIEIK\ IKSTM*R*E*\TPTRMTIKD/DINTKCN *GYGAVGMLIHQW/NTKMQVPLWKN
912	14813	A	919	51	326	FFVFCPLPSLVFISLNGLGF/PTFFPRI PS L/PYLQIT*LYLFFY*LKPIPLKPPFRDR VSLCHPOMSTVA*S*LIEASKYH/VQ*S SHLSLSS*DY
913	14814	A	920	239	2	DSLTLKSVQ*HDLGSLQPPHPLKQ/PL PSNMHYRCMSPCLAYPLFLVETPTPCRV TQASLELLGLSNLPASASAGI
914	14815	A	921	1	242	PRPRRLLYKFIPLNPLQ/RSRSATQA EVQ*HDSHSL*POTPRLK/HPPASET
915	14816	A	922	249	1	ALFCALKKTLCTGLT/IALFTIAE/SR HNOQTPTCLSTDEILNK/MHRHAGNYS AIKRNEVL IYAKI*MYLENIMLSBII
916	14817	A	923	404	1	SRPQKRLGLKCS*RPKGLNKNQRKPS TFFFFETKPHSPQAGVQWYGC*SHIPY LLHIIFF*VF*MFLLITV/PSRNKDL IGNSEKQIHN/WSSLYFYF*LFFLRWL TLVPSQGVVRNGLGSQPPLPRFK
917	14818	A	924	6	358	FFCSLLHGAGGETPNISPLPHPL*ETKS PPKPPHPLKKKKHSLLFFKI*FLKKNQNG PFFFFPAGPNPRG*NPDPQP/RPPKOPP PPKELINPPPPQGNPPNGERPPLGPF PKKGGY
918	14819	A	925	268	2	HYAFKQID/TAHLRPSAGKKETPAKLL YF/L*RNPNQIQIQKQKKCLPACRGN VAHAMNPSNLGGQAGIT*SQALETSNG NMGKP
919	14820	A	926	74	338	IAGTGVSH*RSKNSY*KQPL/NPQTVA HSCNSNNGGQGNIT*GQEFETSLANN VKP
920	14821	A	927	339	1	LRLFACPLPKWMDYRGEPPEQ IFFSWH

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921	14822	A	928	3	416	FFKKGQGFICPIEKGRLSNCCPQKEVLI *KKVILKI*PFFFFLMESSCSVA*AGVQ WHDLQPLPF\NSWDYRCPSPRAKFCIF
922	14823	A	929	344	69	RCWENKIN/FPWK/S/VWPC/TKVNIH SPYDL/TLSQLPYRDEYLCYSKNIIMFL IVLFIITKNYKQPKCASVG*WLRILWYL /YMYNSAIKMKK
923	14824	A	930	378	1	YKRSPLIAKSA*DGPAWKSILPRS*YKR SPLLIKAKPDQILSGWESPLII/PRAL LQKLKPAASKP*W/NPKKRALIS/KAI PSKNHAKCINMFPNFKV*YRDATATKA* WYKSSSL
924	14825	A	931	479	83	HSKIDPRFPIPYKIL/MLKMFIDLNVK KTIKFL*HIGS/TIPIVDHKK*NP*KK KLVN/WDFIKIKSPCPVH*KPAVGK*RR /QP*TRNYVQTHSTSDRLISRIKELF *LNSKVINIRKWAQSLN
925	14826	A	932	36	440	SRKGLGRGLKRGGFPPPPPKGLPGVA PPGPEGFQSL*KG/DRG*PPLKVGKE KGRKI*EGG/EGGGFLPPPPQKGFSS NFLGFIYAGKENP*GSGPPPLFPGAQK ISLKGKENVPPPPGNLFIYFI
926	14827	A	933	8	398	TTYASIDAEQLPRAKNAPLITTP*HITK NGPILGKIGRKMIADQ/GHRMKHKKCK LITQVINTHYVGPRIILITGTEPLQNLPE LWALLNFIPLITPFKSCSTFEQWNAFFA MTGERVHLYEESTILIRKVKVL
927	14828	A	934	1	441	CLQKKESTLTINWHLRYFLPPPPFFWPK KGARKNGRPPGSGPKNQAPCPKPFEN PGEKTKPKRGFPFKPCPGPQPFPGQ GKPP/HPOKOLLPFVPOAGPQGRGG* WNPFPFG*KGFPAPTTPPK
928	14829	A	935	3	383	TRSHPRALKVETVETINIVMNPANATSL QPMQ*GVILTLKAYILRSTPCKALAAVP SDS/SSDGSQGSQSLTFLKGLFLDLA* NIGDSMEEVKISTLTBMKKLNIPFQND FEGFKTSVEEVADVVKITEEVQVSESD GTEFLQSH
929	14830	A	936	417	1	PGFRASKDLTFFSSGNNAGNFKLQVLI IYHSENPRVLKNYAKSILSVLYKNNKA WMTAHLFTAMFTE\YVETVYCS\KKNIF FKILLILDSVPSPRALREI*QMTITVY NP/STTTSILQPMNQ
930	14831	A	937	412	3	CFFSRDEVSFCGPGGSPSPD/RHDP PSQCWDYRDPFLWVP/PHICFLHKKRS SIMGSMYDF*KP PHQWKSPPPVSVLY GSLPVOVLAPPTINPIYTFSPPPPW GGGRVGVGVCSSEVCEPFGSDENVLY
931	14832	A	938	1	416	KPTRVKKINPPFFKNTKNGGGRVQGSILY SPFPGGLQKNQPTPEAKGSLNLKFPPTA PKSMGTQKQSLPKKKKKKSLKPLNQ KINPKYKQS*GITLPE/FKLYYKEATV TKTAWRYKRNPIQNNGTGRNKAH
						KNRHLDQCSGIERPEIDSHKYSLTIDPK GAKVI**RNDNLFNKNYNNWMTCAR INLDTLTLYFQNGSQT*P*NIKLENS MGNLGD/LGMSQ*VSSSSSRRIHDKK LVS/WDFIKIRNISKSGIKRMKSQTT

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932	14833	A	939	4	443	D DFPDYHHDDHYAKLGRTPGSVGGSPDPQ FTP SRMGREGGTHSIL*CS SLGMGVIA DLSTDPTELEKRALEVAGPDQASATSP ASPRRKAGDGGHRRALPGCTSLTGTTG KSGEAGUGKPPGD/GPIGYSILPGSGP GSGESVMG
933	14834	A	940	3	404	LPMFLFFFF*KRSC*VSQAGMQCYLIK ALQAPPFFRPT/SLSS*DYNSLPPPLA NFLYP*ETRGFTGLTRISIPQPTMG LSQTAKLIFP*K/HRVLVDS/HG*SAR AVHGGDLHLLEP*EPGLK*YS/CISL
934	14835	A	941	397	1	PVNSQVANAKKKPLKESSTVLSGT RKONT*ADME*V*M/WIKDQPSYSLPL SQSVIQ/SRALTLFDCTKASERNRGLKQ WEPAY/EGSGKGLMRPKERSHLNLIKVQ DEAVYPEDLDKMDAVNTKHQI
935	14836	A	942	441	29	SVTLCKHIVHVPTFLRKGKRCPLPGQQ PWPSPG/PHPLSMSPV*PRPQ\PIPLHS APPLALGPFIPLMSVWGLPFPQSGGLR NWKPPFPQPSLIQ**HFKPLKPIRGLR PFPESTLSILPLGTRPRAKGLVNRSL
936	14837	A	943	2	397	ARDAAPEPGRHLQGLSARHGLRPPRDS RPGED\PT\SPHPLPLPAVPITFVPSFG DSWLL*SPFFAPWASEGACAPNPHAL VPSPSGQASGLRGGAPSWKGLDTDGQQ AGRQSGPAPFPPSPPLPPSQDC
937	14838	A	944	3	449	LRQVWHEGEMFNKTTLIYHYTPI*LTNI KVTMTKSLWGCAEASPTSC/HMRIM VKPLMTVQ*TLI**KLQPLPBAVALH \SICPRKVY/CHRGKTRS*MFVI/A LPVTAQTKN
938	14839	A	945	380	175	RAPAVPATGEARVGL/H*TWEDRLNG GEV/CSEPKWCHCPANATKNCVSKKK KKKEKRLNHQDEK
939	14840	A	946	21	331	VAPLKYGPSKETI/IQSVRGTECKRYF AYYPSDTGLITRIYEEL*RLNRKEKLS SVYKYAKDLI*PPSKEDTQMANRR/H*K KCSTSLIREMRFKTTMEVDAV
940	14841	A	947	365	1	GGGPPWFFFFFPLGGFLKIGKIWAYKRT GPSFPQKKKRGPKKKPGGFFFFF*K GFVAPGGQWEGFGLQLPLPGVKQFFC PRFLRW/DSRFFFFFLIKNSAEQFPTL YAGVRRYIK
941	14842	A	948	357	137	ISAHCELRPLGSHSSPALLCSPLSRTP NLKQSSLPSLPKCDYR/LATVPQGLLL F*RHICISIRNTHLHNM
942	14843	A	949	53	352	REDNRHKEKRLNTRKMANEWHRCFSE ETQWVKHEKGLASPIPSMQIRY/L NSLA*KKKESKDNTKLHQGFGETKSV* RYIIN/PYDPTPLGTY
943	14844	A	950	937	3	KVSPYKINIRH*VAFICININQAREK/M NMVLFIATNKKI/SYLVIH*IXEVKYL YNNYK\LLKKNRDNANK*KGTPCS*I* RINIIRNSVLKATYRLSAISLKL*ML FMLEKKE\TILKVIWIKTAHLAKATLT \QSNPGGLTLPGLYYKATVIRITN/HCY KNTHVDQ*/NRRRSPSISLFTTQLPSD

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						KVNRSQ/WKNCISNKNWYSESWLTCRR RKLKLYLSPYKKNSK*IKNLTVKLRKI KIVEHQKSTVLVTGLAKGPMNTNTKVN TKIKVKN*HLTKLKNFCTPKET/T*QIC RQQRVWMLFSNF
944	14845	A	951	246	1	AASTKIGVQTKTCI*MLIAALVITVKRE KQSKSSVE*E*TMWITMTEYISVTKR NDVLITITWMLNSMLSKDSHG
945	14846	A	952	2	255	QCGEKGTFLEKWEQYQLPKKT*/FLK DPDTPIDPDCATPLGTYPKYQSLYYK DT\AKTNWQPKQLWVGTKQWYTVDA A
946	14847	A	953	343	3	GSITYTKEMEPKNNLQK*KASCTDQ*G EFY*TFENEPIILYNLFQKTEAKGTLTN SRDEASTILIPKPEKCTRRKENDK/P/I SLMSIDAKLNLKILAN*IQQSRIYSRHT RLIQ
947	14848	A	954	1	349	AQPPPTLFTLHP\TYCTFSS*S\R*QKT LKT* PQGFICPFFFFPK/CAKSCSRIK GNGPI IAKGTPSLGLRDPPTSPT*VAG TKGGGPHQLKFIK*FYISF*HNGK FCSRRGR
948	14849	A	955	2	351	GLKNYAKSTLPVLYKNN\KA*MTTLF TMSTE*FEPTVETYS/EKKIPFKLLQ LMDNA*SEPRALMEYKELNAVPMYNT ISTLOWDQGVISTFKSYL/RNTFCKA IGATDSGS
949	14850	A	956	336	3	PTKENFEPDGF\TG*PYCTFKELIPPT FLKTSREYFSSSSSSSSSSSSSSSS SSPYRPI/SIMNTD/AKTLNKLTLNQVR LHIKRNTHDLVGFIP\WENIRKTDQS NN
950	14851	A	957	181	1	RNDLTMLPWLVSNS\GLRRSSH/LPKCW DYRFEPPCTA*GWFLIGHWNVS TVVGS PRISRQ
951	14852	A	958	3	293	GGLTSPHVKTYYQATVIRKTMNG*RGVC MDQ/YNKTEPNTDPCKSQLMFSEVTK ATQ*RKDSLNTENWNN*MSIHKSSSR KHLNQLVTPYTKL
952	14853	A	959	350	3	NKKKGQSLVFRSPITLFFFFFL*ISMG\F IMLARLV*NS*RRNMTTSGSGVGITGV SHHARPHKRLPLPSIITTIOWAGV\WHL TIVTSLMDYRREPPRAVLDPFHQRS RMPLSH
953	14854	A	960	349	1	GGFEPFLFFFPF/PPWKGKPPFFQ\A SFPPKKGKGPDPFFPGSPHGWKQFL VKSPLPFFWKKKKPPPP*KKFFPP\VF QKQGRVKKPPYERNWLLGPPTKESPK KSTGS
954	14855	A	961	379	160	PGPOGEPPFFLNPKLWGGGRFL*AP LLRGVRQKNSLNPGGGALKPGS/HMP PSWGKKGFLE*KKKKKK
955	14856	A	962	184	2	TFPSPKKIPPPFFFSKFFFPKTFGFSR EMFFFFF*DG*V*L\CHPGWSAVVPS RLTATS
956	14857	A	963	1	328	ARLVLS*PQ/COLPASASSGCTGV HCASASQAGITGMSHHRPKMISLYLG FWSFNINVLHPCASSLEGESNNELLS

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957	14858	A	964	1	334	KKNWEFLDKRLHSTKLGNNHVCNPF HPIAGRGVGGVPLGF/VVINPPPPQ*GTP FFLKPKNNPGRGAKPVIAPRGG*GGKF LLPREGG/PSMNPNCPPAPPP
958	14859	A	965	206	360	OKSMSLHQO*QDIHSSQAHNRSSW/PGA VAHTCNPSTLGGQGMQITRSGDQD
959	14860	A	966	10	332	NFFSRGAPPPPPPPFGGGFFLKKGPPFF* KKLLGGPPPPKKNPVGVPFFSP/ANKL GFPVPPPPPPFF
960	14861	A	967	1	282	RKCAKLANRESFKEDTWISTECI*H*VS LRKSTLKPMPHPHY*NE*LYKKDDDIK CW*GYGVTVGAVFHFWVSRMVQPLNNW TVPRNVKFTL
961	14862	A	968	339	195	FFFCDGVS/KCCPGWSRTPRPGSTCLLS LPKCMWDR/RL*ATVPSLDLYL
962	14863	A	969	3	342	IKKGPHPLQKKGPPVPPVFGFKISYFPF PPPLFNNPPFFR/DKASLCHPGWSAVML SYFTAAYTSW\VRSSSHLLSS*EWKH TOPCLFF*F*FL/CRSK
963	14864	A	970	384	6	GRKIVAGFFPLSPLYTPPEHGLGPPQTF GAGPPAHKSHQKVGROKRGPGFVPPRPP APLFFFFFK*SVLEKKENLYNSLPAY KILNKVQGETQCEGRAHIC/VCVVCVVC VSVCICVHVCAIAC
964	14865	A	971	427	109	INSQFELQSKRISNLEDNEKIT*SERES KRMARN/E/QSLRETWDTFGYTNIGIM ECPREBK/GKREKTIKKMAANFPHL NKNINLHQLAL*TPRTCTCPGG
965	14866	A	972	389	145	SLQP*TFRLMLSSHLSLSSWDYACVFP HLANFLYF* *R*GFAMLGSSNSA/SAS QSGGIGVSVHAP/VVTFKKKLAVDT
966	14867	A	973	170	419	VSFLFFFFFLERQFYFSPGGGREGGFG LIEFPF/PGRGNFSCLTW/RRWD*GAP PPLPAYFGFLIK/TGFLVGRGGDLRLP SR
967	14868	A	974	212	3	QNSMIRYSRSMRSCLOTTLILSLNRS LKSPR*/WPGVVAHACNPSTLGGRGRI TRSED*DHGQHGGET
968	14869	A	975	28	356	VFETSLFENKRSIVKSTSLDPRTFYKPK LIESI*CLHGIGQNNHANNRVGNQLDA /EACENLIEKGGISQW/SLFNK*QWS ITIHKKKKTRPLHCKIKGTGDKFKLS
969	14870	A	976	350	1	LFCKKKVSLCGRFPFPPGMRKSTLSL PKMBGYR/RIAPPQLRI*PHFFLTSKA TFL/CLORSKGRNSQMFSPFSGVSL CSQAGIQNRDFGSLQPAILLNFK*PSCP ILSSWH
970	14871	A	977	4	343	PLHSSLQHTVRPLHNNNNNDPTKQW* GCKPGPLIHCIWYNNV*LNKTDWQF LIKPNIHLYDSVAHLGIYPR*MKTYL QRL/CP*MFIAAVFLAKNGQLRCPSV SK
971	14872	A	978	3	424	KRMRRQATDWEKTFAGKISDKRLSKIH KELLKLNKKKSPQVACFKMGKQ*TAH LH*TIYR/CRVTHRKDHSRWLLREL QILNT
972	14873	A	979	114	325	QQQNN*IKELAESNRDFSN/EDIQMA NK*RCSTSLVIMNQVTVRYTYLTLI

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973	14874	A	980	339	2	STATTIRKKKQNPKK GPTGPRKPNQGGPPPKGSFFL* KISPPS* NDPFFFGPKQKPKFFPPPYLNPGRNFF SKKPLFFFF* KKQFFKPPFFFFFF* GRVSLCCPGMSAV\A* SRLTVTSTSHVQ T
974	14875	A	981	2	377	QMANHMKSPSTSSAFHM* IKNNKMRSH DTCRMANININDT\CW*GCRSNKILMH SW\WECNQVLL*TW*HFLNK/DTYH DPAISLLGSIKKSKFCT*/T/CNLYL NVLFINNPNMKQSNWYSNG
975	14876	A	982	1	457	INREIARN*TERPKNTELTSSSSSSSS PLVLGTRKRSQN\WEDITTTDTTII/ TIIKDYS* IYA\NKIEQASSSSSSS KT YNLSGPHIEGTESLNRPISEIEIESLSQ NLPTNRSPRADSFTGKFL*TSKDELPT LLK\FQKTEQERTLER
976	14877	A	983	332	2	TPKAGNQVLPFQYQSKVAPAPSVUVAL PPPPPPFFHFCFPQPHCSLPPQIPPPFS RFFLQVKSSQGGPPSLLGWGEQ/NTLP FFFFF*SHSLALLPRLCSGAISTA
977	14878	A	984	365	2	KSSKLFPYPLPFLFLNFGPKPKK/SGPF FCPKNFENFRKPGHNFNGKFFLLKKG PTVE*IKKFWWGPLEPLK*PSGVKRFPH FLIDFERP PFFFFFLLFELVGRHFMVG QASLELLTS
978	14879	A	985	1	153	GVQWQNYNSL*PRPFG\SDPEPTSAFQV AGITGVHHHTLRFVFGIFFNE
979	14880	A	986	225	1	LYTYREEREEREERDRDREHSHTHLYHT RTHLDNLLFCHPGNNAVA*SWFTVALNS WV\KSSSRPSLSSSDSS
980	14881	A	987	2	375	GTDYFILIATLVVVWSHVLFFPFEKIA PFCPPAGKTGANFGLRAPPPGIKEIFW PP*PSEEG\EPKPNPSRGNFWFFKCRG QSPL*PRLFG/HDRP*GNRPP*/PPQRG GNNKGDPPPPPGGIF
981	14882	A	988	55	335	HTYIDVPVSGSWLTV/ISLLELTVFCY NVGAL*ASG\QASNNRISVSDFLPLFSY LPKGL*SFPAFMWGHKILI PERVIPH MLEBE\TCTER
982	14883	A	989	295	369	ILVTHNEL*VLPEQRTFLKAMALRS IPLLKR/WGRPGTVAHACNPNTLGGQGG RIKRSIV*DDP
983	14884	A	990	2	240	KKISNLEHFRNSESQS*KTYIYMIIF T*KLQNGIYK TERYIYIYIYIYIYIY FFFFLEKKLELEFPKSGGGPF
984	14885	A	991	463	0	GERQLSCLSLPSSWYIYHMSHLNPF \TF*VERGFRHNGQGLLELTINDSPSS ASQSAATH/GMSHCTQP
985	14886	A	992	82	365	ETCHQLYRSFLCSFC/DHPSNKSHT MNCVHFIIRLLNFSFFFEKKFRFVQV EGQGSNLG*LVLPPLPKPESCLTLRS WGYRGPPPPPVN
986	14887	A	993	3	317	GLKQSSCLGLPRKCDYRHKPPCPHTIF NTH*IIKVLNVFSFCT/PLCWSIALSD HVO/PV*LYNNLVSSFILLLLFFSIEVV YLACLCFVGSPIILFFF*YILTF
987	14888	A	994	350	139	LFERLRWROHTS\VGQGCCSE*SHCT

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988	14889	A	995	219	1	PAWATE*DPVSRIQKNQNDQTFSSHFFIL ECRTSGVSAFLAL RPRRPLTGKTKAKNHHFTPTRMPIKDN NKC*QGCGEV/WH/CRMVQPLWKT/QPL LRMLNTELF*DRALPLTGGKE
989	14890	A	996	3	498	CLPWAARQPPSPSNIHPPQPGP*LETLA PDITATAVNQALQRQBS*TCG*SPSGWPA VPTVPAPG/PPSAG*GVVDPRANPRENG PPGQHPKSKTYQPVAP*VQLSPSTQTP APMACSSILLPLPAPPAPAPRPPCPAP FLPSRTSLPPLPRLSLSTIKSKTTPGP
990	14891	A	997	2	419	ADTEAASASYPDNLANDDESSYTKQQTEN VDKITALYWKTKPSRTSIARBGKSKPGFK TSKDKLTLILLGNADDDFKLKPMLTYHS KNSRAHKNYAKSTLCFRN*NKANTELFL IAWF/EYFKVTVTNCPERR/VLLLTEN APG
991	14892	A	998	388	405	G*FFPPLSASKFFFCF*ALKELNMEGCHYR PPQQRVFPPLQSSQR/GPISASLKGKGF ASMPANIGPPEKYL*PAPEFFFPFLRLQ SHSVTQAGVQWRNSSLQPPPG/LRRSS HLSLPGSNDH/MPPCPANPCIFCTGG
992	14893	A	999	1	423	WILHD/NLRQPAQMLDQEAAPKHPFFKFN SH/QKQVWVTVCSAGLIIHYSFPLNPGF TSTLEKTYQCIDENH*KLQCAQPALNLR RGLPLQDARPRVTQPLQRLAKLAGC VLPHPYSPDFPLTDVHFFKFDNPLQG KHF
993	14894	A	1000	2	406	SDLFRAT*ETTSVTVYDVSMDYLETDE MIRDLLNTFPV/HLELQQDSGVTQAG ITEASTINAKEINHLMLKGNRQRTQEP AANQTSSSRSHAVLQTVRQSRVKNILQ EVRQGLFMIDLAGEASQTQN
994	14895	A	1001	290	3	VTQLPETVPHFLDRDVSFCCSGS/DHSS LQPQTDLK/YPPTSAT*VGGTCHLQAL IFIPLRDGVS\SVQAGVQWEDLSIL*P PPPGFKRLSLRNR
995	14896	A	1002	143	408	IKKIKREI*KILDTSKK/DIYQINWN ATKAVL*GKFIGINVIIFINRKN*NR*F NSTSGKLKLEKKEQTKIKISKEIKIKI RAKINS
996	14897	A	1003	84	409	DKLALFSSNTHLFGSFLQVTRAPPPPP PPPPPPFVRLVDFVDFRSLFVRLVDFV PRALH*PHPGSLPAC/APGLIGCTRQC S\QTILPKKKPPPLDADPANEPPEP
997	14898	A	1004	392	2	EKNVHFDQKQIVSINRPLQVPTQVCIQ NKTINSNGIAGYPFHPLKRNRPFNALKV PGPFSK*TIHLNVLNLF*F*DRVSFCC PSNSAVVKS*FTAASTSLIKQSSCLNH PSS*DCRHTPLIFFVRMS
998	14899	A	1005	2	421	FVSLILLITSAIWAAGTGTGTVTPLS GNYFHPGAFVHLTIFCLHLEGVSSILRA INFIASITISIIPPATITQYOTPLEG*SGL ITAGILLISVPLAAGITII/LITRPSLF TTFPDGQGGDPILYQHLP*FFGHPEVY
999	14900	A	1006	1	428	DIHYG*TIYRLHADGASIFCILLIHG RGLYGYSPLYSET*SMGIILLATIATA IGYVLP*GQISF*GATETIYLSAIPY



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						IGTDLVO* I*GGYSVDSPTLTRCPTCYF ILFVI IARLPALHL/LFLLLETSNKP IGLAS
1000	14901	A	1007	1	419	SPIVPIVWMAACMLNTERITLGYTLRPG GPNVGGPYRLQPFADAIKFLSKEP/LK PATSTITLYISGPTLTITLIGLVLTPLP IPNPLVNLMLGLLILATSSLAGYSIL* SG*ASNSNYTLIGALRAVACTISYEVTL
1001	14902	A	1008	411	27	GQPGQHRKTPSPSLIPYF/ELAGGGDAS T*PQLLRRL*EARLSGI*CCSEL*LP PCFANVTK*DPVFOGRKKERLSQLRK LAPREKSLVQHYVAIKGNNDPNPGPX ATQGRSCITLGVPLCHR
1002	14903	A	1009	21	377	NSLAGQQDSAQTRTSPOPAGFFGQRSIP DRIGHGFHLGVCKVCACVQVSVCKCVH MCACACMCTRTPMCECVQVCECVQVCVR VMCMVQVCACVVR/CACVCSGAG/CTCV T*NSLACG
1003	14904	A	1010	1	412	HKANTSYTLTLVNTFSG*VRACPTHR TAEVVASTLLEQILPR/GAPFLSKLVK QVTTTLDVNNKLTPIYHQSSEKVERAN SLVQKHLIKALKTRQSWITLPPALAN LWAPQSPGTGINPFELLY/SAPLPLSN
1004	14905	A	1011	1	410	FRVAGASRGNGA\TVILRD IARAREN IHKSLAGSSGPGASSOTSODHGLVIRI ASLEVENQSLRGVVQLEQAISHLEARL NLLENSSPVHRTAPHTQVSP IAPVEP PARKPATPT*DDVDD IDLGRDND
1005	14906	A	1012	269	32	MSRTIYELQIMNKKT\SLGRAGQYAN RNFTYDI*MAKPKMKACTLLVIREWQI KTMRYVYPTPARMATIKETDNNEY
1006	14907	A	1013	21	443	RIRKISYPHYVESTVATPIYLRFPYT IFMCLDQEVILSN*H*ATTETQLSLSF KLDVLSIILIPVALVATNAIIQFSL*YM \NSDPNTKQCLKDLNPLMTILNLTAN NLCCQLIG*SGA*MISFLIS**YARAD A
1007	14908	A	1014	1	309	SSRAAAIHGGACLNQILHRLRWEG*LS VGGQGCSP*LIH*TLANATERDPVSQK KKKKPKQANP/HLET*CKKKKKKMLGSP PKSQRKGGPKAPQGRTLNP
1008	14909	A	1015	3	256	EKNQILQNTMDLSRHSICK/NMQVGNRH MKKC*TSLIRKIQIKTMKYHFTPVVM AIIWPAGATIGMSHRTQPSPTLLITHVV A
1009	14910	A	1016	397	3	LFPSPPPPKGGFFPPPPPPFPAPPPPPPP PPPPPPPPCKGPPPPPPPPGGGAPPL SPDPFFPPPPPPPPPPPPPP/SDPPD PKKK*KKK*KKKKCKTANTPKKKKKPK KKKKBAARDLELVGRVGRV
1010	14911	A	1017	2	154	EKERRE*KEER*KEK/RFEGRGGORE REERKKKKRKRKKRCCMCFIVHPIE
1011	14912	A	1018	1	406	NSSPPKNKN*KN*QHT*EYFNPAFIS DIELVFTYNNKLLQNKGNPKNS*FK NQFNKSGK*PNFYITQSF*RNKPI*KF/ AKDLNKRFSKEDM*IANRKIKTCTPLA IRKRQIKTTVSSPKA/IYMWVVKET
1012	14913	A	1019	302	2	IYELPLGLWLCFLQNPVRVKGDPYFSK

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						SKANPVVFPVT\SKQPFKKAPFVYQKQ LPLF/PALVDKKVL/RFFFF*DRVLL \CCPGWSAMVQSWLTTESTS
1013	14914	A	1020	47	382	AKIALHSSLGDRVSIHTHTHKSNEI ELVIKSSPKKSSGLNGFPFISYCSFK* ELIPIFLKLFQ\VEAVGILPNL*EVS ITLIPK/PRQGSNKITYRPISLMNI GK
1014	14915	A	1021	273	1	QSKERRORTQEWGKTFHNNRENTLFG FSQCLKDEIIIIIFRTGFRSISCAQVQ W/P/NHGSLOPFPFLKQSSCFLPSSW DYMC*LPH
1015	14916	A	1022	327	1	KFLKGWFIYLLKRGFPFVQSGGQMAN SLVPOIYGVK\YPSAFASKINSTWGMCP PAWVTFGMAQLNGD*IF/IFFLRQSA LVAQAGVQWHDRLSPQPPGFKRFS
1016	14917	A	1023	3	407	THLQR*/HNIGTTP/W*TGSLSTVLM NFYLMW*FHFQSIITLFIILRLTTKIMY CGMLDVTQORSYOGHTEPPVQKGLRYI ILFITINTFFLEGLF*ALYHSLSLPTLH *RGDWT/PTGIPLKPLSDPLNITFE
1017	14918	A	1024	3	425	LPPQKRGFPFKIPRPF*RTPPKKIKII FPFGKNWPTK/RFLKGPSPSRFIPFP FPLPSSPSPP
1018	14919	A	1025	430	1	GSFSPFBNFIFPLSFIRG/RGVCPK FPFKGKPSFQNPQGTFWPPQKKKIS SPPPUNFAPRDLKRPPEFFFTFFFTF FFFFLPMHPSFPTSVPQWQITSFLCLL LLQCCVCLVIGM/VGDSQSSPSHILQ FRWL
1019	14920	A	1026	463	494	RKTGFPRLT*HLDLFFFFFFFWGIFV APRAGGRGRNLG*LKPPLGWAPFSGLT PPKSWN*GAPPPPPFNF/CVF*RTGFPP RLTR
1020	14921	A	1027	606	1	AGGPPPPKVPFGAFGW/SING*S*LKG KGSQAPIPQSGPTVFGGIPPKESPLR PPGGMQRRGPRWPGASG/VG*DSVLR QP/GVTGRAPCPGASSPQASQAREGSH GKGGAFTSVWGGCVLSAAMPWGPQPSH G*/PGRRGQSGSGSCPKG*AMWRPCLAG SHSSAKHKWSSSGPAPRGRAISPVSG SICPTAARG
1021	14922	A	1028	436	1	QGAPOGVLLKKAAPFFFWKQNTFVARI IKGKGVLSPQPPPLGKFKPGCTPL/ SRWGFKEGLKPPGSPNFKKKMGPSWNP RWV*\IPGPKEL/PPPTSGRGIQGT/ HRPPTIPPSLF/CFFPMETHSVQAQVR WRDLGSLQPL
1022	14923	A	1029	1	436	PPKIIIFSKPE*IPWGGGPNFPPPKGS FFSQNPFGVFPSP*KKKIFPPPPENN GPPLF/YKRPDPFF
1023	14924	A	1030	28	366	EDHLSFGGWCNEL*LCICTPA\WRQNK TLPKPKDKH
1024	14925	A	1031	3	142	PDCAIQQEFTRELYCPSWSQIPELKRC T HLSPKCMYR/R*ATTPLGRIVLEQK KLRR*CRELLYTPRSVTPNINDI*HNGG TFVTINEIISIH*YIALAGRLFSSSDV LTSASQVGIQTOMSHHWP

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1025	14926	A	1032	7	361	PALRPSARQQYYDSTKNTLCRNAQND SYLPDPNPFSSRSTL/DESHWQLEAPDA *KAPFGLYWGARGVCR\QGISAK*TEA CGLGTIKPSFFLLPLKQGSLLGYPAYNE NLKKGKKK
1026	14927	A	1033	472	3	TRQQMLNVDRTAPYKKMSRTFLANAK SMFGFRASKG*LLGANTTGNFLLQML IYHSKNRTPKMEANSLLVP*K*NNKA LVAAMLT*A*TEYKPEIETQITADN APGHPR*MYKENVVMSAN\TSIL*PMY QGLISCRIPARIEVKG
1027	14928	A	1034	488	0	PLR*TLAQRSQTHSKT*SGEAAZ*KS EARSWSWTLRFKEKSHLENIKAQDKAAT DGKAASYLED\TD*DGENTK*ICNGDKT AFY*KEMPSRMFPAREELMPGFKASKDM LTLLLRANAVGD/VNLKPMIYYTENPKA LKNYDKTQLC/PVLYK
1028	14929	A	1035	114	491	NYPRNPTFSNKGTT/CLT*TLPL*KLPN F*TF*LLC/I*HLA*NTNTLYSCTKI FFIPLFYKHFLKFIYFFYFLDFII*GAY *SLCY*VVYPSQFQVLFHFWGLCC HVLVRLLYPQTDEPFY
1029	14930	A	1036	114	496	LLKAILTYLYLYKYSAMNLSA*FYIHL TYHCVP/DHPVQGR*LLNK*INELFCYR SGF*WVFSYKLSSEDALEBKTLRERS RNVK/DLNVTSSTVKILSEILGKTLDDI GLGKEPMKTSQANITKP
1030	14931	A	1037	381	45	KNRGRKNS*LGCF/GDFVYKTF*KLKQ IYKLPQKNEKGT\*NSRPTSLNIE ANQN/RAVLNMIQKHTKIKIRHNQVV F/IPGR*G*SNCTCKSI\NVITHIKQRR KSIET
1031	14932	A	1038	134	394	SPCDKPFNCISSELQ/SYSPTTIIKIF VLFKIRSGSITQPGVQWHDHSSPQP*TH SWAQTIFLLSSQVVGTMCHETWL/IF LFLFVF
1032	14933	A	1039	483	30	YDGGSEITINYLESRLIGTEKFRVNTD NLSRKTYVGLKGGDTYEYKVSANIV GGQKPSFCTKPICTCKDEL/AYVSTIYET SETCTCFVDL**DINKNDLPL*QLILAPP

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						AHTISQREKTEKKIQI*YKSEKLPLFTSS SLFT*VKNIAMEFAKKLLRLINYNKVER YKINIKNILLARNTWTLKF
1036	14937	A	1043	50	457	TRYQLANNMKIKCTLPITRE/MQIREH EISLTPIMMALSSEONKNKYWGSCREVE TLVHCWW*CKTVOSLRCTVHRPF* ELP*ELPPK/PQSQRDICTPMFIALAFT LAKRFWHPKPCPTUE*IKEMWYIGS
1037	14938	A	1044	2	469	LKQSSCLGLPKCDYR/P*ATVFG*VLL *NTTEDPNLTK*ILNNH/WCHSVGLLI LGSNSNTIKTSI\SFQSASSHONTTVQFL STSPSPKNCQWLAILPR*GLTLSECFEA FERQGL/NSVAQAQAQWLHHGSLKAQPP RLKQ/FLNPCTIMBCYLRQP
1038	14939	A	1045	42	200	LICT*MLIVALLVIARNWQIRQ/SST/ DEWLNKLM*IPMEY*AJEKEPTIGTC
1039	14940	A	1046	475	36	LNNV*LNHP*IKROKLAG/VYKXHDPTIC CLS\QQSRFIFKDTNRNLNIGWRK*TFH ANSNOKIA/GVAVVVSNTK\PIRNKE* NVILLKQSTH**CIIILINICATNS*NLK I*NKLTMBKEBHCSKITVD/YNTLF* TMDROKPEHRMO
1040	14941	A	1047	3	326	FFFFIITIIIFETERDSVSKIIILIKNKK DLF*FLVTONTPETITQYISTLPQSKT KMDRPGTVAKHSNPSITLGGRRRI/TLR SGVEDPQDEIG
1041	14942	A	1048	403	15	EVKNSPSYLLMTEIMPGTVSKLLNCD SGS*LS*SPNVCKDARY*Y/LEBRGNTS FKSLLLMMKLLHSAIFTS*TPRGL* YFIYMYVLETSWHSVAQAQCMQMDQSSL QPSPPGLKEPHRTDIVAR
1042	14943	A	1049	25	457	YMWNSHSHSCMPTLLPSSPPPPSTCFPI LRSILFLLYAELPLAFLLVKDSFILFV* MSVPFHLILKLQ*NHNIYFTLITFKCT VQWH*VYSHFSVAKTAT\LSRTCLIPSS WDYRHMPCLANFPL*RGGLALLPLVL TSWLQ
1043	14944	A	1050	14	478	FEPYCRH*TIKAN\CMWGYELVQSLWKA TEQYVLKPDICVP/LEPGVSLIGMYSEK LCTLC\YQKTRMFIATLFAVKS*LPK SS*MYE*ITKL*YFHTMEYTYAM/INE* ITL*TTIMRN/TLILNERSTOK
1044	14945	A	1051	2	465	GLDPSEKPEL\TQSTCTGTA/LTFPNS VKASREBEAR/ER/VBSAS*PVEQ RSHLNNIKVAGEATADGETAGS\SYPE DPAITDEGSHTKQIIPSVDETCACWKIS SRTFAAKESGMSVSKAKDRITLLIRAS AAGDLKEFPRLV
1045	14946	A	1052	392	24	DFAPRRKKRETRRSKINSLS**KSTEN QVKTNQKGRKQKIKIKVLSREIETLK TFPKKKVNSKRSWFYEK\INKLDGTLAR QINKERKENQ/DTRNNKODIITDPMEI *TTIRGIPPLWR
1046	14947	A	1053	204	488	CAVCYQISTLEWVDL*SLDPGFETVSH LFDVNVQ*DCRRVTUMLVF*NLHFI LFFLFNF/DVFVLRQSFPPVVTQGVQV RDLGSLQPLPPG
1047	14948	A	1054	498	2	SVVVCLFSLPGITSHTYVPMTKGAQR

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						VHWNKSLFNKSCWRNLTSTCTRMKVDPM/LTPGT KINTNWKDLTPSAESII CLK ENIG/THPHD IRLGNA/PWDMTPKA* ATK EN* IPWITSK*QT\FCAKNTVN* VKR* PMD*E/RIFAKHISEKRLLICVITYKLE LN
1048	14949	A	1055	28	209	IDSRERGLWN\CVVLASQLLWEAAGGS LEFKSLRLQ*AMWDCIPW
1049	14950	A	1056	163	479	TSFTGSGAGTTSVS\HCPSEVFFLKLI HMRQGGQVALINATPVCSPPCPQTRAPI PRGRHDFACASLIPVCLILNHLMLPPI VAGRGVSGSLG/CQAGR*L*TC
1050	14951	A	1057	2	1258	ELFPVHPQSPKAAALVAKAIRDVPGT RRWVPVTDGRPEGFALSEPHHSC LGRH QGPERCRHMAASP*EAGNK*PKDKGHP GERTETAAGVHTGCGKGPAAAGGR*AQ GSGSGAGAAAGGAGAAVGGAGAAVGGSA GGRWPAGLLQGHGAG*GEGPGRGHGPPF GVSAGQAASPAKAAQPGPGT*GAAGQP GRG*GFAPGPRGAAARAGAGAMPAQGP AGAAARPAEGEARPGAGDYGAALNHPGA RTGAGGAGGAGAAAGLPRPAQHR/AQ IINGVPVPLGTGGRSSS/GGIDIMSHRLH QRHRSIGEAAGQRHPRPTGSR/LGL QSMLSKIREVAGQGLKVGRLGRLGDC BEAPIQQQVPRLCGSLNR/RPHHWRP *AVLL*NIFHISRREDDWDPMPSSPIC PL
1051	14952	A	1058	2	437	ERSVRTACCKQSGSLSSLLCPPAPRLS *TGSPVTGSSALEPRSPHPQP\PSLRPR SPGPQPLHPIGPRSPSPSPQTVPSHFA RLPSLSPTQTG\FKAQ*SQLPPPSLAL AQPAVAVGGREVASPACPSWIKDSRLR AVPGSA
1052	14953	A	1059	47	456	TRCYTLLRLDAPGKLMTRM*VVASTY ARTDRKSASFRLPLPRPGFQLSIHFS LTSPSCLAFSANTHRGLRGENYHTK/C DMAPKV/HN*TAQVQWHDGSPRP PPF GFRSSCLGLPSGWDISPLMHGQL
1053	14954	A	1060	484	13	PFPSASQNTATTVGSQHQPLIP/LFVE WSGPOT/SPASLKPSLTPASRAA EGVSAHH*PLNFL*WASGFPVPSW* TFLI/KQSSCLSLPV*DCRCYNHAWP HSVFSSQPLSLFPNFSPLFFLSFFK DRISLCRPNMFHQTVOISR
1054	14955	A	1061	1	494	GSPGHVPCGRRRSALNPGQPCSLPGV VSGATGAIVRQRTSSANATAAAGAYV E/TTRFRYT*KAGVCGDLRGAWLKADG LGETKAEHTLDG/PPEDALYGLEGGDD TNPTIQGEVHVCHYTGTLPGTVFDTNI OTSAQKMM/NAKPLSFVK/GIGKVS/G NDE
1055	14956	A	1062	3	395	SDFPSGCGIRPDEMEKPLENYNTLPKLKE /DKINDPTPVK*IGSVMKI PHTVEP/PS HKCFTSEFY*TPKE* IAPIHKL*SRG IMGATPVPMVHLOSHVLPK/PTEIK*T YRPVSLMNTN/KILKLLTK
1056	14957	A	1063	402	260	WCPFKV/LLRFSVYSSPFEVNAVGSIX

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						AEIYMLRFLPFPRTREVD*TP*TCPV/LK GSPKNKDFCP*GAKTFEYFYPATLGLNL KI*IFRQRW
1057	14958	A	1064	66	379	EPORGCGSPKLRQCTFAWVTSEDPVSGG KKGKRRKERT*REPSVSRPESH/VPSQ EAFWVQALSRPVLNFISGRSASGLGK SEATKSLFLYIAVCSITTEQA
1058	14959	A	1065	223	437	KCMSCDNRIFFLRQGLSCSLTQAGVQ WHYLGSLQPLSPQPK*SHLSLLENWDY RR\PFPR
1059	14960	A	1066	414	65	NKSPDRNSLAS*KCTQ*THTSIARDFFA KTIQWGNLSFNWC*DNWISTSKRIKL DPTIIPYTKVNSKNIRDLHVAKTIKL LEKNGPGAVVCNFCNPSYSGGLLEARS LSPAWAT
1060	14961	A	1067	418	1	LWVFFFSRQSL/DSVAQGVQRCDLGSL QPPPPFRFKRSCSLSLRSMWYRCRPPHV ANFVFLVET/GFTMLARWNLNS*PCDL PAAAGCSAGITGVSHHRL*FCGF*YIHR VAQSSQSI*DDHPKIKKFCIL/QPTFFR S
1061	14962	A	1068	24	440	EV*NLISENFKMLKEMRGDLNKKSTP *S/WI*RLNIVKMAVLKLIYRFLNLIPI RIPDFEKFVKSTS*L/CKFIWNCKRLRIA KTIF*K*RTK/GGDLILIDFKTYTKTMV IRTI*Y*QKDRCID*WDRIS/PEMNFY IY
1062	14963	A	1069	442	26	LGNVSTPSSKTPRFFFFFLKRGQGAQ RRNUSL*PTPGKLPQSTASGVSRIL GASHHTPLIFYYFN*GKGGGSCSPV AQAGLQ/LRQMLPPOPPLKWN*RIK PPLSTYPIFLKRTD*SCPSKEKATRPP
1063	14964	A	1070	294	46	KNKLRKRRKRNKKKXNTDNKSM EKIHKKD*FFERNKIDKLLATN/RI TKTQIVFMNKIRDITTYPTDIDKNVR
1064	14965	A	1071	141	469	PKKQGVQLTQNALPFRVGGKRGKCPK KKRRERDREIISIIIIKLP*TKTPGP DGTDELQTYK*LTSILLKVLKRRR CPL/PYSMDPAVPAIALNPP
1065	14966	A	1072	49	472	EFOIIRK*NSFFADTERALWIENONSH NMPLSQSLIQSKALTLFNSMNAERVGKD AREKLEASRGFWMRFKKPS*HKVQGE ANNLDVATASYPELREIIDEQGHGKQ /QINMDRIVFYWMPSRTFFAREERSM PG
1066	14967	A	1073	82	419	LTVGPRETRSSSWCSSSPKRALHLRF TPAKK*FFWSPSRLPFFLRURVLLC CPGWSPTLGK*SSCLGLPKCN\IYRE PP
1067	14968	A	1074	1	407	LEDGFFKI TQSKDKKRT/KKK*K*NLQ EVM\DYVKHNSLQVIRP*EVKCLNLL FEFVIRAMI/PHLASVLDIQIQAQVQRTQ RGYIARQCSFKHVVRLSKVNNQEKILN LPKEKHLITYKNSIRLTKGPSPKPT
1068	14969	A	1075	3	396	LHAYHIVKLP*PLTAGLSE\LLMTSGL TM*PIFHSITLLLSLLNTLTIYQ*WR DVIRESTYQGHITPPVQGLRYGIILFI TSEVFLFAGFF*AFYHSSLAP*PYLGGH

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1069	14970	A	1076	250	47	WFFPTGITPLNPLEVPLNLS VAACQNAFTTSCYWL*NLCCR\NDLD ISLLP*TKVNSRWIAGFNVRLATIKILE ENIGSARGNRHSQ
1070	14971	A	1077	2	393	PLTGALSNLLNSGLVRDDIGSTLLI LGLLTSTLTLYQG\WREVTQES TYQHH TPPGQGLRYGTMLF I TSEGFLYTGFF* AFYHSSLAPTQLGHWPPSGITPLYV ESPLIATSALLA*GVST
1071	14972	A	1078	2	500	LHVIGVSGEEN\GWRKNIPEEINGN F\PNLAKYINA*/IQEQ*TPNGIHLKK TVHRYIIQLVNTNNKRLLLVAREKHH GLPGOTML*NDIDFSBFIKARKIDMF LKYKRLISSAKHC*SRILCVQISFVS KG/EITTPSKDKRLAFIISRPAHNAK GK
1072	14973	A	1079	419	1	LRWGALAAQAVRMNNGSLQPLPSS SNSPGSNRLQ*ANTAPLSSLGNNETL SQKRRK*KDNSEWIKIFANHASDKGLVS K*KLNYSYNITEN\DI*QWTKYLNKHS KQIDKMANKHMKRCSTS
1073	14974	A	1080	468	2	KLQPPFRAGSSAF/PLEFPPTKGFSP PPP*KFFPSNPLFLFGQFPFLFPDPKK NFFLKNPKGFFSP*KKKILFPFPP*I FAPDKFFPKSPDPLFFFFFFFFFFF FFFFFFFFLRTGRTRGRTRGRTRG
1074	14975	A	1081	467	1	PTYKPAIPIKIQ**FKKIGENCILKFL /WMLKEPQLAKTVLK*NRVGGFTLEDFK LTVTKVMS*EKORADE/NK*TESLK IKPYKIDQFFFTF*FSL/HF*YLYT SQHHKLPNRNPKPNKRLVNK*CMEN WISICKLIKIDHYLYPYTK
1075	14976	A	1082	387	3	LKQPPPHKSVFVGNVSLCCPG*F*TP GLKRSS\HFDLPKCNDFRCAVLSLLN NIK*L/CGRGLIKQPF/SVK*K*AP SNSAHLAETFFFRQGLTLFMPGVQNH DEQTVQQTGHK*SSHPSL
1076	14977	A	1083	2	435	FHEPTNAGGSFPFP*KFFSPKALNFG GGVGNFPPPKRFPKPNRGGFYYPEL KKKNFSPPPELKLADPRV/SFKRPPDFF FF
1077	14978	A	1084	447	47	PSRKFFFLAPPKRGFFDPLKNFFPPL GGLFFG/RGVQFPPPPKGGFFPKKPRG VF*PPPKKKKNNFFPRENLGPEGVFLK RPPDFFFFFFFPPPPFGRRFVK
1078	14979	A	1085	438	2	AKNIPKGSFFKFSDFGGGGLIRQG L*KFFFFPKKRLV*KPPKIFF/I FFFFQKVAL/CDEQCNKGVQGFPEF FSRVGKPLFPMPPKMGKKNPPPTGKI FFFFCSFFL*RGGLTTSRLVLNSNA*A ILFLQDDK
1079	14980	A	1086	43	265	IKHKLEYIKTIONFCASSNR/TERQDME WSE\MPANLISDKGLIPRIHKQLL*IN/ TKQONSPI*KWIKDQLWPVYL
1080	14981	A	1087	11	412	LASGLHDFNNKKKKKKGGGPLEKTP GQPKFNROKKKIFSFKGGKTPGGFL EKNPFLGGGGMQNNPPKKKPFGEKINF *GERGEKKPKFGGKMSBSPQENKAP

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1081	14982	A	1088	2	292	RDDPRPPE RSLPASNDSSSLVA/SLAGVDRDVRSTCW PGWS/AV/VQTL* SAR/LGPLKWDYRCE PFCLABAPSFMRSGKASCTLETWEDKH KYEEAERFRFYBNZAT
1082	14983	A	1089	376	3	HIGLYTASCTLLKKEIKGS* IDILCSWI ERLNTVKAILLKSLYGFNTAI/KILS GLPIETERMILKLTGECNRSGTANTILK PNKVGRIALPNFKTYKATVIQVWSH KDRWVGFCVVTQI
1083	14984	A	1090	277	407	QIKAEKSHHQIT*SNRNKHCSEEDYDS *REKAPGYIILK*F*K*LIKKKILNSGR LKNRPKEE*RYAYQDISETIVKRR*EN DIFKVL/KEKKSQPLLPLKIS*IEV KYFFDKSKLKEVITNRSVP*ENLNIULV /INYSDFYEP
1084	14985	A	1091	421	2	GHPGVLPKG*K*ANEKSL*NCSPFNY* SFSNMQTRILKNV/WSTVAHACKPSTLIG GRGGQIT*GG*ETSILANTKCP
1085	14986	A	1092	369	3	FLKEIRSVTPVNT*ENLAD/IGKVLV VWLENQTSN/ILGQSLIQSKVL/TPNS MKTER*/EKLQKPRASRGHMRPKRRSH LA/NIRVQGBASSALVSAAGVYPDPKAT TVKGGTQ*QINVDV
1086	14987	A	1093	71	506	FAKNGIL*LNKCKCKRDLAVFGCTSF VLTRGL*PNPLTGS/SLAPLEFS
1087	14988	A	1094	118	385	SDLGIDFNARTSKGAJHTK*ITWDDY KLRSPTSAQ*TKOST*RRQSTB/HKEK IPADYSNRGLISSRQETQTTQWLKKN KNALCTL
1088	14989	A	1095	419	1	DAKIPGGWAK/RIRPRPKKIPCPDQVW FIPGMQGGHIGKSLNVAHQIQMG*KSF NNIQHPFMI*KKGNLSTGTTHEGDITQH /R*MLHEHTTNAILNREKLKAFPLRTGI RQCCLL*PLLFSIAVKT*P*AMRQEKIN
1089	14990	A	1096	34	464	NSSKKEKKRIPHDGLRPLMDTPRT*ST NGMD/KDFIKK/FCASKDTINKVKKE *EKLQIILV/DKRLVPRIYKDSYYPRIQ LEKHWVNLNKHCFKEDTQIANKHKKES TSISRE*QKTR*RSHPISTRVTKIEMS G/N/HKIQGC
1090	14991	A	1097	458	28	RIIVKLVKCTRNPDLSLEBNHQPFFKSR WPR*NR*FE*SYHK*NN*LNH/VSKGS GPDATGTFEYQTCRELAFLQLNLPQKN ESIRSNSPYKVRITLIP*GDNGS/TKKE NYSVVSFPMNLDKAVLIKILAN*I*VFIK REFH
1091	14992	A	1098	41	500	FWIRHPLSRHKORKN*MDFTIKNLVLA SKDTVKEVKR*ST*WNNYFQI/RMFDTG LVPRVYKEFT*LSNK/DNHI*QWGGKAV SRGSPKGNVQMAKHKMQRCSMFFVIRKN *I/KPKMRYHFTSPSMT*ERNKDNTCFK SDGEYGLIIYYVGI
1092	14993	A	1099	1	484	RRAPFFFFFPPKRSFPPNARAP/LQWAF GLVQNPFPRIQPPGLHFF/SCPNNPKK WGYKPPPTPGKILGF**KGGGPRLNKK IFISRECPDPAPTE/QQGGIQGGTTPPR



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						PFFFFFVSCSVQAQGVQSCDLRS LQAL PPGFEQFSCRGMP LKWIGSHPSPH
1093	14994	A	1100	144	260	TLILDSALGHPEPEHFNFGIBVVLPL NTMYIIQLPDQ
1094	14995	A	1101	265	457	DPAAPLVITYTRET\*MYITKRYTAALF IRTKNWK\RPKCPSGKG\*INKLWYICTM EYCSAIKNE
1095	14996	A	1102	387	40	RLRADILRLVYNNPQLRLKKQRYLFTG PQYRFLFLLEMLWCVCVCVCVCVRANF *IISRDKVLCCPV\CPCFLNPPCVVCVC VCVVCVRCALINKLLVETRSCSVAQS GLR
1096	14997	A	1103	465	208	QNWIKTFQDYRLSLMKYIARKQQYRFR Y\*RMLNHYQMGFTGLRSGWNT\*K\SIY IHN\* *EKKIMITLIRSEAFDKC\QSL II
1097	14998	A	1104	37	250	MTCSRMQ\RNILRLRYKSEKL\*ENETS RNEITILSEEDGPTNVKLEN\*MKTIVKQ KRTSKRTGVYKAIKKQISBFGKTSNF Y\*EQINT\*EKKNFKENWSL
1098	14999	A	1105	2	378	YVDPKQGGILKVLKGEFTISNERANP GRGSPSSVSND/L\*CNQIKTIESKKTCL IQKLKIVKABYERESRKTMEINETK/ SQPFPEKI\NKID\*/PLARLTKKKKKTQV LKSEK\GNI\TINHTIKRV
1099	15000	A	1106	291	1	VSIYVSYNLSDCKGQIRIKSCDDQYIFK RLYFFEITFLKFLN\*K\VLKKIRDNVLL C/YGWFQIPGLKQSSCLSLPSSWDYRH VPLALAPINFLW
1100	15001	A	1107	24	397	DIDRWBFETVYFYHQAGLKLKLLTSDP TALASQASGITGVSHRTPSGHFNTPF EPPEASSLSHPKLHKSPTV\*NGAGL/Y GSSKLLSCVLNGPISLVHSTLRLRGGP QGNISQISLMAPP
1101	15002	A	1108	64	414	AQLIPTQFGRAALHGHV\*RTAPLCL FMAEKNAASFFLPFSPSICINKE/HFK KKKKKKKKKKKKKTKTKKKKGPEKPR KQPGGGLLISKILNVAPPGGFFLTREGP PPIFF
1102	15003	A	1109	62	475	PEPLPYL/CLLNLFFQLQDRHFFPLPLTV DLVNTWGCPLPSSPQ\*EWLLAAPHRSTP PPLSSGFPARRQLEPGAGARGP/HIIQA LHLSSFFVFRLRL/DSVAQGVQWRGL GSIQLPFGFV\ILSSFLSLPLSY
1103	15004	A	1110	76	477	EEWKLYRWRRNINSLISCKELI\*C\IN/ NQTPNIOFLKTNPTKOVNLDKFTINED TQKFTLIHQ\*R\SEKRS\*S\*LFI\*KMG NSTALPLYPPTTQRIQTDETIKTRWG CGILHSM\*TRKMGHSL\*KAFNP?
1104	15005	A	1111	1105	3	KEERSETLAKGKLIAAGA\*YN\*KEERSQ INNLTLHLKGGKKINKDKSKR/QR/I\*Q IRARISIRLRPRKKKKNNNEFVPLKINKN FKTHSYIKKKRKISNTK\INKRGDSITD ATEMKKITRD\*CEQPSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSPPKKKIPGPNPTQEFYQTQBEL MPALCKIFQ\NVOKPEGDI/PNPFYQVN IYLVPEPDE/OPFVITKLKELVIYGN/Y



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						N*TSIWKRMI/GLDPVLT/PHTKINSKRIK DLNIRTKTLCSSWRKKRKNFLAKKKRKL
1117	15018	A	1124	206	24	CSIFFCIYLYFIYLYFIYLYLRQSL/DS VTQAGVQWHYFSSQLPLPPGT/GLP*RT SYSWDF
1118	15019	A	1125	3	351	ERGRGPTILVQAQTPDLK/HPPNLASQS AGITGVSHCARPCLCFRKGQF/NSVAQ ARVQWHDHGLSLQLPLTLR*YYHLS/SW DYRDM/PAMLGFFVFYAYPGITLLPRP WISGLNELP
1119	15020	A	1126	2	349	SINHKD/GTLYLLFGA*AGVLGTDLSLL IRAEGLGQGNLLGNHDTYNYIVTAH/FV IIFIVIPILIGGL/GIMILP
1120	15021	A	1127	362	2	RVSLECPGWSQTPBELKSSCLSLPKC*D YRCEPFPAYLTSFITEDSKNFVYVTL F*NNIY*TMFIELPP*VHYIGARLF*IQ LSTFF*SF*N*FFVCLFRRQSHSVAQAG /VQ*CDLGS
1121	15022	A	1128	1	349	IYFLTRSHSVSRAGVQWSSGSLQ*PP RFRKSSPPLSLLSSWDHRTWG/HMP/H SSSFSSSLFLRSGWGKGGLWS
1122	15023	A	1129	367	24	INCVFYPCRGVTKRPYYT/HF*RKGFII INLPHGPFKLTFCVCEGKNSSETLYPPC FLPLSLAIKRSRPLGVFLV*KGPLSPPL QNTGVGVGVGFFFSAFVIFIKGLVLS PYHN
1123	15024	A	1130	61	299	IPRVNHYGVVREHLFSLPFFFKRSLV/ SVTQAGA*WRDLSLLQLPLPGGKQF/SC FNLLDNHCYRDVPLLLNTLCIFTK
1124	15025	A	1131	2	261	FFFFLVFSFPLRLQLLPLSPSSDPPSVF FFLPSSFSL/CLVSRDLTLSTQTKVQR DLGSLQLPLSPRFRFSLCLSPSS*DYGR TPLN
1125	15026	A	1132	2	381	EFYFFF*SSQMESPSIAQAGVHWRDL/ SIAPYASWVQVILPQPPPGFESFSL RFPSTWDRHAPPRLAKRKNKI
1126	15027	A	1133	2	221	PSLKKLARHSRGL*SQLRLNLRNRR /CVPANVTK/GETPPSKKKKNTPPPGP GAOTFETPGGKPKGIKV
1127	15028	A	1134	331	2	RGPPLPLKPSGVRIFQFNLSESGGG ERKQSPPLGPPIRRGLSPKPPPEKGL TVFFFFFRCKDGVSFCCPG/WISRTPG LK*SSCLGLPKCWDYRHPHPAPAL
1128	15029	A	1135	3	391	AVNFMKRRK*KSLADVSEV*VNNIEDQ TSHNPLAQSLVQSRL/T*RAKCSMA ERKKAAGKLAASRG*SMRTKNN/RL HNKVGQGTASADVEAAASY*DAQKIT GGCGYTKQQLFNDETAFY
1129	15030	A	1136	107	350	YSISVAIVMRFFYFFIIFYFLRMSLAVVI QACCCHPGNWHDGSLQPLPPGTHKFSCL SLLSS*GYRCPPPCOA/IFIFLVNMG
1130	15031	A	1137	35	297	TLMHYTNRVKKNIIISIEAEKAFDRIO HPHM/IKYLTNIKAVYNRTASIIISLG* NLKAPPLKSVTQGGCLSPILLNIIIEV LSTRP
1131	15032	A	1138	378	1	PPTKINLKWITDLNIRKTKFLLEDITIG ENLDNLGHDYDILDPTPCA*AMKKILIN

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						VALC*NHESFCSNDTVIRMRK*ATDRK KIFAGDMIKDCYSXC/NRKAENVNMKKK NPITYKAKDLNMLL
1132	15033	A	1139	271	361	KW/YMNPHTISQVCL*GPRTYQHVVQ MTKQRCQGNM/NAKDSLNNKNC*NKNI FF/C/RI*NINSYLTPYRKIK*KWIRDQ NITVTTLKLEENRFSFAFGIGKD
1133	15034	A	1140	28	340	LLYP*YKRGFTMLSRIVSNRQ/CDPP TSASHTAGIADGSHHARLLFLEK/RPA PQPAGRKAGRF*RPSPFGFRGIPP/ LPPRWMDVGGSPPEKRGTF
1134	15035	A	1141	94	128	GSQNPRLHYD*WIRHLATLES/CYSR\ VYPRFKPLFLEHDIGSTQKSHS
1135	15036	A	1142	85	492	VNWGLLSLRGSSPKFGNPTFRVGLSSG GPSANRLFPFPVYFLRQL/NSVAQGVQ QWRDLSSLQPLPPGFK*VLKRGVCLFV CFETESHSLAQAGTQWCDLSLQPLSPE FKRFSCLRNSRLRDIEPSEGNQC
1136	15037	A	1143	372	3	KMRN*PISTKEIDPIVKNPK/KFGPDG FTGILY/RHFKKBIQTVNCLQKTSKE GMLS\IYKASLAQIPKPKDKQKTQVTD/ YKPSGTRAKTINRILANGIQYIHDQV RFTPGMGWSNIQI
1137	15038	A	1144	56	482	TKMTLLYNOKNG*VDQNGIESPEIDPY K\YIQLVFDRAKTONV/RKDSLNVKNC TYAKKKKTLNLFPTPTKITSKTYLRNW N/SVNFINTPLGKLGLDLPVRDEKFLN TPKAKLSLSEH/MDTLNFFGKIKCS*KNM VKDKKT
1138	15039	A	1145	190	482	RQGLALSRLRSCSVITAYRSLKLVGSS DPTLASQIAGTTGIRHC*PKTLFLAS VIMPAHNS*PSLSPVPSL/SLSPPLLA SQSRRSQ
1139	15040	A	1146	138	485	IFFPSV*TIPLLLALFFS*MYLIPVKS SLSIYSVYQF/SPLCFWSPISDPKSRF SLSPFIVCFVFPFRNRLCHFGWSAVV *S*LTAVSNS\LLQSS
1140	15041	A	1147	101	426	GDWRKFTYIRGSESKPLILFEKKKQVL EYSGSFDI*AIKVIYHSRKRK/KNL ANLDAEKALNKI*HPFMKTTQQFSNR SPLHLREGIYKKPTANMIIKEQITF
1141	15042	A	1148	458	15	VFVCLKICRHRGTAKQNYFNWGLPLY MRSVVDQNGTM*EMTIYAPNIGAPKYIS QILMGANREVNSTIILGDFSIPLSTL/ DKRLPLNFT*NKIDLDIYRTFPHMAA KTYTFAGHTSTPSKMCVFGDIRVLIVE FRRSTYGLDW
1142	15043	A	1149	1	507	KGPDPDPYVYKK*GGGPKKFP*SIPE KRPGRDP/YKPRNLKPPWAKKENPFP KKKQKGGKGNPDENKVKDEKSE*PSPK KTKIWPDPGGGKKKKKPPDKKKKKK KSSVSPPKNI/YRSLFCTNLKKSFT*F *NLMP/TKLPV*EFPPPPYNSF*SAP
1143	15044	A	1150	436	32	NLCMYVNYHLYIVRTVCTIYSIYSIYL IDLSLYHHYLSICMCVSIYPIYLSLIY LCTSLIYHLFNLCITYSIYLYLS/YVC M/SST*SMYVCTIYIVCTIYSIYLYLY IYLSIITIYLYLQWCLFVLSSERF

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						QPPVETVYCSGKRTPFKLLWIDNVPCRP GALMEMYEEINVNTATNTTIL*P/VT SGVIS
1155	15056	A	1162	216	464	SSEGGPGSGELPYGAQEFVNKAPQGITLV IR* T* FFETESHSAEAGVQWCDLSLLQ LPPLRFNQPCLSLP\SWDYRRPERIPAN
1156	15057	A	1163	29	433	AVEFGGDSCTGHPNLNPLGSPQHSPPP LGIGCT/REE*GWGGGLVVPCTPALPYP STPSGGICVCVKGAGVAPP*HPILT* LGGGSTPTSLAPGAPRHPGHPHLVLIQ TLNPGDHTPARKPYINKVLSGVDP
1157	15058	A	1164	486	11	STCLGLDFKCYDEKIPRDLACRPFPLN ILLFLKFTLSEINPTDAFF*LVFAWYI FFSLFSP*P/DLEHYI*SGICVDTM*VG SSCFNPT/MSISSF*LVCLDLYFFLF FPFLRQSL/DSVAQAGVQGDLSLQPP PWWKRFPSCLSRIPAHFWSRA
1158	15059	A	1165	467	131	NRSLEWAKMYKPYDEKIVLNTLPT/RKS PGLCKITAKFYHIYKDLGLVLLNTLQEI OVGFHPNS*YQ\IILIPKYSGETTKKGN CRPIPLVNIETKILHEIRAI*VHQKIRT LE
1159	15060	A	1166	455	32	EEGVLEKAKRGCKSGLLHQTQVQVN/AN LEKFLKIKSDTPVNI*MIKK*INLTAD KEKVA*IQDTSNNLEI\QSLIQSRALT LENSMYTERGEAGEKFKASRG*PMGF KRYSHPHKKSASKAASADVEAVASYLN S
1160	15061	A	1167	26	418	KINDYVQKTL*ITGTPERGGEK/NMLE NIFEALVQ/ESVPSIFKEVDTPQEQIQR ASSSSSS
1161	15062	A	1168	64	313	KWCKGNYSIKDLKELKFLGV/OLK*VQ /DL*SENVQILLKEIKEDLNKNDIPCS *IRRLNIKMWIFSGLIYRFNAIPKILA A
1162	15063	A	1169	464	36	QQEMAESL\DPGGGCSBELRSCHCTPA WATEQSINK*SIHQSIK*ESKLC/CWEN TLVKHIFHKRLTSRIYKEL\QOLNKKTN NSL*K*EKDVNRYFIKKIYDI*MANEN IL\IKLVIREIQMLKMLSWPCCCCCC FVLFVF
1163	15064	A	1170	290	487	GSLEPHKTEK*DFLF/CVFTQGRSVT* AGVQNNIRGGLQ*PPGLKRSSHSLFP LIFLPSVDMGV
1164	15065	A	1171	2	413	GKVFIT*FSTLH/GCNMK*SRSL*ALR PIPLPTARGITQIVLANSIHTIADTY YMGTHPHVLYIGARPAIGGFTH*LP PSGYTLDTQTSKIHYTILILIDINLTFFP HHSILGSGRPRRY*DYDPAVTRYILS
1165	15066	A	1172	381	2	PFKLQNNFFSSTGKPFLLGGRAQSPDP KKGFQSQIPRRFFPLPKKKIYPCDP CPGPPPTFLRAPPPFFFLLLPCSF VGKFLFLF/FYLPFIRDTV*LCYPGWS AVVQSLTAALTTPP
1166	15067	A	1173	9	405	NLDKGRNRTPQSFQNPMPMSFSEK KCKKKKKGGGALKKPGWAGKPKGK KENFFLKGA\BKTFRGILEKKPPFGGG KKGFNPPKKKFLKCKK*GKGEKKP

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1167	15068	A	1174	410	0	*KFPFKKKKKPPPSKKTF FSYYPPPTRGCCSPSPFQTLPLPPPLLV FPFSPPLKIFPPFGQFKTFGGVVPFSP PKRKVFPPKPRSVYQNPPEKKEKK*SLQP EG*VMAPPGIKKK/PPPPFFFYIFS
1168	15069	A	1176	319	3	KEARSVFRVGRG*KNFSASQPPGQGNP GGGRPGRGPRVFLIKKGQPPPGPEG/SP FDF/GGPPPPPPSPSGSGVNPFPFPF FFPFEMESRVSQSGVFTADADAW
1169	15070	A	1177	385	1	SASGLGKCMVYRHEPTKASVSVTVTS SRLSCA*ARSGKGLVFWAQVVFRI LTKYSDHSRSPSSLQLCMSTPSKAEPT VAKADKRLCCTAKSSTAKSIAQIKQND AGRSPQESLHVSGRV
1170	15071	A	1178	147	808	KLKBTIKLLLENAGINLVYDLRQSCFLD MTPKAKQKKENLAKMDVIRMKNSCASKD TITFTN\YRSDKGLV/SKKYKELNSITE RQPNF*KDLNKPDK/SQMAKST*KTTE RLFIEMKTKTT/NE/VHFLSTRMAKI* KDSNR/RLCRKTGTLHCW*GTAPANLL ENQQLPLFP*GTWQPLKRLNLELEDDP AIPFLVICPKEMKI/C/CYTEICTQMT AA*III
1171	15072	A	1179	1	398	SRSHCTPAWVRVTLVLKKKEKEKEKEE KKRCPCLIVSHQSL*KKRQFL/RNVK/ LELPYDPAI/PLLGKLEKI*KIATYKT CM*MFALFIIAKKYQLKRLSTDEWIN KMWYHAI
1172	15073	A	1180	3	389	GYDRVIPNP*PLTGA/LKALLTLGGLAM *FYLQSMNVLIIGLLTDLTIYHRNSDV ARKSTYQHHSPPAQGLRYGIMLYMTS EVLILLGLF*AFYHS/SLCPTPOLGQHW APTGMTPLDPVEVPLLNT
1173	15074	A	1181	354	2	ANSSDACTLDGHRALPLQLPFCGYSISF AAQSSVEMPELLIPPHCNRTPSLWHY SPASNPTNPSY)*TAPSPPPPIKPNP FS*KFPYTVWVYTSLTTCQPPVSSPNF TQPSVL
1174	15075	A	1182	3	384	GANVSG/DL/KLKPVLIISSNPR/ALK NYARSILPMLCKQEKKEKKK\AMWTAH LPTAMPT*YFKSTGET/CAKSKI PFKIL VLDSACSHPRALMECKELIVFMEPVN *HSI/LFCMQPMDQALSTYKS
1175	15076	A	1183	1	410	BPLP*KFFSPGGVGS*KGRFNPBPVG VLPSSSP/LIPTFGNWCFSPPSP*KF FFSPKGFIPQGGVGPFPFPKRFPSKI PPLVPFSPPFKKKIIFPPPVNIGPPRV FFKRPDSIEFF
1176	15077	A	1184	406	62	PPIINMLCSLAPFFSPDPLRGVLFPFP LKNFFFP*GVYFWOOGDHF/SPDPKGG FPKFPWVFNPPPLRKK/YHNPDPDG EGPVRVFFKAPP
1177	15078	A	1185	337	383	RSYISPOK*VKDLNHPKDDTQMAN/K HIKRYSTLIVIREMKIKMTRYHPT*RM AVPF
1178	15079	A	1186	3	471	LAPSDK*ENRLPGRNPL*EVRSRSPARQ PHLRSEPLRPATPSGK*GASPPSSHA VREGGGQPPPGQPPRRRGEGRLCAAP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
						LKPVPTI\YHSENPRLKNYAKYT/PVLY KNSNKAMMIANLFA*FIKYFKPTVETC YSDKKIPFKILLIENADPHLRALMEMY KEIHAVFMPANTTSILQMDQGVLLT
1206	15107	A	1214	3	340	KIRVEVNMKNRKLLEBKIKISLFFEN INKIDQLPRLKTRQRQINKIRNBQG GISINIMETKYSYKEML*AIICKLNNL HEMNKFL/EHRVPLKTQVEIENLANYTK K
1207	15108	A	1215	1	57	RGLKIQWNEIKS*CFEKIKIDKFLARQ NFKRRKRFKRD*KGDIIMDITET*GII RAY*QL*GNYLENLENGKGFVTEILP KLNH/DIEMLKKPVTT/REKSVIKSLP LKXSPLDHSTPAQFYQTPEEE*VSVLKR
1208	15109	A	1216	350	1	QSSFFSYTPNFHLLSPKPCPDFTFPYA SVLATNLSLPFFPQISRYFP/PFERERE RERENNVL/CCLGNSAVMQS*LTALNY W/VROQSILSLQAS*SYROGPPHANI HFIFCR
1209	15110	A	1217	139	358	KNTFFVVEAKRLFPVQAGQGGNLSFK FPAPP/NLRG*SASSPSGGYRTPPCP ANFFFFKKNRISPGWGSW
1210	15111	A	1218	361	50	WGDHGLSKQPPPLRSKNPPLASLVGT Q*LG/HPVAPFPQILFFFFFLRSL/D SLAQAGACWCDLSSLAQPPRPTPLGL SLKKKGNPVFVTWMLNLDIMLS
1211	15112	A	1219	1	361	LKQHVSNVETAFYKWTQSKTFVARE*K GELSSNRGECLLQSFYQPLLLGANAA GDFVVA\PMILLOSEN/PRALQNTTS
1212	15113	A	1220	292	362	HTPVVATQQAWEVGSLEPRRSRE*PPR LK*SSHLGLLNSWDYRNLB/RLANPCI FLCPVR\FKLLGSHNQNSVQSARLTG VSHHANPILKKLFLVCLFMGSHYVAR AGLK/PPGLK*SSRLSLQNCWESREPP HPDTIH
1213	15114	A	1221	372	3	RLFFLLPPRPKGDFPPTLLIN*RHGSP PHVFKPPPLMLILGALKKKFFLPS/LPY VKFYFFKRAPLFFF/IFFRDRVSLCWS *PPGLKQYTHLGLPGIMDYRHESACLAN NIRNNNTNFFFTS
1214	15115	A	1222	3	291	RSQDQDCPGQGHETLSLSLT\PNVLSLI CNL*TLSLIFVKIQLANHGVR/L*SQL /LRLRLQENHLNQG\DCIPANATEKDS VSKKKKKKGPPF
1215	15116	A	1223	379	19	HWQILTIMRYTPIRMAMKKIGYTK/C W*GCRATSY\WECHRVQSL/WQNTWAD S*KLNTLSYDAIQFL/GFYSKEIGY IHTKPT*WYTAIILIKSQI/HKQYKCL STDWIKQNRGIV
1216	15117	A	1224	387	40	KKTLSTP\PEKHPTPLPHPPQXGGA PPSKPPPCKHPPPKGISPPPP*IPPP PIYPPPPPAKPPPDFL*SPPPPPPS PPPP*TPPPFSPPLFFFTFFFLIR LLV
1217	15118	A	1225	21	477	IVSRLITVRLQKFLDPVRPVRERKEN YSSV/SFINIDRNVLKIL/SSQIQQYI KKLIRH*FWF/IPGIQGWNLKSVIV TVVWKQWKKHITISVDIKKAPKHY

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						LALNLIKKKKKKKRALPOSFIPGDLFKK PNGGFFGLKMMGRAPGE
1218	15119	A	1226	1	398	BRINHTLFFLAERQKRLPTGTSGRGFA IPHINTPORAPDHAYLPAJALAAQHRAGGQ QAPFPFG(SSPSSSPYDEVKDRLEGVITASH GLRGNGWGSF*ATSLVLNLMYNTATYKG DEVFGPRMENAWNATANTENK
1219	15120	A	1227	3	238	DAMVAGHG/RTP*SQLIKLIRWEHRS SGDRVSDP*SCLCGLAWVAE*DSSSKKK KGGFFKGTGKPMNRGGGKINFFYGA
1220	15121	A	1228	207	2	NRVSPCCPVQAHDESLQ/PRTFGLKRP \SASAF*VAGTGVHHAQLLPHFFFFFY *DRVQGVQRRL
1221	15122	A	1229	15	413	RKSNVLIHHSLLKKKVMILISIDTKK SFDKI*YPMFKLSLSEN*DSLNLNINII/ AKP/VANTILHSKRLNAFTKQCCQCC \PPFLFNIILEVLASTKGRKEIKSLQIR VBEI/KPLSLFADNM/IVYIENPKES
1222	15123	A	1230	363	1	AADPFACRPVSPHPLVLTSSQSLLTS VSPKKQPPSAGMQLGVDSLSGHWGRT KKTRLAFFKTRLSAAQTKRQWCEHRSQ P*PPGLIKRSSHLSLPS*NRHMPHFL AN/LCLFV
1223	15124	A	1231	3	402	QANSCIFSRDPSGVQAGLEPLTPGDFF ASASPRORDYRC(GPAAQLLTPC*ISI LILV/CIS*NRDYFITCIYFNYISQI FYRASDFFPFLRQGLALSMDHDSLSQ PHPPRLN/HPETSAGVGT
1224	15125	A	1232	3	396	LSQRHFFLPFPFAGIDKLLKLPFWKDN* MYEKED*RGVITLP/QYKASVATVVK WVHWQGDIDVDQWNRPRRPNYMSQ *FPL*TVSQENMLPLHINPYMNVINGF ICNSRQKQSRPSTGEWVKL
1225	15126	A	1233	3	395	LPKCNDRR*PPHPALP/LFP*GHRFP KMQVK/WRKH*TEHRLVMYFSEKRGD*L KDQKILYVLDNAFQFIFFTYVMYSIL FKFNIR*LTLSVVGAVFLVETGF*TML ARMVLIS*LRDLPTSASQAGI
1226	15127	A	1234	416	2	KIDKLILTFIWKCKRPLLAAILVKKKK I*RLFLPSFKTYGRQV/TK/TGWGPK NRPIKGTGF*VQKKKTPHYGLVEDSG ARTITN/WY*DN*IST*KKKLDLYLTI YKINSKWKIDLVRAKNTIFLENIWVI LD
1227	15128	A	1235	384	22	FFQRI*NAIPVNTQWVRKONSHPANIEK VL/VVWLGQTSNNIPLSQSLTQSKALT LPSHKA/E/RGDKAEEKMETCRGFM RFRRRKIVINIKV*GEARSCGSLAAGS PLKHLILLNLTIC
1228	15129	A	1236	379	2	SPYTKHSKCLRGIANVRLPTKPFLEENP G/VNVVDLGPCKKPTS*APKAWATTKI IQWGYIGLK/APCPAKALPRVKTWPS SFGIPAGHAFYBGFIPQIFKGIQPHSK KKKDLILKLDLSADIS
1229	15130	A	1237	1	407	YRVQAGLKLTLT*SAHGLPKKMDGCR EPPCLTIAL*SVFSLVLPVLLKILNF F\CRDGGQTMPLRLVSNWPQMIC/LPW PPKVLGLQ

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						H*WIKKT*/HTDMNEYYSATERNGLISF AATGMSPKDIMLSIEICQAKNRY
1244	15145	A	1252	1	253	VADVRESLDPGD*GCSELRCLCHCTPANA T\SRRTSQOQLKKQNTT*KTGIGIQLM NCQIANYCSKILYFRKMSNLQSNLKKKK K
1245	15146	A	1253	3	372	KKQAQKSGTIVLPNPNYSYGG*VGENA\ MARSDGLIS*EQO*QOONQOQTSKTD PYTYG/YLIHRRGGK\MTQGWDRLLNRK GWIWIAFQRKIKLELYLTPYTRTNSTW IKULAVAGCGGSL
1246	15147	A	1254	2	410	KNLFPVQJKAATN*ESLPQT/SRRKK KKKKKKKKRQALKKKFKGGGQKKNF FKGGKKKKLGGGVKKRGGKKPGGKKKK RPGKKSPFSRGGKKKNRSSSSSSSSSS SSSS
1247	15148	A	1255	61	487	GRPGPTHAPVVIDSFPNPNARFNNHSC DPNCBMQKWSVNGVYRIGLYALKMDPAG TELTYDYNFHSVNVKQCLQCGFEKCR GIIGGKSQRVNGLTSSKNSQPMATHIKKS GRSY/RE*KKNKKRGGGRFKGQSFSPPG MQG
1248	15149	A	1256	118	5	MFIAELFLIA/RRWK*PKCLTDWINK M*YSHTM*HY
1249	15150	A	1257	390	1	TQNTPTPKPKPTSQQHQKRNKPTPGF FFFSPPGK\GGFFPSPLFWVPDGFPPPP VKTRPPEFIFGAP*KKFFSPPRSILNF FFLRGPPSFFFFFFFFS*VGKSGSSPSH EMPLFPPTGW
1250	15151	A	1258	378	3	QAFVFFPPPEKQFTPTPTFFFGQGFV SPDFPIPPQIFFFPGKKKKCLPPPPQ KIFFFLRPPELFFFFFTFFFTFFFTFF FFFL\DLQ*NVLSGTSAPEKQQLLGMV AYACNPSTLGRRG
1251	15152	A	1259	462	287	RDG\FHHVGQDLHLHLS*STRLSLPEC WDYRCDLPCPAIPAVTLQIQYRPLGLE SKA
1252	15153	A	1260	446	34	NVRABT/IKTLEVNTGVNLHDS*/GKA FLDARPKAQVAKEKSRQPSLHRRLR/PC ASKDPKEVKRQPT/WEKINHVSDEGL EFKIHKEILEKLSNNPI*KWDKDLNGHF SK/ELQIASKHMRCSASLVIRKCNETV DPD
1253	15154	A	1261	2	383	GSQRKNFLEMBSTPGDNAIDIVEVITKG FHYTMNLVDKAAVQPERIDSNFERSSSV SKLLSHSLACYR*IPCKKKSLMQ/QTS LWFFFKLLPDPQPSRAPTLLISQQLTLL RQDPSPAKSL*PTDGL
1254	15155	A	1262	476	50	FFFFFFSDTGSBSVV*AAVQMHDSLQF *PPGP\SDPPTKSSREF
1255	15156	A	1263	143	472	TGAVPIRPSNI/RPPAKIFF*NAQGLLF AEFLASQRAITLNEFFKAYHESVLKSKA KGLAECKPGKLHQRLVQVYDNLALHPSH QTRTKSSSTRQFR
1256	15157	A	1264	179	489	YIFFFLSLFFFLWPRPEYRGALTVECSL NLPGSSDPTASASSVAGTKPH*YIFFFL SLF/CFVQAQ*VQGGHSSLPQPPGGL KLYPTASASSVAGTKPHLPIFFP*KKK

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						FL\CFVPVQAGGQGHDFG*L*PPFSLKQGGGLTSLRIGDYRGPP
1257	15158	A	1265	1	536	FRGGWGSVRRAPGTASCTYALAGGPPQCPRAISCPSPLWGS*TE/PYVPRRPGDPSAAP/PSW*VPRPGVPRNVPGRGRVGDGCGQAQDIQAASLADTAPDSPGSAGSVRALPACVPEISGS/SGLPFGAALP*VAA/RPTPGRHVDTHPRQHSFCGQGEDIRAFPTLYLEVYGP
1258	15159	A	1266	403	2	TSLSHPRGYVLLRQCTSAFCGYMLPRGSLHPRGYVRLKCTGVWRCTPWVHAPSQTGVHLCTPWEHTPS*RPISAPLGAASHVT/GSLSTQHIVYPVCLLRQGL/NSVTQAGVQVGNLGSQKPLGPAQVILTK
1259	15160	A	1267	2	401	FVLNPGGRSCSEPRSLHCTPAMATKAYLQLGKKKKKKKKERGEENHQQPPRPLKREVGTPGQKKPL/WGSGNAGQKQPA/QKKGKKKKA\HKGQRGN*KRKREGGGS\TKNNSRGTGAKA*NPTIWGGGKKI
1260	15161	A	1268	49	416	LIRGRALDRLLERCGLGAPFAPVVALRAGT\CTR/CTL*APPRA/DRSPWPRSPMCKAG/DECGDIPG/MKAMSGLTRQCPWP*PKLPQSGHPAWRT*PLPQTA/CGPGPAAPCG
1261	15162	A	1269	420	47	GGPGWASFLNFPFKARR*GEWKTPGESGGAFTSPGKFN\AQGM*RRPNNPPPGPKGSG\QTGGAGLGNNPFRFWGGPNNPGNK*GGOTKKKEGPPPLEFFFLNTDFCNLIKRDRLGVGAHL
1262	15163	A	1270	404	1	AETLELVNVDILKGVSESLNRSIDQAEERISELEDRLEFENTQSESK*KRI*KNEARQQDLENSFKKANLRVIGLKEEVEREMGVESLFPKNIIENSFNLEKHIHVQBOYRAP\FNSNKTSRHSIINSHTK
1263	15164	A	1271	387	2	KRERKEVITTFVLLPLK*FQNTQWLVRELEKKPTGKYVV\FA*RKILPKPTQKRCTKNRQKRPRIHAPTAHVALLDESVFPGEIVGRRIRVRNTQQLTRVHSDQAQCN NVREIVQTFSGIDKKLR
1264	15165	A	1272	1	393	FRMRLPFGGAPHFSFGVAGQRRSSPHRRSRRABALLTQTRGLRGAPHISDDGRGRDAP/PS*TGWQVGRGAPHPD/GQFGRGAPHLPDGRGRDAPHPYGVVAAGQLQSHHGRPPQAGRWAL
1265	15166	A	1273	3	317	SSYETGGWLDSSSSSSNDHAFIRIKTNASDSTETIILPVVEVTTG*WKTDIEISCFVPVSIAYSGEVKNNC*LFFFP\APGIYSTEMLDFTLRTQGGKIF
1266	15167	A	1274	92	368	LCPPGGRAGGQGNLNVGPPSPGPKGFWGPITYGGGGGKRTTRPGGKPEKSPD/GPPGPPGGTGKNPAPKNTFAQKERGEPFGNGGPGNKL
1267	15168	A	1275	401	3	DMCDWPKKESDTPPKA*SIKSRQLTSPIKIKSSCSPS\KNTIKGLTRQEKLMGKIFANHMSDKGLVSRIVBELSKLN\*K*KLNF*KWAKQ*DHLLKTH*QICKERYSLGEGKITMRVHSTSIIMCIKTIS
1268	15169	A	1276	298	426	GATMLVLLF*LAFDLRQL/NCFQAGV

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1269	15170	A	1277	421	1	QWRDLGSLQSPSPHFK VSFRDQKT*INKENHPLEKWKIKCNQPL PQIRYMDANKHILKIPSTSLAARETNMKI TT/RILWKTVQFPFKVSYLPLEPATLS SYLFTQEK*KHIDGSCSPRVATAKLLA LQWRRPSMNCMHQRAGSWKQIGAPPFSK L
1270	15171	A	1278	1	218	TRSGVDQDPNQHGELSLLLKIQRLASYG GVCV*SCLLRELRQKNCILNGPFSHHC PAWATAEONS1*KKKG
1271	15172	A	1279	88	396	TELFSSSFFFGGVPKCPQLRQ\BN FASLHPPPPGGGFGPSLTPPA*WNGR PPQATLGAFLGEG*TFPPQRPEP*L WGPDPDPQQRGMVMTPL
1272	15173	A	1280	94	399	TDLFPL*TDLFILGSLKNIWNEPR YGGFSLGVSNQALPPSQEVNDAIKQMK KHLKLA/KDKLSIVRCITKGM*LLGVR SSNQVKRITWQLVLNMLAYAVFGI
1273	15174	A	1281	236	2	TQSLVFFVYNTGPAVYLNNHALRTHGGS HLCFFFCFENESHVSQTQA\VMKRLS SSQPPPPRLKRFSCISGFS*DY
1274	15175	A	1282	37	410	KKTKLKKIKCLCPGKGSPNPPYVLS KVFPKRGILFFKVTVFSLTPFFKKKNP KIGGSGFPPLWFFFFY/RDRVLCH PGWNAVTRS*LTISVSSDPS/CLRLPS SLDY
1275	15176	A	1283	404	232	LSSWDYRCPLPPHPANPLYF**RRGPTVL ARW/GPRDSPASSSQAGITGWSHCAQ PG
1276	15177	A	1284	3	402	WQITLWRYCTGVNMP*KKK\SRTEPR C*GGGT*TKILPCWGDYKIGS/PLH/K SVWQFLIK*NNHLLXDPALLPLPYTRE MKTIVITITKYCNHNEK/CMQGFTEALF /TLPKTE/SQFHSST
1277	15178	A	1285	1	253	LRGKPTLHS/SILKRG*SQINN*TATL IK*KKKGKIKPK/RSRRKVIIMNRK*D *KQNNKFNETRSMFFKMKKIYKSLVR VT
1278	15179	A	1286	400	105	FNFRKKKKKKRNEVSE*QY*QANYLRN FTKNI*VABKHKNAQYVIREMLI*LTM RYYYTPIK\MAKIKLTDNRKCCQLKPSY MVGKFGKFLIKLM
1279	15180	A	1287	400	119	TVFHHIGQAGLELTSDDPPVSAQSAG ITGLSHW\PASSSFHNSCPVLEPHQ VQQLDSFGYEKVCFSN*VPGAQKNDL SEN
1280	15181	A	1288	157	386	NDLQHPFPYCLF/DLFCQSLKKGQWH DLQSLQPLLPRFRILCLSLPSSWDGCH VS/PNDG*FCITYHLYFLVMGF
1281	15182	A	1289	400	124	FDAKAGQGGDFGSPPPPFG/AQKIFP PHFSQ*IG*KRGAWQQTIFVSFSKTGA PPPGQGGFQIPTPCGGPPQNFQICGAP APGPGGGFF
1282	15183	A	1290	419	3	KNFFFLERGGFFFPFGGAGGGFF*FPF FFFGKKISGPPPKKRGPPGAPQK/L/R EILVLVKKKGPPPLWPGGFLNPAPKNFA RANFPKRGSGRVGPPSGGNLNLNLGGN FFRFFFFFFFFFFLVFTFRFFCCGNSA

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1283	15184	A	1291	397	39	WGQVNAKDWHIGLGEKTKGCEPFLPVGCP/SLIPPNLFFYGIPTGGLKIFVEKONPPFP IKKRPANMIATFFPGVFLFFL/CFETRSHSVTQAGVQ*RDVLSL*PTSGFKRFSCLSLPSSR
1284	15185	A	1292	399	1	LNFFFLHRQKLNILGSSDDKVPAPSIYPKPRICVYVSLLEIIFSDFNKKIRIYKRVSRIVYKDLKFNKNDNPVKKVAADINRHFSKDIQKVKHIRNC*TLAIK/RMQNTTTHW*HLMENRMAKIRTI
1285	15186	A	1293	412	1	ARKWISIRPLGTPIWRSQGGKGNKRVSPPTRPNPLFLNPKKCKKSRD*NKPPLLKKKKKMGKCPAQ/SCKQGNRP/SPTRGLPPSPSTPPSRPSTPLAPWAS*LAISPAHTHCNMRKLSOTHTLSICPLKLRPG
1286	15187	A	1294	229	1	FFETRSHSVTQAGVQWCKNPGFKRSCFGLSSGWDYIYAPRP\ANP\*FLVETGFIYVQAQGLKLLSPGDLEPALAS
1287	15188	A	1295	401	2	STLPVH*KWTIKAMWTAHL/PTANFTEYFKPTVQNYCSEKIPFKILVLIDNAPHGPOALMGWKNKMSVVFIPV/NTTSLQP\ADQGVIFTLKSYCIRNLFGQCTPAMVTTQLDSVSKK*INIFQPGMAHACN
1288	15189	A	1296	1	336	KRTPRKTRKHEHNGEK\LRAPFLRSGIKQ/GCAP*P/YILNIVVA/VLAKYEGKEIKASFRIBELKLCLEIDNIFVEIPEPNSPQKL\IN*FSKVAG*VSTQNSVAFLEFFFFF
1289	15190	A	1297	3	384	HTNMQKVLV/VKTSBQPSHNLPLNQLILQNKSLTLFHSIKASRSRA*EKCDORGNPFRFKKKK/RISTHQGEAASAVIQAGTSYPPKDLAK/DBGSYTKQITZNNVETVLY*KMI/PTEDFVVRKDKSM
1290	15191	A	1298	3	395	SRSVTRAGVQWHDGLSLSPFPKQFCGLSLLRSWDYIRLPPHQMGGILF/VLPLFFFPGKGVFLGGPQAGKGNLIG*WNPFRGLGEFFGLNDPFRGWGF/HPPHPQLF/CCFPRGKGSPPRAGRPNP
1291	15192	A	1299	260	4	GFIVSSAVFPLLKCLDLTVSSSVLLYCLWNFKIQKSFRTYNLSPLVSSFKNSH*NSNI/WPGAVAHACNPSTLGGRGGRITRSGD
1292	15193	A	1300	91	219	LSRLSANDY*HVPTHVFFVMGPHRVVQASLELLS*GDPPALA
1293	15194	A	1301	277	441	TVER*GVQSMKEET\ELCLFKDDMSVYENIKELTRN\LLK*ISNYSKVAGYKVNIKATAVLHTSNBQ*NFEIGNTLL/TISPKHLG\NLTKAAGLYEENYGNLMBNRIKSLNTW/RDILCS
1294	15195	A	1302	256	482	YNVYFKICIGPSTVAHACNPSTLGG*GGRITLRSRGVQQVQHG
1295	15196	A	1303	182	460	VGRFLDMTKGEFIYKFLYIRKIN*SSSKLKTFTVLPTLLRD*KAKLQVGRKYL*IITYPVKGLVSRICKLKLKSLNKKTTQLKKWAKDNNRH
1296	15197	A	1304	1	468	FKQPSLSLLSSWDYRHPNPNFCETAPYKQNPAGCSNFTDNPVIST*QGLQALS



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						<p>PNNVEQS PWRETKKTAVALDGVTKPCQ  VFLRKPKRTKNGQ/HBQQIRGF/CPFSR  TESHSVTOAGVQ*IHHLGSL*PLPPPPFR  NSTTRTSYDQGP/HVPP/HFA</p>
1297	15198	A	1305	880	1026	<p>EEHGAGLGGQDAAGGVFAG*GGWAQLN  VTRKASLFLDKTHMPVDQNLGSLYTTIE  ATAKGLMQKLELGRYKETHAKWLEK  QELGGFSTQ/SQDGPETTVALEAL  TFRFRAVFPKQIQDLHVQISAEKALATV  NNYIDHSNAYQORSAKFLAQDDLEIKAS  GNGRGTSITLTHYKHSPPESRDNCNLVH  LNATLHSALEENKKGGEFRLRMETRFQ  NN*EATMTIMEVSLTGTFYFNQDDLKQL  TSDVRVYAFQYKTKTSTSDSTVVLYLEX  LSHEINTELGRFVRMLQABFLQALVLT  IYDYDPSRRCSFTFNLPTDSSL</p>
1298	15199	A	1306	3	726	<p>RTDHYQFQSLKHLCTDGEALNPDVREK  KROTGVELYEGYQSBTVVTKWLSYE  DNTYIVK*KTL*TKKEG/IICNPKG  MKIKSVSWKESLPYTVHIVDGBGNVLP  PVEERNVTVRIKPTQLLILNCYLDKCE  KTAVS*QGDYITGDRARDKDGKFWFMA  GRNDVINSSTRTGSPVEESALVEMTA  VLESTVSSPYTIGDEVCAYIVLTRY  SSHT*ALTRVLQSHVVK</p>
1299	15200	A	1307	230	486	<p>NATCPNBSKSLGLSGSVTYTGVRK*J  HSLIQPRPGLK/YPTPSAS*VA/GPQA  GVONHGLSDLTQPPG/FKRFSCLSLPS  SMDY</p>
1300	15201	A	1308	463	440	<p>SALPHT*RRRKQTSLNADMEKV*VWVI  EDQISHNIPLNKSLIQGKALTLPFNKMA  KRSEBAGEGKFBSRGRQ/MKFKERSHLY  NVKVGQEAAGADGEANASYPEDLAQSTD  EGGYTKQCNFSIDV/TTFYNKINSRI  IAEFHHTD*GDGSGVP</p>
1301	15202	A	1309	463	59	<p>EVI STLKAGKILKTNKX/CAQDCGTR  RTFTHCWGVELVQPLMKRV/YTFPYNL  AIPILIGIY*/NMKIYSHERTCTQMF/I  NSLPISKNHGLHRYTPPREWK/HYS  HYDYIQAIRKMLDPSNHEGSGQHYG  PQGGKGGTPDAPDFPPDPDPKGVQWPT  GEPPPELEKPPPNKAPPEGAHPH/SL  PPFPVRVFKKTFPTKKKFPFGGGGKKP  PPPLQGGKKMGSALKFPPSGGKPPWGISP  QT</p>
1302	15203	A	1310	438	29	<p>PGQGGGGTPDAPDFPPDPDPKGVQWPT  GEPPPELEKPPPNKAPPEGAHPH/SL  PPFPVRVFKKTFPTKKKFPFGGGGKKP  PPPLQGGKKMGSALKFPPSGGKPPWGISP  QT</p>
1303	15204	A	1311	2	310	<p>HNQKNEFGPYVTSYVKVKA*IAKTRK  LLEENIGVNIHDLGSGFLAMMP/EA*  AIRLKIEKLDPIKIKNSCASKDTINKVK  KTRGPGVAHAYNPSTLGG</p>
1304	15205	A	1312	19	348	<p>RGQDDVLP*RGQDDVLPGRGTYSEYOL  IFSAKNPSMEV*SVNHRPFPHHGV/HQ  NCSDSGSYFISKRCGN/WVSACGTH*CC  LVPCLPKAADLGE*WNGDFSLSGKCKK  EPYLMTFSQ</p>
1305	15206	A	1313	2	424	<p>ENKLTNIGKGTNGGQAQSQ/PPECEPRTH  LQRLGRCRGGEPWQGGQPD/PPSNSSL  KNPQAGVPPFSSLKGVKRDERSVSDSG  EQRRAGTQ*TFVWKKKKKKKKKAKKA</p>

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1306	15207	A	1314	375	3	AYSFDSKA/FSSKSSPKSS KKRTLLTFLANMDAT/MNKILAN* TQGH IKRIIHNDQVQFVPMQGWFNIGQIN INV IPYY*LFY*CYINRIKQDTLLISIDTE KNDKIQNSFIVKTLRK\IKENFTLTKR IY*KSSNNKNKD
1307	15208	A	1315	403	3	LRGVSTFFPRVASQSGILSCNPPLRF HHFS/CPHLLSKNGYRPPSPPA/FFFF FLKTGFFFFCKNFALCSPP*KGASPPPP LTVFFFS/HHPFFFFFPLFFFLRWGPA LVAGAGVQVHDLGLSLQPPSLGFKKF PEKPAIRPRPSAWQVHPLLSSEPLRP AAAPSEK*GASPPGSHINIVRSARQ PPRPGGRWGVNPPQGPFRPGGGRIC PAAPTGK*GAPLPGQPPRGGRWGGYPP ARSAASYGR*GAPLSGR
1308	15209	A	1316	38	427	LTFFFLLEGARPPPPGNGPQAHQGYTA PLFNGQGGQGNFP*PPGEGES/QGPPFP GGNVFFWKKKGSAPRAGGPWTGGKGLP RPPPPPKGC*RGNPPPTPKFLGFTTFQ KKGKNGSP
1309	15210	A	1317	43	399	MNEGGRGRLSSIG*FAR*D*GKNVGR GR/BGVTFSPREPKEESLWSTPQKIV GVINHPRGVRDRQAGGGCEGFPALRAQ TGGPPA*ETRAGEQKAGGSGKAQTLQ RETRPPRGQGGGRSASL
1310	15211	A	1318	437	54	GOGNASTVLTSSQVGRSGRTPLQPDGAA RQRPPPPRGGSWAFAPTSQGRPGRGA PHLDGGRGRDAPLP
1311	15212	A	1319	351	133	KINSFQKQKQKQKQKQKQKQKQKQKQ HTEETSTQINWKGKSSIG/LAIKMGQ IQITKSYCIIIRLCK*LKNSDSIKCWQ GCBEI/GSLHICWRKLKONSTALQMVYK
1312	15213	A	1320	474	11	CPASRVAGITGAHGHMFLVFLVWGF HHVGAGLE/LPVSWSNGHL/RLCLLF GYGQCCYKES*RRFFCVSYIRA*K*G FVCLFV*MVSCCVTRLEFVTVHRCNHSK LQP*IPGLKCS/PASGF*VARTIGLYHG VNVHNSSTALTSGLQ
1313	15214	A	1321	485	33	THPPGRPRGGVFKVRKLNPPWLKESNPL FIKKKKKKKPGGPGPFIPTPSBG*/GKK KGFNPKEKRSNKPAPSNPQTGLGKKK KPPSLKKKKKKKIVYSLIF
1314	15215	A	1322	451	145	GKAEHRHDPGGRACSPSCHWTANAT \SHTPFKKKKKKGLCISMGIVSSCFDVR T*I*LRQYVLLFLQPNVITYLFTCL HDKANWVPLDKYVCTFLD
1315	15216	A	1323	470	151	TWGGKSNLTSQRTATPLPSLNDARK LRLKKKSVGLSPSILLAKNQIKKPP PTMA/SK/RIKYLINLTVDKDLYNEN Y*TLAKNLKGGANCSPTSL
1316	15217	A	1324	64	367	AQLFKTSMGNSITLSLQKKKKK*TL PSSNDYRHPPPPPVNPV*FLGRMGFRVR AQAGLEL
1317	15218	A	1325	193	381	GFFPPY*LPK/SLRC*GKDFYNGSGQA RWLPVIPPPLAQAGGP*GRSLRPTW PWSNPSFLKKPTPLFLKFS*GRILNLT PKAKVSVWDSPPALQPGGSKTFPKK
1318	15219	A	1326	410	7	

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1319	15220	A	1327	295	3	KKKLRIITGPGVVAHACNPNLTLD VCHFGIYFVCVSLYFTCLYFFFLPL*V TLTFLVYFDFTVLFIISL*YFNDCSRD CNIHM*LLSLPVLI FHCC\FVERDRVS LCHPGWSALASSLL
1320	15221	A	1328	2	392	RQASRPP*SAPPAFAGKRGSGR*PPSPK /PPPPPPKVVPKRGFPFPAGPPPPPPPP KKSPPPKTNFPPPPP/IKPPPPPPPPPP PPFFFPFPFP
1321	15222	A	1329	378	7	TDDLILKFT*ERYKPNQF*YKTKLKDLSL PQFENYKAKVVKR*YK*YK\KHLDGM KRLRSK*QIFNLASLI/HIEKTYLCKNK CYRTTHGEKWNLKPL*TKIPSK*I TDLNKTTTINKLL
1322	15223	A	1330	403	2	VRTGFRHQGQKLLRLITGDLPLPLASGC WDYKHEPLRLGELRSLTAAMAMQDQVPS PNK*IKIK*I/P*SEOPSGI*SINNVVO NRHFYDPDTFHHSKVKVLIHTYVSPHS FLSPFTGNHQCLLSVSMDFSL
1323	15224	A	1331	1	389	KMKQALDLKIFTKHISDRGLGVGLYK ELL*FN/R/RQCTQLKNGR*TNSTSM GMSFWMVSKHMKRCSCAFFSLVTRHQ VH/TTSLFVERHYHTPRVAVIKQSDQV W*EOGIRTLIHC*WCKRMAT
1324	15225	A	1332	392	3	NNMPSSA/PPPPPPPPGGPRVSPPP FFKPPPPPPPPPGQKKKIFSPPLKFF FFLRPPPPPPPPPPPPPPPPQNLGKGF P*PRPEKKKPPPGVFFPSLFLKRCV ALSPLSCGAGAHNCI
1325	15226	A	1333	394	1	SOVVGPTALHYCNLVKFTLGHFSKTTI SAPLLK*TSRATTSKSPS/CPRMERA BGRMFLGKSLKQIVLLF/LISGSCVT AS*PL/CFFQTESHVAQARVO*HDLGS LOPLSSRLKRFSCFSLPSRTKG
1326	15227	A	1334	416	1	LTLLFKPTPTYNTRKENYPTSLINIDAK IL/NILAGKIPQYIKVH*NMGLTPMQ GLFNI*K/RKSVNVI CHNRKESKILL INA*IVFDKNTMI*KNWQ\GSEYIY SNILLNGKMLKACH\KTRIN*GOQLSP DAN
1327	15228	A	1335	391	57	WURVCNMDKNLYOKKQODNVREK/WAT DLI INFTHEMQSVNQLKOTHPHSLVI REMQIKTTSY/HLLAKILNSDNSSY*G CGMGTL*CGWVSKSHALNBIWVFY SK
1328	15229	A	1336	285	2	IFFPPNRGETI*HLSLINKSRONERAH VKMGDFSLIKSLKMLIKYKILNQITI KMFYFKKHTSTIKISHLGSKGLNAC QRISVLQTKGV
1329	15230	A	1337	34	391	AKIASLYSSLGNEANSVKONKKTQON LKN/IKTAGLGVVAHSCSPSTLGLH DPGV*GCREL*WCKCTPAMASQRTLSQ K*INEGKERKKMKNCNMWNNSLQLTS FSFTKTWSS
1330	15231	A	1338	292	1	GGGISKTPGEGEAINPKKPPALPGGKK RAPSPQKKKQGERA*RDISSEDI*MAN KHKSCPLLMIREMQIKSTMYRFIP RME\ILKQKNS

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1331	15232	A	1339	369	16	DPWQNRQLSRVTCPPRRASMRFRIT*YK VTIAALMAYSVGPRVASCIRALWTTYG\ IMDNYYKRHRRFLKPL*WPGMVAHACNP STLGGHGRHERVGRVRSIPDCVVRVAG VKAS I
1332	15233	A	1340	394	1	TQSGQVRINDAGSLQPQPRLLKQSPHPSL DSAQDHRVPPPCARPCCSHDSYVLREG PQGRW/HESRGRVFLVLFVS**LSLMRS GGFKKGEPCTSSH/SLCP*PSI*DVICS SLPSAMVGLPDIHFGF
1333	15234	A	1341	400	161	KIGSNLECFSTKRPKKIKTIQFWPKRV F*/SPPPPKKILFPFPFPPSGFFP/PLP PLPKSPFPPIKINLFPSPGDFIDPPP
1334	15235	A	1342	377	3	NRHFPKASTLKASKHKLRLHLLVIREV QIKTINICHNIATRLAKI*KADNTKQWE SCEPVLTFY/C*WEYKLVQLP*KVWQK PKVCVPYYLAILLLQHIPESTCAS/CY* DIHKRLLTAMLFAM
1335	15236	A	1343	170	369	RCNENKITYKEVYFGEIVFELDNKEKNTS FFYFYFLFY/CWR*GLALLPRLVLNS*A QVLLLPWPPRML
1336	15237	A	1344	385	2	SDLRRSTHLGLPKCMYDRC/RAT*VPGRL FIFLNVSLKHSFKP**RPYLYFLSL MLLVSYLRNH*LIQGHOLLPMFSSKSF MLVLTSRS LSLSLFCFLFVLRQLG/L SVYTAGVQRNHWESLQDP
1337	15238	A	1345	1	281	HWATYKRC*/SEMTLKQINMTTPO HONG*N*K*LNVFKQWQ*GAYVNLHLC W*CKLAQPEWKIDLSIAKISMSYSHV VRKIFKLKXK
1338	15239	A	1346	176	1	SVIWNKEP*IAKTIKLTITVGLTVP DFKTYTKAMVI/KTV*SWLKDQRQWY RED
1339	15240	A	1347	398	2	PRPGPVRRRCPS/LTATSGSSSPSSP FYLGYPCGFPLPAVINRGPFILFWGPHK KNITLPARGR*IGSS*TA*PPFF/SLPS FILLPSFLLFDTSYSVPQAVQVFNHGS LKPQDPGLKLSQLLRRLGW
1340	15241	A	1348	9	395	GLQNPVGFLVSGVSGVPPPKKGLGV PPKKI/RGPNPANGPVGEPLATGPFVWG PLKKNPAPPRALFWGPPPPPWG*HPP PFLARGSPFFKFPFGGDPFFYRTNPRG PNRGPPMPKMGNNPPPK
1341	15242	A	1349	119	1	ENVFRNH/WGIMAHCTNTSLGGQGEW ITRSYV*DGQDQ
1342	15243	A	1350	58	396	GLRWGVKFLIFRGFFFPFGKWSLDP GRKTGKPL/LIKPPFGVKGIPLDPPD GGG/CGPPFPRVIVV*CKGFPD*GD GGF*PPAPKGSAPPPVLMKNWGRIPG GR
1343	15244	A	1351	396	1	GPTKGDPFLDGFPPTTLKQNFPPA LFFPPIGKRLIIGG\PKPGGLQPP* KPLRFKPGGESDCFPKF*GRIVCFQQS LCFPPPKKKTAFGKRFKKITLFFFF SDGVSLCHPGWSTVAQRL
1344	15245	A	1352	1	250	RRL*SQLGLRLRRQNVILGSACSEERS /CSERRSRCTPAWATKRSVS KTKCR RHQVGSILTVRLRPGYWRRCQCHWP

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1345	15246	A	1353	249	3	CGATLCPKKYMKITPSPFVEIDN/ATLK FIWKFPGPRIAKTTLK*QKG*RTTHPH HNILQKATIVKTMGY*YKHRQSPGRVAH
1346	15247	A	1354	15	416	LTLTSSSLKTTHTNKGRT*SPTRHNIT IFIAITNLLGLLPH*PTPTTQLFNILAM AIP\*AGAVIIIGFRSKINGLAHSLPQG TPTFLIPILVLIETISILLIQPALA\AR LTANI TAGHLMPLIGSANTLT
1347	15248	A	1355	2	416	IKYLNVRPFTLKLK*/ENIE*NPNNIGL GSDFFNLTSNSQGTAEKIDESSYFKLKS CCTSGTDMRIQLWNEKCLQITQDGL LTP*KKLK*LY/KQKTNNH*K/NSKRLK YPSRKDIIMAKRY/KKKCSTSIITRENKP K
1348	15249	A	1356	426	85	HARLVL*VFV/LFETAYLSVAQA/QGAN AQSAHFSLELPGSSDTAITSQVVCYHRN T/RLLF*IFQGYG/RCLCLGWSRTERLK QSSHLPLKPCWDYRWEPLYARPLYSCFP ENARIG
1349	15250	A	1357	2	301	GGLELVKQDQLGQHNKTPSL/TKITYIL PIYTKQN*KNLTRHGMCL*SQLARLR *ED*SSPGI*GCREP*WRHMTFVMTIQQ DSKSRGEEKQVIFTHYT
1350	15251	A	1358	2	389	FLHVGQSGCELPSTVLDPASASQNAIT GVSHRWLKSLLDVPSPLT/P/VSSAVP LISYLATGWRQAALIASPIFLQLARPA QPAREAAADS*LPADSAPFPKQWTC**M FTRALFKKKKCPVAKK
1351	15252	A	1359	309	3	KWDHILKLGKCTAK*/INKVQRPWEN* K/IFVNYVVDKGLITRIYKELQLYRKK KSNNLTFKMSKS*SSLAIRENQIKTTMR YHLTPVRLVYVLPKRAES
1352	15253	A	1360	300	2	KRAFH*KKMPSRPTAREGKSMPCFK/A SGWATPVIPAL*EAKVGESLEPRSSRPA WATREDSCLF*K*K*INK*KLTLILGANA AGNLTLKMLILCHSKS
1353	15254	A	1361	396	60	HKVTRKSDGMLCHSGPCISINQLAFCLF FQPGGPRGTLP/PYKPPQKTPKKTGP GGGGLYSPPPGGGGRGNPFPGAGGFF* PPSPPPPPPPGGRKKIFLPKKKKSLLF FF
1354	15255	A	1362	37	385	ALPSPSPFFPGFWGKKIFFPGQGRAGG HNNLPSPPPPGGGAAPRNNLSGGGE*RG PPLS\GEIFPGFLKATGVPPGGRGWFKPP APKEPPPPAPPRGIGGQDPLPPVPVLPG WKKRN
1355	15256	A	1363	12	421	EWSPDTGLGCTHLQLTLEHYQVLMKML VVTVRYHLTPVKNMPTFRKTYDAGW*KK KKGYGSKRGKGLI/HPPWAL*MSIV KKTYWGTFFKKIQKELPNDPATPNLMGY PKBGNSVFQRMGLSPVIGTLFPFAG
1356	15257	A	1364	278	3	CCTGKKLETFLR*ATRGCPHLPDNNV EVLNANVRYEKSITKIQNGKKVKV\SL PTDGEIV/YAENPHKS*PKNSL/KLKSD CSKVNITQKPIAF
1357	15258	A	1365	265	330	WPGAXAHANPSTLGGRGERTT
1358	15259	A	1366	379	1	KRLNVCWWECK*TPQPKVTVHPLKLL KLELPYDSVILLLYTLKRS/PVYARDI

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						CTFRKFIATLFIILRCSLTHD*TKQWVYLSIMEYYSAIKNE/YLPFATTQMNLEDNIFSEESQA*KHGVPFIFP
1359	15260	A	1367	1	376	HLFGASSQPPPV/DNSWDRPAGRTQLLWTPA/DPHSYG*GGAGPHPCSPQGCCAPVQSCS*APSEAGSLGNADS/GPAATLPA RQLITKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKDDSGKG
1360	15261	A	1368	2	409	EEAMPKAKMG*RPFPAPNSQILNAKKLLKEIKSVTFVNI*MIRK*NSLIADMKBV*VWIEDQTSINIPLSQSQIQSKVIRMLPSSMKAARKEEASBEKLEVSRLGKISAGFMRPKESRSLHNINVKQIGIATSDGEGA
1361	15262	A	1369	220	416	PQFLFDWQWYTYTTLNDHTLNRGRLESPGGQSCSELCHCCTPI*MT/SETLSQKKKKKMGQARGLS
1362	15263	A	1370	310	289	AFR*AFHSKGSK*H*EKKN/NWFTKTNFCTACIDILKRMKQPTKMEVIFANHIIYLGILS/KIYKELRTQ*PBTQSLK
1363	15264	A	1371	3	322	HASERTHRRGKSTETTTTAWATERGVSVKQKINKKTNK/RNTGSSIHNMVSDPBEQVTQTF*SSMQSNKKLKRYSVTIEMN IKPEYHFTPTIRNAIIKKDINTKC
1364	15265	A	1372	3	332	GREVS*EDTNMLHVAPNNRASKHNKQNLIEMQGEI/DE/HPVIIIGDS/TPLSIIRDSGQKIKINDIV/ELR/STVKQLDL/DIYHTLYLKRVEYVF/FTSLSKTFPATINCI LGHKV
1365	15266	A	1373	381	2	CSVAQGVKKNCHSSLQ*TKQV*SSCFSLSGSHSDYRHE/PALFEKFFVQNGSVT ML*FS*ESCIKSGRQCSYTYLHSPPIFSSLPFSIAPESIKRQEPSFPFEMESCSVTQAGVQMRHLSLQA
1366	15267	A	1374	1	385	YRKGINAKIPNKI**V/ESAISHDQWIVLVLQGLSLI/RNKSISVTHVNRKLN/HMLI*IDAEGAQDIQQSSHGKIGIKGNFTDLLKSIYRKPMANVILNRMKCLPC KC/KTSQGCQLSPLFLFFF
1367	15268	A	1375	1	357	CSGVISPHGLGLFGLSNDPALASRVAGIIGMTP/HAQLIKNFCCWWR*CLARGG*RFKTMCRPIVK*NKSINK*NRIVCMSCGDS/RQLLGRLRNSGLRNVQGCSEP*WHHCTSACL
1368	15269	A	1376	1	375	HRPKFSISLLENNMGSEFHDGL/GSDLIDMAPIVQSIROKTSDFLEIKKSCSSKGTV*IMKQATDW/RITFVKHTSNKGSIMBEL*ML*KL*WNP*KGAREFSRHL/BDQATKHMK/KCSIAL
1369	15270	A	1377	260	400	KRGLGKIVP*WPKKENG*PFFPKTTSKRGRILANVNP*PKYYSVKKKKKKGGGLPPFCIKI*FPNLIQTTFWPKINPLILKRRKKPKKTPTWGHFFERGIKKTQGGKKNPKKGGNEKLFLLGQKKKMA*PFFOKPQOR/WRKTLNVNDEP*NLLKQNM
1370	15271	A	1378	403	1	TGVSQALSLEFFKYFKPMVEFLVPSER*KGSPVYGLQIFFSIPKVPFPCPFWAR/SLV*SSPPCLSLILLPAGVLPKRSLLRPMLOQSPMFFARIG*FOILLNFQSL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
1371	15272	A	1379	195	381	S*FFFFFGDRVSLCRPGMSAVAP AERYQTISRSTADRI SCLET* SAEI/VFP DSGKKTGGNNNNNNNNNNNNNNNNK ISLSLKP
1372	15273	A	1380	361	39	PPVKETAKDVNRFFPKQPM/NET* SDA* VDEVVCL*FQLIGRLK*SRRIA*AQBFK AS/HQHQSEFTLSLKNYLKKKGFSTLLFL RSMQIKTITRYHFTIRNAKK/SHHYKC *QGLAMLPRLAHSWAQILLISLPI SMNYRHTTSSTQASLHVLFVIGLGNRL LTSFAVSFTGG
1373	15274	A	1381	400	90	LPSSNDYRCAPPLLANCVF/M*SQGFT RLVSN* PQDPPPTSAQSAGITGVSHHA WPAFFIMWFSSYSR/TMH* QGPHV*K LHICPN*KS\LSCPQVPTIIV
1374	15275	A	1382	1	431	DNI PKKSAYVYMITLFFKGDVDEDEAY SGTLAISIC/ENIHLCVLSDEQHST ACTANTIDITVGLAYTITAKRKINKL CT*MPKLSYPLF*KIL\KNTKNTV\ P NQLQIKABLPVILHNCDDPPTMLGGV ASTYN
1375	15276	A	1383	2	432	ELSADVSFFFTITPLSGVL*QWNGIAP IPIELRSPTVITFSFDVNGGPFESLQS PFIHSDHQWHVVRERMKASL/QVDQ LTPNTCPAPADGHVLLQNSHLFVGTA TQKGLSCIRAL/RNKGWTLDEERAQ VTPVQ
1376	15277	A	1384	1	421	NFFALASQRAGIADTCHCMPELLRLSKP QFSNL*SKKFAIGDV*SSNLL*YIYFF EMESRSVTOAGVQRHDLGLSQ\LPKPL SLLPKL SLLPPK\ SASCRLAGSWNYM HVPRPRANFCIFSGDGVPCWPGRTPT G
1377	15278	A	1385	2	416	IFSVDETALYWNMPSRINYL/RKEKSM SGFRDSEERLTFL/GLNAPGELSLIL LI*HPEILGPLANYVKPTLSVFY*WINEA LITAHMFIANLTFCFKPSVBTYCLGEEM PFNILLIGNAPGYPRAPMEIQENIIV
1378	15279	A	1386	170	1	DGVFLIPGGQNEKLNQRDQ/DLTQLFR LA*NSWARQSSCLAPSKCWYQREPPCL A
1379	15280	A	1387	47	418	FWGFFFLKKKKAAALGWTPFPQGGG PFPFPSPGKRGPNPRTIIGFVGR GPPPGGGGKPPPPGGA/PAGPQTGG PQNNPPAPGP*KG*GASKGAP*KGVD GGERSQVNRGA
1380	15281	A	1388	58	503	RPTRPNGYIMKEPIFQKDRTI*NVAP KNLALKYIKQKLNIGKGRDKLT/LVAN ISTCP*VTIDISR*KICKGTEEL*QPA \DLIDIYRTLYPTAA*YTFSSAYNYSK IGNSIGHKTFSN/CKRNDNIQNLFSNIN GIK*EINIII
1381	15282	A	1389	2	401	LVSQVNVENRILKKIKNSTPVRI/RQM IRKQNNLIADMETVLVNNIEDQTSNII\ SQSMQSKALTLFNSVKAERGEEAA\RA GRGWTRFKERROL*NLCVSEPPS\AD VEAVASYPEDVAKIIDGGYTKOR
1382	15283	A	1390	294	3	KIVIPDFNDVKNCSS*KIVIFDFNDVKS

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1383	15284	A	1391	3	422	CSKTVIBGKVS DCKKIFSKHISDKYLI SIIYKELSNLNNQQPN*KWAKDL/NNM SSKHKIKCSISFGKQIKTQLRNHYIPT DAM
1384	15285	A	1392	3	400	PLFKKESGTFNPPPPWGRFFPGGKSFS PFFFPFPPPIKGGPKVSKGPRFFFFFF F*DGVS LCRPGWILFPPQVTEALLRGFL ALGSLCFRLDKFFFFFR*RGHLLSRMDY RHEPPPHLRIS*RKTKS/KGLIMLTRVLV FLYITRDIYR*YKTFQINNKLRIYPR* EKDLSKLTAKDQNTNML*HGSLLLI KQWIKTWMGHSSLECLHFNANTTC WKR LGPAGTLLLRK*ECKSVKPL/WETP *QCLIQIOMQRNYH/DPATPLIG
1385	15286	A	1393	409	2	IYEHFSDKRDITSTNEMKGGFISLVREV QIBETTMGHHHITVRVKIKTDIFASAN TKC**GYGKTRTLINS/YNECKIVQPL/ WKNILAVAYIKHTFFPPRIHLSGSQKS HFSIYSKEMKTLRQKHIDFNATLSQN
1386	15287	A	1394	409	24	KSPFFFEKGFSPPPGGANQGGFPPE PPPVPVK*FSPPTPNKMGNRPPPSH/P G*LFFFCSPGGFPPLNNFLTPLPR*SY PGLPKRWGFKQKPMGRG*RAFFCPPKI SKKLWGKKKKGRPLAI
1387	15288	A	1395	83	411	QRDSVSKTKQKIKNNKRTDLNRHPTKE DRWM/ANKHLKRYST*LVIREVQIKTM EYIYI SIKKSKINKPDHNCWQCORPG TLIYC/MS/CRWPSLK*TFW*FLKLN
1388	15289	A	1396	308	14	NFFFFYSMSNLIYQKGTAT*PTSKDID FN*KIISROK*QYMLIKGSIK/DITII NTYTSNNNSPKYIKQTLGLKGELAPST IVVGVFNTLSIIK
1389	15290	A	1397	321	1	KQ*CSIEYS/FKYTR***SKL/WPGAVA HAYSPSTLIGRGRIT*GQEFKISLA
1390	15291	A	1398	183	48	KWPAVNHACNPTSLGQGORI/TIRSG V*DGQGHGSPSLVGRVR
1391	15292	A	1399	18	422	KAGMALLIDKVDPTKNIITE*/BRHFI ITKGSVREBNISVLNV/WPHYRASKHMK Q/ILIBLHVELGEHTIIVG/DFNISPSV LNRIKESARR*NI*NTNHLQLNLVDI Y*KTIKNTNGRTTFPSAHLFTIILHI
1392	15293	A	1400	28	339	YSCDHSVQPTGLKQSLCPPE*TAG ITDAPHHIWPIFF/LKRSFVFIAGQTQ WRGLI*KKKKVGFFKSGCLTLPGRGDY RRFREEKILIPGRGFCNELI
1393	15294	A	1401	390	1	PGIAGHIVLHTSEKQSIKEDT*LDLFLK IKNN*SKZITKMKRQNRKIPRHH QS/DDFF*WALDLFPKEDKVAWKIK RCLRLLLA\SMKYHYH*NKKTHTKCR RRG\RLRLLCN*EYRMVQ
1394	15295	A	1402	149	402	RFWIHLRYRVRVFPPLNPVTTNKEKGF VFVFVF*DEVIJ.CHPGSAVPNS*1TAA STSWA\K*SSHLSLPSY*DHQHASPCLC N
1395	15296	A	1403	1	403	KRKSVPELIC/APRC*APCSYRPLNFS PGPHLDVPGTPTTSPRPGPARGPAA RPKEPAKPKKERRGI/PAPGG
1396	15297	A	1404	342	3	KEDNIDKGGSPKQQLFRVN*YALY/YT



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						ALYSKKTPPRTLIAGKEKILPGFKASKN R/TLILGANAG\DFKLKRLIDHSEL* /RPKSTLPLV*KKA*LRHLFIATFTKH FKKPTVS
1397	15298	A	1405	498	66	KNYAKSTLPM.*KANSKALMTAHLFTAW FTK\PFMTVETVCSEKKRF/SPKMLLL IDNAHSHPALMEIYKEINIAFMSAKTA STLKPMQ\KVILAYKSSYLENI\PEKT TAAKSDSSDASGQSKFK*TWKGFTRTR GRTGSAK
1398	15299	A	1406	3	411	VSPLCGERSQTPETK*SSPLGLDKGVY RHEPIYASMGVLNCPISNIGQCTPP*V AMWSLLGC\PIAMLNIVQTOLPSVLIQ PRAPGPR\HPPVSAS*VAGITGTHYAN LGMLLGSTL*DVPPFLSPSLPSEE
1399	15300	A	1407	361	2	IRVPOKKIKSPGRGHKIPSF*RGPPF FFSFFFLRQKESHVTAQREQWHDHGL QSRLGPK*FSH\PPPHPPVTGTTLPLF IYIYYFLRQSL/DSVALGVQWHDGLS LHPRVRPRV
1400	15301	A	1408	393	2	PGFNISVLKRSAGGLFFFSPLGKRGFFS QPFFFGSPRVPPPPFFNPFFFFFCCL L*KIFFSPPLKIFFFFFKGAPPPFFFFF FFFPDRVSL\CCPGWSAMVQSRFSATST LRAQAIL
1401	15302	A	1409	393	60	LNVNPKL*SYLQKRGMLYHILQSKLEFL SKTSFAQAEVFLCKWDNKLKMFCTAK KTL/IKVR*STE*KKIVKI/STK/G *TYRIKFKLNNKNTQPKRAETSRSKM AE
1402	15303	A	1410	422	2	VNDREMDGWNWNGEGR*TKMKKGGRK REKERSMFLGGRKGRERERERESQ KERQKRGKARQQRQARQKGR/EREK ERERERGRERERERGRKSS*TGSKVVK IILLVIMLVLHKLHLKVCVFSFSRS
1403	15304	A	1411	398	64	PGFFFKLIVENFFGHQFFPPPPPKG KNPL*PPQKGP*RPFGVPPPLKKGSK KKFPPPPRGTPRWGKKLLPKRGKGF GPRVSFFCLIEIGWFWAQVKKKKK
1404	15305	A	1412	391	125	EPAPFFFFPPGKRGFFA*PP*FGYPPG FSPPPLFKTPPGNFFLGKKKFFFPFPP GKICFL*RAPPFFHHFFHHFFWPPRQA ICFIIIE
1405	15306	A	1413	3	387	TDLK*LTRLSLPK*WDYRRATPG/LF FFKVPASLGSISM*YISIVCLASKRLIL TDSFSPSATAKIPLASIPAMLSPPA LIQPHSSESLYSSYCPVPIILF/IYLF IFLQSL/DSVAQWQWMD
1406	15307	A	1414	409	1	KRSQPPFF/SDPPKKGSPAKOFFLSP VFFPPDSDP\GFFFSPPDKRGFFPNP FFWAGDFFPPPLF*NPDPFFFWGKK KKNFPPPRGKFFFKGPPPLFFFFFF FFFFFFFFFKIISIKGEIGRSSVVR
1407	15308	A	1415	3	385	HRPPVNLGSPEDAAAGVGPAPVLAH QHHAQLARP*LPHQAGLRTCSPCLLS LPNPPWAPWPHPP**ALPPAP/AVDG PIN
1408	15309	A	1416	2	238	PGRGCSSELLPRHCTFANVT/SEKPSQK

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						RKKREKFGSL*EKTLPFCQTLVFGPKKK NGPFLGRVWAKRKGQHPPLXN
1409	15310	A	1417	3	394	NKRLKRCSTSSVIRENQIKTINKRHFSE *KHN/IINMCW*EGQTSLSALLIRC*\
1410	15311	A	1418	307	357	WDSENVQPLWERKETYKBITABSSWDPA IPLLDI\YPKRNEASC
1411	15312	A	1419	341	3	LETRKIAEKIKRRAGPER*NLSTNNGEN TISQNLRDVAKEVRREKFIAMNA*\SKK KEKE*INNLMLEKLEKEDBQTKPKVRR KKKILNIRAEIIRD*KNSGKD*KSXWF IYVFLVGRGFFPLTRNVLFWHDPPFL P*VLSGLFH/LPAPFQAQALRQVPPH *KNKILPPKRNKTFLLPPPPFFFF*DR VLCHCPQWRAVQSWLATASTSQAPAIL PPR
1412	15313	A	1420	405	1	WGEBLVPQRVHELFSSALRSERDTSV CSGGQCHCPGALPGAAKGAACRGDPAS RVGVETGSTMNGGFFSFFIKPYFFRD RVLPCHA\AMQAS*LTAAST*\VKSSF CLSLRSSWDVRCVSPHLANPKTF
1413	15314	A	1421	1	399	OPTLLTGLRFPVPPHATNMLLY*IN TILHYSYKNNYFLPLRQGLQPLQAGVQ WQNHGSLQL*TRGVSLSSWDHNPANF FIIFFLERQGLTLLPQVLNS*AQ/CNT PASAFQSGAIGMNSHCSFPYKN
1414	15315	A	1422	168	414	BWRBEGESLEPGVGGCSLRLCHCTP ANVTEDQSSYKKKKTPGGKGQV/C*K LGGGIMP*ERVCPGKGPPTKKKTGGA E
1415	15316	A	1423	369	1	BHCKQQLDSVPKKKYITTYERSVFP INLNTIKFLERQKLS*QIEBALINLNS IV*/PNESEPI*SLPITKAPGVGYTE FYSPKGRAMQILHKLQKRG*RHSPSN VIKTLKSKPEK
1416	15317	A	1424	403	1	KNTESKRYSTIPQRYCGPSSREFFHPLV HMKVMFPLFKCALCLQKQYIVFFETE SCSVTR*/EVQQQDHGSQQPQPPRQ/H PPTSASQIAETAILNPRKICIFYLRQ SL/HSATQA*VQWRNHGSPQAPPDG
1417	15318	A	1425	401	3	FFFFFKINFFFFFQVGRGRKLG*QFPF PG/LKNFSAPPLPGGN*R/RPPPARLF FFFL*KRGFSPINQQGLSGPPFFSP/R APKNVGFQGITPPKGNFFFFFSEAES RSVTQAGVQWRREGS/QPLPPGF
1418	15319	A	1426	386	27	CRINGVILITACEKMAQTL*IPGNPL QKKLDLTCDSTPLGLIYPRDKTYIVH/ KIKCT*HPTAALLITKWEKLLRPSBG EWIHSRHPYDRIVLSNYSTENWIKIQRH YAAKCTV
1419	15320	A	1427	398	2	GLQVHATIKFFKFFVETGSCYLRQGLE LLVSSNPPG/SSFPKCDWYRCKTRRNP LKFSLPLIFVF*LNRLFCLHLPLFLIK LNLPCFMYLFIIPALYLSLILALFRND CDLSPILHLEVKYFSKKDL
1420	15321	A	1428	401	70	BHAOLRCFPNFSVVEVGSLCCPGHSQTP GLKRSILNFSKCDYKR/AALITLPSF* *IALF*BNPNCNLSLPTPLSPPKLAALG NSCLHPWLPQPPVKGLSDSFVCMHPS RGGGCTQRH/RGFKQNNFNPQGGSS*
1421	15322	A	1429	388	131	

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						PRSNYC PPAWGAQQGSSLSQKKKKKKKK KNYQKILSTQCTQKSRVFIWNSHCCTRH CEK
1422	15323	A	1430	184	413	VSPLFDYPLFF*RW/RSISVTCAAVQ* CDGSLQPFILFYFLRQSL/NSVAQAG/ VGSLLPLPPGFKQFSCLLSLIND
1423	15324	A	1431	76	533	SKRRTTGRQPDLPTRPPTRFQSFALVA HAGG*WRDLRSLQPPPPGFKRFS CISSV LWCTKA/NDFDQRIYFS S*1*GFDSFE VNFPPLEMGVSL/PARAGLKLQSGKLP ASASE/SGLIIGVCHWAQLL
1424	15325	A	1432	373	29	KQGFPPKRNVLSSKKKFKQIPHSKIF PGCGAPLIPPSRGEAGKFP*P*QGGK A1KQNYC/HCPPTWKKKNFVSKKKKK EKQMKQK*RCVKDQ* T*MLLFP SLKS IYYFK
1425	15326	A	1433	389	73	TDCPAIGRRNRDPVRELLSSPHRKI/V NLYYYYIIVRIILTIGSTDLN*ISPVVLV LTRVCVCVCVCVCVCILPS/CYVPCRF MYPTTIVKQNISIGQKQKIKT
1426	15327	A	1434	402	39	QAGLQLASSDLFALSSQSGAGITGVSHC ASPSISL*APLGLDTFSDPFCFNLDLSF EHHSGML/SECP*TG*DLSPFS*VYN GYGFLEDRHGKVPFFITSYSQSYTPPTQL I1ADV KFBQLV
1427	15328	A	1435	105	387	EFKVAQVYKINTYKSIIVLYNSNE*PEN /KKI1PPI LASKRIKYLKI/QFAKAVQD FYABNYKTW*RI1KEDLNK*KNVLC*W1 GR/LN/LGVLLP
1428	15329	A	1436	242	2	FQGGFWVGTENKNGPPFCILKNLE/IR PPEN* KPP/LPPIAFSLGLQVFFFF *DIVSLCCPGWSA*AGSLJAJALSPG
1429	15330	A	1437	411	0	LLFVAQCELRNFSALGQPVFCS/VPAN QOPGVWV*QS/EHVTVLQRFCLMPVLG PAYQIWEVPSTLK/PPPPQFK*FS*V SLLSANDCRCTP/PIDPANFCIFSRDAV
1430	15331	A	1438	41	412	FFCTD*GSLCCSSVTQSGLGRFHLSE PNCWNYGH/RASVVLGLIFTFFLRKKI/C P*KKFL*NEDLLCCQLGLELLAPRDS LGPQSVGTANVTPRPW/LLFL*TDNYLN SSRVRFSPAPLKYKEV
1431	15332	A	1439	1	406	HAYNIV/NPSPVSLTGLSSLLMTYGLT MGCHFLSITLLILGLLINTLTIYH*WRD VTRESTYQRRHTPPSQ*GPRIYIILIT SQVIFTRFF*AFYHSSLSPTQLRRHW PPTGITPLNLEVPVLANTCVLR
1432	15333	A	1440	3	422	MEKSVVVLDTGSHNPLSQSLIQNSAL SLFSSMKT*GSEANSEKFSASAWLAR /FEERCHWNVQGAENASGDRATQSY PDDLAKI1DUSGYPKH1FNLC*KPTDT DIVDETALC*KKPSTYPLFFLKQSLAL PP
1433	15334	A	1441	375	2	KVSSPRARNVILYNCPLLEFFFLCDQ/CH SVTQAARQWRHSSLP* TGL/ASOVAG TAGAHLPSQNLIGRGIRSLA/SVATC VQWRNIGSWQPLVRKQFSSLSKSSW EYRCPPCPD/LFIFL
1434	15335	A	1442	397	122	QASLELPTSGDPPASASQSVRTIGMSH

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						CARFILGSCISLFAYPFCFLKCFLE/CCREVILL*CSGWS*TPGLKQSSGLSLPKCWDYRCRPP
1435	15336	A	1443	3	299	WEKFMAYLSD*ATVSRPYR*LLQUNKTKYLLKLSQS/MNRRHPTGDVAMNIGHTKRKSTSLVIRBIKIDRHYLLKRMARVQK/SVKCWQBCG*GGGKCG
1436	15337	A	1444	10	410	CTLFLSLSPDSAGGLCTNLLPQNTLNFKISLALGVSDKCPNPLINTIVRNVPYIHKKKCLILYCPSCANTHWTGLMTHIHLKQFFLRGLTLLPRLKCGATTAHCSLDLCSDSP**ENYPTVM/ENYFLTPRVCTKYANTDATHHTPTETTFPTGSHSVAQGVQWRNYCSLQPRPGIR*SSYLSLPGS*NHRHVPP
1437	15338	A	1445	431	9	GPAQSLDSSVSLPTITSTVKMRHAYLAGLSGGL/PCDCFLGPRVPWGSICQWHWAVSPTLS\PTVPRPLFRETLYFT*V*VPPLETCPQ*HISHCRCVINWCEDTHIPK KHLVCVHACVVCVVCVVCVCLGRSQSRH
1438	15339	A	1446	85	416	PGCLSLPKINDYRCRPPRPPHFFIPSSYOGPLTDFPLTLEQVQLSPTAKGLKKIPFFFF**RRGVPLARVVPKS*PDLAASASQKPGITGVSPHVRPIFLY/CSSTQGPLTDFPLTLEQVQLSPTAKGLKKIPFFFFLQGLTARQSTHGLPKCWD*GCEP/PWPGLECEFFKG
1439	15340	A	1447	376	3	IKSEITHTESRKPETKTS/RAQSCFCGNVVEIDKLARLDKMKQTQNNIN*RD EINTDPTDIKRIIENYQDYGTGFNNLDETDFLERHQLPKLTQBEKDNLSFITIKDLEITV*NLSTG
1440	15341	A	1448	2	192	SKWIESHLNKLKP*DS*KKPEGNHLIRFGNDFLOVTPEN/MATKCKIDN*TLKPFKMLMRIWRN
1441	15342	A	1449	411	3	VFLPPLPFPCFLNFF*GGGFFPKFIFF*KKKGVEGQLGPPPPGPFKKFFPF*IFLKAFLVFPVTLKPLF/CPPKKQWNNP PPFPPCFVKKIQYFFFFFLLRNRVLLCHPRNSVMV*SLAVASTSNAQATCP
1442	15343	A	1450	413	1	EA*IGSWCNPGGGACHEPR*PPCFPPWATERGFVSKKKKQEK/SRIMBCFQDNLGFFQILSVNKRQGR*FWIK/VQITKYNA*NVGSS*VWKRREBSCITYVKLLFQSTLS*YVGRAB*KGQCNLAETALW
1443	15344	A	1451	4	384	DEAIDPLLTYPREMKTYHTKCTQMAAVL*PIVARTSKRPKCPDTE/VNKI*CTYI/MTVYSAMKDR
1444	15345	A	1452	3	390	LPDHPGSGVSTPRGVITIGRGFWLLFPNVSPFFFFFLKRLSLLPNNRGGQNLNKSPPPRGF*NFLA*PPQGRKKGPDPHPGAQDKNP/QPFFFGSKKKIPNPTGGEKKKPPSPFKGGGGGN
1445	15346	A	1453	37	381	LTLVINVCVVCVYIYTHIQMSHTVAEAGVQWCNLGMW*P*TPGLK*/FLLSGDYRLTLPHLANLYIFFFFFSRQGL/FFPLLKLV*NSQPKATLPRVGTIGLTHTPRYP

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1446	15347	A	1454	3	400	GDLPFF TERVMTETENVLHISVADPLDPRGRGV NLMLTAEFLYGGTEAFSSFDV*GPCS ETVECFSD/L*A*GPP*NT*SPIYRFAS FLIAFCIYLLETRSP\SVTQSGGK/WQD LTSLQPLPPRLK*SSCLSLPSSWE
1447	15348	A	1455	77	398	RAETVFLYSSLGNRVSPSQRMYYIEQ LHAHTFGNLAEMDKLVERYKVLKFT*E BI\NNSPVSKRETF\AVISLPQKETLG PDSFTGGFYIPKESLWPLQLRFP
1448	15349	A	1456	397	69	CFPGLSLGNVAVP/REAPDPDP AGIDAGLDDCPLOQTHH/PPAAGASAP AGCAAGPARGAPGRSPSPRGGAADPP PWDPAAAASSAGSSAPCASSPAADPT
1449	15350	A	1457	400	2	ALFPWADKKKKNFSPPPKKFPFPPKFP PLFFFFFFFFFFFPPPPPPPPPPPP FF*RRPIFILFYFLNQNLIRDPFFFF FLRDRVFCQPGWTAMV*SQLTAA\*TP GLKQSSKSLSPSS*DYRWVPPC
1450	15351	A	1458	343	11	QGVHSRKYKETSGLNS*KNPFRKWARD TNRHFTKDNIQMENKMDVQARCSGS* F*KN*NPKSYAL*PKCEI/KSVTGTIN WRNSQIYDKLSTLQNT*WFSRSLYNFE
1451	15352	A	1459	109	401	QNYRQLGQWDRISTVIDPCKYKGLTFD QSAKATEWRKDS*NHQTS/WWKESPTRV KALESTTKRKVNSLASISVRTDVHVHKV *LKKKKKKRGRFKK
1452	15353	A	1460	42	424	CPANFNSFSRDR/SLMPLRLILNLSWFQ VWLL/SWPKWGLQ
1453	15354	A	1461	419	69	IFPLKKKKSGSGVGPLPPLPPPLGAKRG SP*KQNLKPRPHKESGPFYKKKKKGG RGGAFFPFPPLGGTKKKFPLPK/IKVS FNPMLFPFPFPFGGKKKFPFKKKKKKK SRNTVNF
1454	15355	A	1462	1	277	CHTNFLCMSPP*ATSHHPLMPHPVSR VAQAGV*WCDLARG/CSELSRCHCTPAN MTERDSISQLIRKKKKLIKIKKKNINX SVIFLGGGS
1455	15356	A	1463	382	3	KAGGSINQSPFPFPQKCKKTPPRKK KKKKNPFWGGPRILPHNPPFFPR*R*KI FLGPKFLTPLGPKIKLPLFFFKKKKK RMTY/HSAVAGSPLLKDTLQAG\LSXA* RSPPKKSMGQSFHEN
1456	15357	A	1464	561	86	NDPLISLKAETKFGKIQDSFLVSSSL\N KPGIENGLLS*+KASTKQHPIMHLRV\N DVPFLRS*TRQVCLSLPLINVLIELIL ALITISQRIKKKIOI*YSEKSLPLFTSS SLPI*WMLWEFAKLELLEINIEYKHYER YKIHINILLAKNTWTLKF
1457	15358	A	1465	3	221	RFHVSQDGLDLTTS*SRRLGLPKC/W YRLPFPCTACTCLLWGS*VFLCYLSC FKAQRPSPQNSWGAFTLL
1458	15359	A	1466	2	396	WNPART*HTPLGQTSRFSPLPCNDYRRE PP\PGLVKFLL/IQYRVTHQVGLGDWV QDHHPHIRICLKSVI*NGIVFAYNLRT SSLTLFYLRRGLF/SAPQAGVQRHKL LEPLPPSFRRSS/CSSILSSWDYR
1459	15360	A	1467	349	413	REGL*PRKDTT/HVSLRDTG/WFGAV

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
1460	15361	A	1468	403	2	AHACNHSIMAGHRRQTPRSGV*QDPGQ LPVSWROGIGFSGPHPPPLRLKKFPSPTP PKS*D/YRGGPPPPGYFFFFFLKRGFS FGRVIFKFPFPGVPPPPQNGFGKGRS /HPSRAI.FFFFFKRVF*YPPFFFFFMS PRSVPOAGVQWMDLGLSLQALPPRFM
1461	15362	A	1469	423	3	IEFSFFAPS RDKGAILLGSITLPLPRFNN FFCPPPP INKDIRGPPPPRPNFFFFRKR QGFPHMACMFLSNLQECPPSPDPQ/SV GF*GRN/HPPRAQFFFFKKFF*CYFFF FFFEHPSRVPQAGVQWMDLGLSLQALPP RFM
1462	15363	A	1470	13	427	ETRGLVFDKTEPKPKIKKKKA(GPFL RGNRS LK KKKATFPKNLAFNFGPKPKI KKVLSDLQKNLNP PPRMGNF TPSLLK* NKSSKQQTITRDRDLTS PLDQDL*KIY KTFYKTKTETYSAPHGFI/S*FDKIKI
1463	15364	A	1471	378	1	FVRPPFFFFSSRRFPFKVQGFPLPAPQ FFFKTPRGNFLLRG*IDPPQTPVGGAG SDPW/VPDGFPPKGGGVFFQQGL*KIS PPGPADP*LAVGGESPPFKKKSRPGVV AHACNLALWEAKAG
1464	15365	A	1472	412	53	SRLSPFLSSSEPHGPPSPPLGFPAKNKVF C*/PPPP*PSPPKFFFF*GPKSVLYF YQR*PPTSELFPFKGAGPP/PPWGFV NPKKKL/KPSPKSPSPAARKFNPGTKL QPFKKKKKL
1465	15366	A	1473	116	34	DNNIKPVLSN/NTGLMSIITLLQLF LL*LFFFK/WELTFPOKTHQRVDPSPQ GSLGRGRQFPLTKTEYHIFFLKVPNS ETEGAGLAT*IK
1466	15367	A	1474	42	428	ETIMESTNRFDVITF*NFCL*CYLMSKI NRQASSV/ENV*NQYVGEKILIFLIYKE CIQINKK\KLRPKIDTQVKDKISEEGM QMANQHMICQ/QPSLVNKNQIETIAGSH HLPYQINKSGIMVEERQ
1467	15368	A	1475	87	433	PQSSPFSHCHSQRLPLHLVKSTYRLQ KIRKIKHSQGNNEYFGGFFLFSLFFF ETGFNFVPOAGVQGDIG*LQPLPLGFK GFS/CPQPPRTFF*FFFLRWVGFIQKK KFLFV
1468	15369	A	1476	212	430	SLTLMTSNGIHFIYFLLLLFFFF*DR VSACHGWRAMS*SYFT*ALTSQVK/QS YLSLSS*NRHTATIP
1469	15370	A	1477	493	2	PGAAHACNHSITLGSQGWITRSKIDEP DQATLNPDSY*KTGCLLQAD
1470	15371	A	1478	454	492	HRVGERF/CLFETESHSLQDFQWHD LGSLQPPPPRFQPSVYH*PHAN
1471	15372	A	1479	2	213	IDQRENLWQDRERDITETDAEFMARE /RNRIRERERLGR/RRERRKRDRT*M PRERERENLNSLYRETYRDFETENVMDR ERORLKRLL*AVIVPSHSLGSRKTP FQKKR*REGEXSEFLIQIDI
1472	15373	A	1480	77	453	SFGDSLTSPLAVQVWVLSL*PPFPE LK\YSPTSASQVIHYLLFFFFFGKKVS FCPQGGGGPPFGLLEIFAPGLMPFFCL NPPEKGVNR/RPPTMPKLFVFFFKRGF SPGEPGVSFPPECT

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1473	15374	A	1481	398	96	KRPVVCFFSPPPKGGFFFLPVGRRFF SPPPVFK/SPPPFLFFPP*KKKLSP PRKILFF*KPPPPFFFFFFFTFFFT FFFTFFFTFFVILLIS
1474	15375	A	1482	484	64	QKRQWANKYKIKCSPLPVIREQNTTIT RYDDIPTRVAIGNKTNK*KSNSKYQEC ESARP* IYCWKYGVOELMK/S/VWQY LLKLN*LPYDPVPLLSMYPSQIKTCI PTKTCQMYLVTLPIITNQKLAHSARV G
1475	15376	A	1483	2	400	YKKGQVAPRYVDVBDANFPEELAKLI DGGYTKQSPNIDYALYWKTPVCSY SWR* IY/SLASKDRIT/LIANGVGD LKPVLIHCSKNPRVFENYTKSTL.PVLCK WNSKAMITAILTAWVAEYFPT
1476	15377	A	1484	459	65	GGFFPHKRTIDFPFFFFPRGSSPPPKK KKKKKK*DNAEDQAS*RPFPIS*EKI MELICALTEY**LTARILASNIHISTG SAYIILTEMLELSKLS*WVPLFYPNQ LRT/RAEL*WVILNK*DQGF
1477	15378	A	1485	2	518	PPPPQRFGLRGGAAPPKKKG*DNAED EQAS*RPFPIS*EKIMELICALTEY** LTARILANNIHISTGSAIILTEMLELS KLS*WVPLFYPNQLRT/RAELSMVIL NK*TSDF
1478	15379	A	1486	122	501	PRDPPALALQNAGITGLKQSYFLSLSS WYKHKPPCAPGLK/VFFLEN*YLAAY VF**SYQGISVLTQPSLIPHS PGVS VOLPQK/DLQHGCLTPSISGYSVWD GVQWRDKGSL*P*PRF
1479	15380	A	1487	491	425	TPKNDI*AEF*FINKE/CNKKWVKKGP EAESTICQALYEEIVCSNTEFVHGWL *ENRGQIMKGFNGSVKLEHN*KFYEG* LLYRFE*LAAGFIVEQQ*VSKIVKAMP GTVAHCNPSITLGRGGWITRSGRDHP G*HA
1480	15381	A	1488	441	17	KRTNIYDQLIFNKGKSTGLRKNLSLNK WQDKIS/IIGKKVDYPLISNI/NLKW LKIDINVTAKTILKLGKNTGAILHDLGFC NAFLDGHKPAQTTEKKQVK*TSSEKSR CQWLIPITSLMBTEAGSPELRSSKPA WPT
1481	15382	A	1489	413	1	LPWKEMVFLPWGRVGRGPK/GWLRLR PFP*FSQFPWGPVGLLFPKHTTY*P PGKAGHNPFGKGG*GWRVGGKFN *PKGKCPGKATQKPVQKQKKKNI KNRIVKVKVTKTYIVYVYLVQVSH
1482	15383	A	1490	359	407	HKHMTFF*TVTQNFYLL*KKWDLIQ ED*RTNP/RQKHHTPHIILKLSNQ/ NSKRILKTRKK*LVVY*GTHIRLSTYFW PKS
1483	15384	A	1491	397	39	RKFRGRSFAITLFGSGKG/G/PKGNGLI PEGPPPPFFWPAEDGFFFPQGQLPQ PIRGPGPFLGFPVPPPEGGPPPTGP*K PGKRPKKKGSQKKGPKKKTLPFFFF CQMESRSVT
1484	15385	A	1492	378	1	FGVFWPLAPRRKGFFPSHILWVPPGFS PPPGV/SNPGGKIFGGPIKIFPCPPR

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						GGKFGPPFGAGPPPPPPFQDGVCSVAQ AGVLQ*AEIVP/FPPT*ATEQDPVSKKK PTRPPTRPPTRPPTRP
1485	15386	A	1493	3	428	IKSP*PDRFTAEFYQTFRELM/PIILKKRF HKI/EBGTLPs*FYR/ACVTIAPKPGKD TTK
1486	15387	A	1494	3	417	ILNNARIKPFILR*TTROGILLISLLEFN KI*VLEFLAGAISQEKIKVIQVRNEEM SKTLFSQITTS*GRNPFFIKIPLPMQSVV N/NFIKVTYKYSIH
1487	15388	A	1495	429	4	PPCLGSKRFPFPFPFPFGGRF*KKKXIF GPPRGCPPLFPPLWAKGGGPRAGGSGG PPPEKGNPLFINPKW/PPFPQGAIPQ SRFLGGVNEKIFLFPQGGKFLTDGFPFSS LPGGGKKKPRPQKKKKRKKRVKEKKY FL
1488	15389	A	1496	3	433	FSKEDTPMNVNKHMD/CCTSLVIREVQI KTTTRVHMLTTRMAMCIYIFNYILFLK/ SKNNK*RYREIGTLIH/AQNKYKMLQ LLW/KTIWQLLRMLNTKLSKQCE/IFLL GI*KKKKKKKKKGGRRFGINFTDPGVE RINFYNSAPK
1489	15390	A	1497	3	326	WPACL*AAVAALLVPEATRLTMGNLIT VCTPHSIAELSSSG/DLWLTDR/LLK YQALLLE/DLQRLTFCLNPAFF/VPPE TGEPEHDCENVVVQTKRNNKHCHLXSL
1490	15391	A	1498	345	22	KSKWLTDLHGKCKLKE*YRKPTK*YLG HONDFLDTTSHAWFL/RKIDKLDPLINK NVCSKRVVREKKR*TTDRKISSSGIS DKRLCKIYIKLLTTQO
1491	15392	A	1499	194	432	PVVGVGVGVGVGVGVVPTQS/HVARAGM Q*HNISLQL*TPGLQVSCNLSSWD YRTPN*FFFF/CNLYLERGGVS
1492	15393	A	1500	2	417	RD*FMRFKIKSYSCIKIQREASANV ETMASY*EDLAKILNBSYTK/SQIFNV DEVAL/KIMPTRTTIVREKSIPOFKAS KDRLLILFLG/ANAPGNIKWPKVLYHST NPRAFNDKASILLVLYKLNKAWRIAH LF
1493	15394	A	1501	414	0	SSSSSSSSSSSPKMTGALQF/LLSRTP LKDSSSEKSSQ*AEI*AVHLVVHPANKE KWPDM*LYTDSLAVASGLAGWSGT/NKK HOWKICDK/DWGRGMMNLS
1494	15395	A	1502	3	125	RIGLPRC*DYR/HAATTGLGH*F*SWKE QRQ*IALGRKPVNRENTQYKIHITTY TH/PLTHVYICITHTHITV*YTHIY IILYKVLVGTPLRRLG/SVAGQGVW RDHSSMQRPYPYKLTCT*LASQSARI TGGSHHTWPAIILKLETEAPVISFTE TSK
1495	15396	A	1503	406	172	DTILDR*QKQRLRLAQKQRETEFE/R DRGREGRYRQGRVQGRQGRQRLRHR Q*QRIIDRLRQGR/RAEDRGRGRDRDR GRDRGRDRERQRLRQGR*REGRQRGR /REKDRQGRQDRGRGRDRDRETDGLDR G*DRGIDRGRCSDRGGDRDRGLDGSDR
1496	15397	A	1504	3	420	ITGVSHRAMLPs*FLFPPVVVMESHVS



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						AQAGLK/PSGLKSSHLDELPCWDYRHE P/PHLAFFOFF
1497	15398	A	1505	407	1	PISIIYHS/OPGLSKSYKSTLIVF* KGN NKTNLITAYLFTAWFPKPKPTVETTC/S RKKSPFKMLLLTANAPSHPRALMEMHKE I PVVPMASVTS ILQPMDOGVVLTFKSY L RNTFCALAAIDNDSSGGSGQIQ
1498	15399	A	1506	1	408	PPGFKFPCLSLTSWNYRHPPT/ RGP* P FVFLGGTRFHHVGYTASQHLTSRRTTHAY ALQ
1499	15400	A	1507	2	416	EPSSHCTPAWQLSKTSLQKKKKKKRRR NYFTGKKGKLFQW/LEGLSTLSRRPL GPGLIDRLAQKRLPKFKF*HINFG GAHPOGPKSWERGGGRK* TPVGKYSAN PRYHICIPPGKRNQNPFLQKKKKRRAD
1500	15401	A	1508	276	14	SPFPYFLILIR*GRKGRGQF**LELFFI I NLRQCL/DSVQAGFQHNHSSLOPRT P GPK*PSFLSLPSSNDYSAPQLLAFYGA NCFN
1501	15402	A	1509	1	391	NIFKEIMSENFPSIMSENFPSLGKTES QIQEAQRTPNKONPKRSTPEQVI IK*V RE/MLKTAREK*IVICKGFTLRPAVDFT ASTLQIRRE*DDTFTKLGKKKKKKTL P AKLTFPS ILVFKKTRGGR
1502	15403	A	1510	2	419	PRVSRATNVIISKYQHKKQNTSK*IKO LNVKPEPIKLL/EXTTGKLLDLIELND FLDS/TPKTRAPKANLTP*NYFLKLSFL TAKETFN/KTPPRGANHISDRGLISKI YKELTIQ*QKNLISK*AKDLKRFHFSK DV
1503	15404	A	1511	392	122	SVSLCVSLQSSGNTRC/LPTMPLAR*RO ENPLTSAGGCSERGRHPCPTPAW/TQD SVSKK*IMK*IK*/Q/LRQNVKIKPSPI FCBQGRKK
1504	15405	A	1512	2	281	GGCSELESCHCTPAWFT/SETLSQKKKK RKKICIECNTLKSH/ILSFVCGGKYHSP VSCTCL*WSLGRSLKSLERHQKLNNDP YPIFQNETNIH
1505	15406	A	1513	242	382	QQPNLG* LHPPPGOLGFSPLTLRLSWX NRLPLQHPFYCFFRKNV
1506	15407	A	1514	1	388	KTEGTERDT/REFRERRERDRRGYRN RYRERERERERES*V*RDVRDGDVID RERESQSERERL/REEDWEDTYIVRE TETERETEGDIERERDIVERDRIM/RD RDRDILRE*ERDRETALDSEK
1507	15408	A	1515	4	285	TRKQICNGDKTALY*KEHPSRMFFPARVE IAPGPKASKDTLLTLRLPNAVDNMLKP WMTYSRPPALWYDKQLCLYSTNGN KAWMDYRPT
1508	15409	A	1516	415	2	WDRRESLPFSRVFLPFLAPCPKGLLHP V*FGSVRSFSIERCYR*QRNEFWGPI VVKASSSRAG*VVFSTAPLPLF/CFPE TESCSVAQAGGQ*CDPSSLRPLPKFKG FLCPSLPDAW
1509	15410	A	1517	1	324	PTPRPMGRHHAAPAGLELLSSDLPTSA SQSGGIGTGSIRTNWILASNNY/SMDKL CAI/CERFILFFLNILLWILILFIPIY FCLIK* CITINFSQNSLPLPSHLYI

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1510	15411	A	1518	2	163	ACRYPLNPFVLLVENG(L)TMASDLRNS G*PQ/CDLPASASQSAQITAESSHGW P
1511	15412	A	1519	425	52	VLRGAGPLFQEARLKWDPFGGWAFPCN PPPLGV*KGPLPKG/GGNPPPG*PRGNP VPSKKPKITPPGGGAPKVPVPPMGGAARK FFYPGGPRVQGT/RTKPPPPPGRQKOT PLPKOKKKKKPWSL
1512	15413	A	1520	3	404	THASGKSNIRGLTLFVFRTYYKAAVIR/ TVWF/MLRANTNRQNL/DGPEVDPYKC SQMIFDGAQAIQ*RTDNLLNKM*/ES *TSYCKSKKKQF/DPAELYTKFNS NGRKNLRVIGKT*KVLKGFQKMGDLG
1513	15414	A	1521	332	39	TSRRTONFQDLITAFNLNEGVPLPLWRKG KKGIDIGIGOTKEMP*FPI*LLMESYIVI ERERKPE/LGLSPGLCSGMLAHKONS LPGSSDHDPAERVAG
1514	15415	A	1522	482	0	EARTSGVLLCSFGMS*TPDLR*SLCSF PKRMGYRT*ATVPGLLYSLYSRFP/DE LKGCEKTSRA
1515	15416	A	1523	1	417	NRC**RCEBKMPVYYWYBCK*QDPFWK TKERFFPKNL/NIELPYNTAALLNMRP Q*I*SQ*RVKCSMLCAT\PTPNK*IKT MW*VCLVEYSSPLKN\LLPSTTWINLE DISSNR/LRRHRSKISRPHLL
1516	15417	A	1524	1	397	RDSYQGHITPPVQ*GLRYGVLLFITSE VFFTAGFL/MSAFTRSSLATPQLGGHW PRYGLTRLNRLVPLPNTTFVLLASGVSI T*AHLSLIESNRRLIQALLITLLGLY FTLLQASVYFSSCTISDIY
1517	15418	A	1525	2	376	LRKATGQLGLHLCTVSKFVNAREKPKK ELL/KSATPVDI*MIRKRTSLITDMETV *VV*KEDQTSHPILS*SLTQSKALNF KAMKTDGRKGAVE*KSEANRGWPMQKE RSC/RFCNKKVQG
1518	15419	A	1526	3	386	ESMLFARTGQLQLLHQVPVSKFVNAREK FWKELL/KSATPVDI*MIRKRTSLITDM ETV*VV*KEDQTSHPILS*SLTQSKAL NLFKAMKTDGRKGAVE*KSEANRGWPMQ FKERSC/RFCNKKVQG
1519	15420	A	1527	127	388	KRKQINNLQFRELK/QRETQPKAS RRNKKKIRVDLLKIKKGKPLGVKKKG GFF*RTNRKDKPLKLPKKKGGRIRTF HKTS
1520	15421	A	1528	3	402	HENHMRICSTSVIRELQIKTMK*YTT FVRTAIQNTDITCKQK*REQ/GSLIY CW*QCRWQ/PLKRVWQFPPTKLGSLN I*SAVVLQIYAKSEKENVKICT*TM FLAK*PQCSSVDEERKKN/WMYGFGF
1521	15422	A	1529	2	365	IREKLYSKAKFFCRDRVSLCCFQNSRTI GLKQSSCFPPKCDMYR/R*AAALGRLL LTISSH/REQTQKFTHTYPEKSAKLPQ DGPFRK/HPTTRPQASNIQKPSFFLR QSL/NSLAQNG
1522	15423	A	1530	1	418	GTDTT*ACDKIQKFPFDRKRLKLG/IRK KHLQDKYL/WKNPASITLKSRLKSV RLRPGDGRQGCSPANLENIILGLLARA IR*EKQKQKQGG/QIGKKEVNLGLIED IMLYIENLKESTKCPILIIINEPSKEDF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,151,26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end-nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						RP
1523	15424	A	1531	381	3	TLQGFVIRKRSKIFQKACHTSDMLTIN LSCLHMKGFLPHRLYSSTCVLLELRKEV MRKTTLSCCFLT*DFFLPLPPCFR*F ILLIF*LYFCCKDKVSLCCPSWKLPL/Q QSSCLSLPKYDYKA
1524	15425	A	1532	38	479	DEACGPDQPYLTPYVKTQWIKD*TRNGK IQPLEENGKN\FDIGFSSDLLDMTPKTR ATKVKL\NDIRLRNFCASKDPTNLSLLC RAK*FVWEKISANHISDEKGLSGIYR QPPILNKSITSLT*K*ARDPNRHPSEED QSALYRWVL
1525	15426	A	1533	105	447	LTFCRVFEEYHLHSLHLPQICLSALPFR PTFCVII CEVDVVGSVFKVPPCKSKNNV AVHTMLTYQIFVSLFT*PONMKQPKCPA TVERINOMMYTHV\BYYSANTR
1526	15427	A	1534	76	471	VWVCLSLSGSCSKFQNSTIEFGVLSBG GPSAWRLFFVYVFLRQSL\NSVAQAQVQ QWRDLSSLQPLPPGPK*VLKQRCVGLV CFETESHSTAQAGTQWCLDLSLQPLSP FKRPSCL\SLSPWPSPG
1527	15428	A	1535	45	338	SNNPEFLDWVM*RKVDPIRQPMNTSSV VGPRRRSKALPKAKLAPKKVMVTWSS ARLHCSFLNASET IASPECTQIDDH *KLQRLQALINRK
1528	15429	A	1536	425	1	FFNTTFHSVSFSPLSQRCILTL*ILLKS TVKNNMNPQRSILVK*AKDMNRHPTDD HYONAS/KHMKRCSLVIGKQKXNTVS YHYPPTRIMIKVRNLSNTCK*CGCGTGS LMRCW/NK*NQLLWKTGIPPHGLVSTR SRVF
1529	15430	A	1537	4	443	ETFDHYQCGGRPFPSDLQLHGRITALL FKAVRGHLSLQRLLSF\VCCLCAPRPG GAYRGQVSLSCGLEPVRASWLLCLPK *AWTNGTSTPASLPPCSLISDCCASNQ RDSVIGPSEPGAEYNLLVPRFLPSPSEK RSIHWGV
1530	15431	A	1538	487	3	TQNGVILSPSRVSFSPITLR/CHLQAO C*AFWNGCTQQAASSTAMRAVKPLGIN AGGAAGILPKLGPQD/LPLSAEADPAGK ELSTGRQANRQPDQSAEPFPSQAFRP GYPPSPQPLSMRRGPGANPLRLARPLRG VVRRLRAGSSERQKRKRGSGGFLG TLLFT*FTESRSVAHQWQWRLDLSLQ SPVQ
1531	15432	A	1539	394	489	POQWSPFPDPSLKNQCGGPPVSIIP PPGNGBGCTDCAAGSGT*NEPPFLKI N/LEGGKGGPGGPLNPPFPKPKPGG KKKKKKK
1533	15434	A	1541	14	468	LSMWNNSRLKARLLVLSQVVA\KERF LKEIKSVIPMTLMYERNLSLIVAVEKV LVA*VKEQTSNIPLCQSLVQSKALTL HSVKAKRG*EAAREKLEAGKHWFLRFKG KGRLLNLIKVGQEATSTDGELQVITYFDL VKIVGEGDYPKQ
1534	15435	A	1542	479	141	EKTSWDLIT\SPSTAK*ATNEAGGQT BWRKTFANYASDKGLISRKELQINKK ANSPIKK*AKDTKQPTNMKKRTSLII

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						REMGIKTMRVHLTTESE*LLIKSQGRA L
1535	15436	A	1543	17	474	NPKRKKKKKKIDLLDTYYTLYPK/AEYTF SSE IHKNMLYIN*LRANINKFLN*KIKT ILSDHNRRQRPINKNKTKR/RVT/TQK FRNLILSNYVWKGELQTQIAREPLKRNVN KNTIYLN*NTIKVLNSGGST/ALNTYI DRNFKKRVPS
1536	15437	A	1544	89	481	ICLRVVISLRQENATSVACIVSCLESGSR ASENLVLHNASPNSCGLAFTCLCNV SSGNKLTDCVD*LSSS/MLQFFFFFLK KSFILFVAGAGGQGNH*PKPLPPGLKQ FLPFRANFCFLEKTOFFLF
1537	15438	A	1545	1	300	PPFPAPKXCRFP*XPXKXPPVYSSNRHG SGAAGQAVLAGPGVGRQGPGAASVGI P LCPENQGCRRPGPGHVPAPGALPSLRS LTGGIGGTRAAQAVG
1538	15439	A	1546	2	436	GAPETKSIIRKYND/RLCTTKFYNLDEM DKFLVRHKLPLI*E*IDNLNRWITSQE TDW*I*QQSSSSSSSSSS/PSSSSSRPN GFTTESYQSFRDKLPIICKLJKLIDKE \GHFFQL*GITQIPKPDYH/IENYRP ISLM
1539	15440	A	1547	54	419	PATWEDHLSQGGRCDESPRLHCTPAMV RE*DPSTSKKKKK/NDQ*LLIP*S*RRL *RSSHQTSHLMDWNSEAGR*EATFLRSY SKL\KSELELLILLDNNDHNSD*YLL SEYSGEIVLS
1540	15441	A	1548	37	339	KRWKCLR*LTMRPRAD*LNPDGVYS EL*SRHCTPAMVTEQLDLSISTHRIER HTLRYSHQVYS*P*TG/EESEYPSAL* QREIIDYSFIQMTDQL
1541	15442	A	1549	477	1	PGSHDLGSYT*PQ/VVSSPEVTSRDAPS HPSAPKFCSPNCRGMITSKQPKLRIT SAVPGAPGARGTFHALGGAAGAGGESA SRPSAALCRPLPLPMTLTSPLLSGPG RLAWGNCR*IKGG
1542	15443	A	1550	430	8	CWPGSSGTPDLK*STRPGLPTCWDYRRE PLCPASKTFLSPQIETPPYLNNNHSPR RPALVNYSLLSVMDLPIL\AFHTNGIT GYVASPPVVRNGSHVAGQVPWPNLQ SL*PPPPRLK*SSRLSLLSWDYSHMT LN
1543	15444	A	1551	2	419	BTSFSLQWGLVLPKRGAKTSRFLIIR PQGSFKDGFENPGEIKTPAKKKKK KDSRSPKALQA*GAGLMAASAFRD PQAVPLSAQPRAGPLAVGTSRDGSSG PTPGQESAV\PNRKHQPPPPQGG
1544	15445	A	1552	2	387	FRHVAQMLBLG\SSDPSVSASQGTGI RGMTYRAQPL*LFNSKNSILSGPKV/L QDYM
1545	15446	A	1553	393	2	KNPIFFFLKGGPPPPP*LEGRGKFLAPC HLCPGSKKG/LPHPPQLGAGPPPPSP GFFFLKRGFS/LFCPGGFSLLRRKGGPP PALPKF\GFLRVTPLAGGNPSFFFFF RDGVSLECHPGMSAVAASRLTA
1546	15447	A	1554	1	427	LLLLILYATVAVT*TBGAGYPLPGSY SHRGASGHRAIFALHI.TGGCCT*GAMHC



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						FIKYFRPTVEM*CSYNKILVLDTGLDH PRPLISTYK\FINLHVCLVFNITPIVQP LPR
1560	15461	A	1568	453	39	TALYWRKTPSRISLAREKSGVPGFKGQA HFLFRGKHFKPLVSKLIDHFPND/R/AL KNYAKS/TLAYKNNKAMIAHLFSP\W IKYFRPTVEM*CSYNKILVLDTGLDHP RTLITTYK\FINLHVCLVFNITPIVQP PRNQ
1561	15462	A	1569	1	352	FGTKERERERERERERERERERGRGQA GRQPSLEGGRKIVGALTY*CRCK\GSK ISGTSYTIKWDIRDSAKIRTLTSSQ GISGDACAATFTRAITSAQGEH*INQIA LRPSGT
1562	15463	A	1570	394	3	TLDWQPSRGSGTGKPYVPSVCCCCCCC CFNFCQEARKNNARGLLHQAGRTDQGS FAPSHD\A/PRGTEV/DLLESTLQTSI KQVLSKPR\BQARTGAGGQKSKATQNP KSVLTSMTYKSGQSGRGLPGNR
1563	15464	A	1571	399	2	KHQLPVPWQYNKKANTRTFLDMLHCC FVFEVRKYASRGLPPKVVILIDNAPGH PPRTP*VQY\KGIEVYILPNTMSLI*F LDQGVIRTYR/SHYTQYSMQRTISAMQE NSNKENIKVWKDSTDDCAIVA
1564	15465	A	1572	37	400	RGITGEAASADQETLADKLSDAINKIME BKGY*LPSEQVFNLDSTLFWG/KKKPK RTLSKSKKRAPGPKTGDRILTLPC/A NAVKLITRTLYKASNPQALKENVKHQ LVPCLITRGL
1565	15466	A	1573	84	485	AGHKDSFRPHQTFPSNLHLNDPARGLQ VELPASP\GRALLASP\NVDTGGRPGA CGTTRRGSGPTGAHGAQGRLMHGLQV PSPAPREGS*GPARYQAQRMMWARTAGP STPSAGASRVSPHCPGP
1566	15467	A	1574	3	463	TPAQGLRDPNSMRKHAYGGCCV/CITLC VGAQNIQRAVOGLYSTCPLCVYEHEHI CVNE*VCEHVCESESRVCESTH/LPLC A*TCGPIFGCMSEKHVFSYTPCVHRVCV CVCVHLGCCVC/VVCVVCVVCVVCV
1567	15468	A	1575	1	383	FLSPGFAPQAGSGGHNG*GPP*F/PKA KGIFFPHPPREKQRVHATPPCKFLDFF FFWKGGLNLGPKNKLGPQGGKNTLVSP PKGGKKKETPGPGGVFWGGIFFFFPP PCSPG*FLSLKKPKGG
1568	15469	A	1576	35	469	RTPKHQVQVGGCREGAKQGPFGDA DSHPASPRNH/*SLEDDIPGGGQ CRNMGMPRMTAGICAPQNS*SRHH PWAAAAGDDSPITSLGSHVPGKRSSD GCRQALCTPGSPAPSKAEVCGSPELRS LRPAA
1569	15470	A	1577	473	62	SLEINPYISGLITFNQIAKTNH*SMRKE \SFFNKWCLDN*ISTGRMKLDPLYLPH IKLNSK/LEDLNIIRDTMINLHDLGPN GF*TMITK*ALKKILN/NDPIKI*NPCA SNDIIKKVKRPNTVAYTCNPSITLGGPR
1570	15471	A	1578	59	426	LERRSPGALSPFPAPQPEMKKGPGSF* KFFFSKALNFGGGVVPFFPPPKKRRFS KNPQBGITPPPLKKKKCSQPP/YKGP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						FFLFLSFFPPSFFFFERASLCHLWSA MA*SWLITAVTSQ/VKQSSHL
1585	15486	A	1593	3	396	HSATLFFL*DRVSLCHLSWKAVAQSLT ATSTLL/VLKQSSHLNLP
1586	15487	A	1594	300	62	KMTGVLSKSCQKSPKQVGLVCVCVF/ SFKRQGLAS/VAQTGMQGDHSSIQPPA PGLR*SSCISLISSWDYRVPRRPG
1587	15488	A	1595	1	412	FURPAALQKQSLKASGVQKQKRGTY HWSLQDQVLMWTH*VSLQGDSTL YISNLPICDELQENLWLEPPQVYSTR ILLDYSCFTFRQDGFARMESTDKDAVIE HYNVLLIMTPGVSAPEPLLCCKFAE
1588	15489	A	1596	428	2	QSESEPEPFLPPTSTSLLLVHCLST CVVNSTLSCVPHFHLTFNSILLTSGP RRVHFC*LSLSLISIKNLLNTLPGVIR VASEIFGLRTIRNFPFLSHSVLPFSLIS ESHVTOQGVQMHGLSLQPLPHGQWL SCL
1589	15490	A	1597	2	442	QSSL*PHPMK*SLTSAFMYRHVSPL LANYFLFF*KGGLAVLGLAIN*AG/C HLPALASQSGAGITGVSHGALFFFNLQ CYLI*FLILIFVRRNSPVAREVLNKGSD LGLLKPPFPLNGSFCNLNLSKYPKPP ATSPGYIC
1590	15491	A	1598	419	121	NLGTPRVSPPPPLLPDPPFVSGPKKK FY/PPPPPAQLIDP*TPPPFFFTDGS SHYVAQNGLELLASSDLPASALQSTOIT KHEPHLAETIFLVFL
1591	15492	A	1599	45	397	DRVSLCYPMGSAVVA*G*LPASNSWV K*SACFSLLSRGDYMCTLHIANIKMF LGRVRSGL*SVHLKCLK*RTKSGFL SFFWKGKRFGLQKXILNRLKVFLPG PPKGLGY
1592	15493	A	1600	3	397	SRKPRGRSLMLTLWSHS*VCDALARE EQNSGCFKSH*LEVNFWGSDREV/C GY/LKTVLGSDLDNDVSTQI*D*LMKPR CPEKQDESLLKFGGGA*RIATVVRPGA VAHACNPALGAKGERIDPSG
1593	15494	A	1601	244	2	KTKTSFISLIDSQGVLSYSEFQI*KKM LTK/VLHLRAVPRHVIRFIDLRQEKV LRAUREKG*VHGKQPIRLTADLSA
1594	15495	A	1602	435	2	PQRAYTPTQHPYGAICRIARIGSRD Q/SVEMKHQOLITIPSGP/LGKSLPLP PVALCFADLEVFIPKGMLSPGVTIISL NMKLALPWVLQ*RIETPLARVIPPQYGR EHTLLINSENKRSYVWNTDPLGLHNVLP PCPMVIX
1595	15496	A	1603	288	8	EFTLLIRNQIKPMRYLITPV*MD*RW *GGKRGOTLWCM*CKLNGVCESSK NITIELPCDPAVLILGWTKERKLRFCS WTRGVGQYVC
1596	15497	A	1604	411	236	LIPSHHFFFS*G*APDESILAPTPQLR RHRPPTGILLPLSLQGA/LITPSVLSL* GGHFKGFNFTPGGGGCIFFMGFPKSNP GPGV
1597	15498	A	1605	2	437	KCLRIISPCAGPRRPMCSFEPFVCSWFL GVPPQV/PEGP*GEQ/GFEGDVRQLMQ GVKKKKNTLAKRGWPMFKKRGFSLTPT



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						WFGPQGLMEPCLNPGGFLFLIGGFQKGP KVLITGKGTGPKKKNNRPRKRGLGPP GKDDFPL
1598	15499	A	1606	31	467	EPFGRRFRGGCSRLRLRVCTPAWTTBG DGSNNI*LVNIN/HTVNSWKCSGS
1599	15500	A	1607	418	32	VQVQGLELLTSSDFPASAYFK*WYKR\ DPRAQPNPNTLKAQSNRPPRQR*PASS FSNQNSCMHRCISLP*VLFLIFFKNRP* MNSFGYNSSGWSGLNLTNSC*FWFLFG NSDTEIRICRSFHRGREV
1600	15501	A	1608	379	3	FFLLSFSNPSSTELP***SLGSLFEP YDPFSVWMSFLFELMKSHVTAQATW RNHSLQPSFQLEKHPASASAGTCTN CHBAW/LIYLCVYLFLMRSHCVSQD*V QWHNHSLSQPETPTK
1601	15502	A	1609	456	99	PFPTFPFPPHNSWGLGGLC/L/EPMTF SGLGLKGPS*SPPAHRLSGAQLCPVLR AFVLGSPQMPGPKKGF/DARGPWRKGV FVMSGQSDPLQPS CQELGPRQSTQGV PGA
1602	15503	A	1610	1	420	FRFSDGAGQKCSFPFRGGRABVLLT SQTGRQGRGAPHISDNGQGRDAP\PS* M*WRPGRGAP\PS*VGRPGGDAPHF\Q TQGPGRGAPHIPDDGRPGDAPHPPPDGV GAGQLRQTRHFGRTAAWKKVTVTSLR
1603	15504	A	1611	426	3	ICNPLLEAKVSNFMPKPPALFPGEQRDS VSQKKKKLLHKKKMSKH*PFCRE\VC ESALLLHQNTHAGKSKSYCNK*GRGFN KSHPTVQRTSHGKKAL*KKCS*DFL*K ALLTAYQKTHSGKKSFKVCKR*DFTQK TK
1604	15505	A	1612	428	273	HHA*LIPLIF/CVETRVSLCPGWS*TP ELK*SSLLGCPCKMDYREPPRPTT
1605	15506	A	1613	311	4	ANKPKNLNEIKPPAENLFPKFTQGGN NPVSLY*KN*TVSLRLFP\KKKKSGDD FTGEFN*TSKEEVPSLHKLQKI*BRNT LPNLFHARVTVQSKSEM
1606	15507	A	1614	338	88	PNPFPFSKGL/GFPPTPGRKKTRFPF PPGKFLGP*KRGFPFPPRGGP/NPAPG GPPFPNPPKGGTGRPPSPGCVFFFP
1607	15508	A	1615	2	162	KNGCTCLYSLLGLRLHESCLNLCGGC RE/PE/SHCPAWATE*DSVSEKKKYL
1608	15509	A	1616	3	399	PEVREYLTSGFLPFKVLITLDNAGLSE PQRFTNGEINVFYLLNPRSLIQLDQG VHTFKSHYTYSTERIANMSENPORT VS*KSRIWPL/LDAIWTBKAEMAIKPK TILSCHRLCATOVVIE/FRFT
1609	15510	A	1617	390	1	KNGCFPTLPFGRLALGFLK/VIFF VYRGEKGFPPSPFKGZPTDPPFACPF LGALKE*RGVPSKPPPPGPKKFKLP FPRKSYGGCFKCLGGPTFPFGPPPPQX KKKKNPATARDLEPNAM
1610	15511	A	1618	468	0	NKLVNITWLLNAILGKKHGDRLERK SFEKAPCPGCSHLTLKVFSSTVAEYV IVAPNGYFTAKARNSFISRALKSSEVHN WRIIPRNSPSSDYP*WP/VALKKKKKK AGV/LPLENYSIITV
1611	15512	A	1619	421	2	SSRLSLPKCNDYRREPPRPAQPRILKTI

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						S**BPFFLLKCK*LRTOGLRGRHKGLNSTYVLHKFMD**LQQLANGLANMLDESSFCNVLKHITQ\WRDYYFVCLFVCFVRQS L/NPVSQAGVORRDHGSLEAPPPGFAPFS
1612	15513	A	1620	406	2	GTRKASSNGFINGPGAARKKSQTAPILA KPGAPPSILLDEKNRPQIKP PACFP /S I RESQTSYYPVFFVWSFGQFFFWGKPEP LLLKEAGKVPFLFLFLGFL*DOVSLQCP GWNVLRSLTAES NPHASAEAS
1613	15514	A	1621	411	0	PPPKKKKSGPPPP/PSSSSSPSPPRKF LGGPRVFPPPPFPKPPKPNF*GPPPKKK KFP PPPGKKKFP*RAPPP
1614	15515	A	1622	2	403	TARGHLNFCSSSLPFTAS*VAGTITGTH HHAQLTLLIFCGDRLSL\CPGWS/PNS SHLGLPKCNDYR
1615	15516	A	1623	298	411	LI INVCWPGFLVAHANPSTLGG*GRI/ TMRSGVRDQP
1616	15517	A	1624	263	2	DSVSKKKKKNFK*LTPLVLKLFONTIEE GILPNSLYKG\VLPIPKDKDT*REK IY RPISLINIDAKIVSKILANKIQ*PIKKIY TDAW
1617	15518	A	1625	3	281	PFSCLSLPSCWDYRRPPRPANFF/VYF YKGNTRTQCTVKHGFTVLTRVLIS*P CDPPSLASQSAGITGVSHRTQPHTVFLL NNPALFKLQT
1618	15519	A	1626	300	20	NPGPRGFPFPPGPKRLDFRGGAIPRPGF* YLFHFLGFFWFQKNFLVFLGNKTPFP PQFFFF/RDRMSLCHPGWSEVAQAWLK AALTSQTPAI
1619	15520	A	1627	394	40	FQFAAASLFSGLFFFFFPVTSPPPPFFK TPPIRIFFWPP*RIEFT\PPPAFTFFTF LGAPPPFFFTFFFTFFFP*DRVSLCRP GWSAVAQS*LTAALNSQT
1620	15521	A	1628	386	3	IFPTRCTHLHLTNKLPICSPFDQAKNN PFCS\HHSRGVGLRARLFCERLTIEGAG TPA CPAP*FPGEFTRP/PGRVRNLTPAI PALWAEATGS*YVARTGLELLVSNPFL SASQSARTOVSHRTWP
1621	15522	A	1629	401	93	ARGVLPLNPPFPGGGRGGSF*CKNSKFP RPRGNPPPLLPQKLPPPGGGPPPLPL LGG*SKKTPPPPKGGAPINQKPPPLGP PGKRGAPFPKKKKKKDKNIRTKKGARRS GSILQSQHPGRPR/RGGPLTKNPPLAS PPQEKRGPPFPQKKKKKKTKI
1622	15523	A	1630	417	47	PPPTISSPFP/QKNLKGKGGGGNFRN PPTGGGRG/BSLWAKGSRPPGPPEGNP PLFKKKKLNQGGPPPPVPPRGRADAG SLYPGGGPPQ*POMGPPPPPPGAKKGFP PKKKKKKKPKRET
1623	15524	A	1631	416	54	EYWCGR*IDWNRN*PKMDQHLHSQFI FN*ATKAIQMGKESLNRLCLCNLITR DK\IYIDACITTY\KINSWSHSGARL* SQILERLRQESASLSPGI*VQPRQHSKTP SLKXFFFKFSS
1624	15525	A	1632	2	373	LVFLDNNKLIRHSALASACFPEDLAKI NDEGGYTKQIFKVHGTAFCKWKMPGRT FVVREQSVPGFK/ATD*LLLGNNAGN\

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1639	15540	A	1647	392	1	QKLEIMUREBGMILKARTQKQLGLLQAV THLVNAKEKFLKINVLQGTIN*ESET AKSLILFNMSKARKGE*AAEEKFAASRG WFM/RFKERNCLHLKVGQSAASAVVA VANYIEDLVKKIDKGGCIN
1640	15541	A	1648	425	148	SQSLI*SKALTLCNSMRT/ERAEVAGK KLEASNF/LKFKRS CV/RNVNQKQVA SLDGEAAASSPDLVNFIDEGGYTKQII FN*DKTSFFF
1641	15542	A	1649	271	462	RQKLRHKRCILS PLLFDIVLEV/PARTI *QKKTKIGTQIGKEV/KILSLPADDV LYL
1642	15543	A	1650	70	398	RPEASTLRHNCINAGQLLAKRAKIGALS SFFFWKKSALFAPQPGQGNGLG**KPP LPGLRGFSGLTLLRN/WE*RNVPVPT/ NFGPLIKTGTFVNGQAGDLRLTLGLLR
1643	15544	A	1651	425	3	FGFFPKVGFGLPFRFSRVFFPGTLFFP PKRGRCFFPGGAP*KIWTPGALPQG GVGPALPG/ALQKFGKPNPGFFSGPPQ MAP\GGFPGG*RPFRGGAPFFFLRQG FPVQARVHLFGSSDFFISAPQVAGTDD VC
1644	15545	A	1652	385	2	KGNNEPPEIKFFFFF*KGLPLPQGG GQWGFSLQPPESRLKLFSCPNLNN EYRGP*/RL*LTIGRTSGSKTKVPTV CSP*PNLNLGLTQARNFS/RLVFFFE TSFPVQAGTGLDLHS
1645	15546	A	1653	242	3	KGNPSTLRGFFFTTKVQOFFFFFLQVK LEFFFRNLKFLKAMP*/VFPDLPSP FFFFFLDRLVLLCCPGHNVVQSL
1646	15547	A	1654	3	285	HFITYTDLNRFSSKSDI*YITZHV/KK CSPSLAVREMQIKTTVRPGTVAGTCNPN TLGGQGRRIVQDLKQSKTSLQKKIL FRLRHGGTCD
1647	15548	A	1655	1	373	KVSLFFFFEGLLCCPGSAVSSSLQPG CPRVKQFSHVS/LPSN*EYSCPTNTSL QVCVS IHKYI*YIYIYIFKPF/CR/DRT LARLRLVSNASQALPPWPVKVILGLQ
1648	15549	A	1656	189	2	VQPGQQRNSTSKTKNTKQLPTKPS GPD*FKELIPILHKL/P/HKTEDGKTL HNSFYVYTI
1649	15550	A	1657	385	13	GGPPFWGARSPPKL*NPPPPRKKPPGPP PPPGGAPPLGGFFLFPFGPPGPGGK /SPSRFFFFFPLGGGGIFLPSPGGG PRTVSPAPPLVFKPAFFSKKKKGSS GSKKPADGTFK
1650	15551	A	1658	352	2	HSLSENDSIRDF/RCPVTFNVLN IYFL*KGWVLMPLVLND/PIASQVAV ITDWSWAKLRV/CYVFTSGSLSQ AGVQRVHSGVQGPSRV*SHHSILWK YRYPPRR
1651	15552	A	1659	265	3	HSQQRDEGRMRGQWLESHGVTRASCM TLKTSFLTMAKI*NLKCLFMDEWIKK MWHITIMEYYSATK/DELSPFVATWME LEVIN
1652	15553	A	1660	1	163	NQQRNRRKTIKIGTK*LFKKIKKFD KPLRWI/RGKNQITIHIN*RRDVI
1653	15554	A	1661	56	320	KFFMYSAGESTIKICLF/SLCLFLFLR/Q

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1654	15555	A	1662	3	421	ESRSVSQDGG*SEPRSCYCTPAMATE*D SVSKKQNNKPKKNNKCFASSLLITLP PARHKA GLITDTFPNTERGINIQVKV/RRPFSR FNPKKTTSRDLIIKLPKIKDKGS*KQKE KTSKSARLPQPHGLLGLGLGKSASSPIK KERKQ\QITYSGAPIFLVDFSVETLQV REWHDFVKVLKEK/DFYPRIVYLVKIS F
1655	15556	A	1663	362	2	VIFADEAQILKCKDKLDTIGHTTSVCK TISTEYKDNHREKIFVYSQIDKELISRV YKGLIKLANTDKNLILFL*RLGHSVTQ GRVQCNHSSLHPQTPGLK*NPPTSAS* AAGNTGVHL
1656	15557	A	1664	79	355	IHLPSLIGDNFLFTGISLLICLVLFVFI FETGSCSVAQ/S/GVQWNNHLLQPRPS GLRQSSHLSPSSNNHRRGPG*FIYF/C VEIRAHYHP
1657	15558	A	1665	47	384	KEKASGPLINFFFPKICKLAPFFFLPF FLWGGGGGKFSRNPQKHPPR*KRVFVNF FFFFFLLRCLTVLSHCHPGWSAVA*S QLTAGSNFW/VKQSSHLSPSSWDHRH APP
1658	15559	A	1666	163	601	IPCKGGVLPCCGGLADLHFTSTNSISFY YSSGLLRMTNKETPTMSTIPKGVGVAMR FNSSECIPOELPLTLHLLMLTSLASFIH SHRASNLVGRSLTVWQGRGCVGVSD PAANLRDLKQCF*DKSHSVTQSGGQC NLSSLP*APELKRSCLSPSSWDHWH VPPFLANF*IPCKGGVLP/PAQGN
1659	15560	A	1667	418	3	SVCLGLPKCNDTGKPLCPAPSPFY/EG SITLIPKSEMHLPNENTRSGFLN/M/ DAKILNRILANCIN*I*NH*\*KVKET PGKKD\PNRKPDTIILYP*QIREKSL VSSTMAKVFNKIQPVRLTLTISKGNF LNL
1660	15561	A	1668	411	1	LRHLVGRIT/LFRAVSGHLSLQRFLL PSVEICAPRGGVYRGQASLSCGGLHR VRASQLL/FLTQASMDGPPPPVLLPPC SLI*DCANNKGGFIVGVFPFCVGNL LVSHLLRPSKPSIRVGT*FSRC
1661	15562	A	1669	151	1	PLEKAEITGP*PHAILF/CFP*TESR YLAQAMNWHNLSLQPT*PGFK
1662	15563	A	1670	1	389	TFPPKIKMLSEPCILKAKISGLALIC LVSVQVNSKELIKEISATPST*MI RK*NSGVANFV*ESISTSHILPS*S SIQKDLTFPNSLKAWHQEVSEKSSA SSGWFNFKERSHLTIK
1663	15564	A	1671	1	363	ECTGPKIAKILTEKNVGGGLP/DPNFK I*YKAPVI*FWLKVPVPSSSAILMTV *Y\YFKDRNQDEYRLVKNINSHIYQG LI\FSKGTKTQW*KSLENK*GVNNWLF TCKRMKLD
1664	15565	A	1672	203	2	ALNKTTPMS**TERNCI/KCLFSPKM N*VFNVT/IQCPSGHFFTTDKSILKF IKWSK*PRIAKRTL
1665	15566	A	1673	15	378	NYIHNNQNEHYHSLPNFFFFFGKGP PG/PEGGGRG*REP*IPGGKGFPL*PP

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						KRGPPGGTTPPPGKDKIWDPPKGGPP LSPGGAQTGPKGDGPPWPPKSGKPGG TKQPGPKKFF
1666	15567	A	1674	2	349	LPLTVIARIIVSNS*PQ/CDPPATASQSA EITGMSHRAQPRGIR*I*CGSYTTCPL LLLT/YLFIYFSTESHISVIQAGVQWHD GSLQSQLRRLT/CILTLPSND*PIVTL PG*FCLF
1667	15568	A	1675	348	78	LGPWVPPVIFAPLGG*GGSPRPPGLN PQPKGPRVPLKILQNLKGV/EGRAPLPP /SGPSGCKSP*PLGSPFLTLNFSPP FWGPPGPKF
1668	15569	A	1676	2	385	TSRRDYRP/GHNNQLI*/SFCRDGASL CCPCNSGTPGKIKKSCILVFPCCDYRCE PGL*I*MGKNPT/LFNNGL*CDCIPLIH SIADIRKKPHS*IQGL*LGCHQNSQTES CSVTQAGVQ*CDLGSLOP
1669	15570	A	1677	386	1	KSTRPVLYKNNRKA*INTEHLEPTA*FTEY FKATLETFCSEK*IPLKILLILCNVPSH PRALMGWYKELNVSMPTDITCLIQPMH QGVISTFKSYLKNPTDFAIAT/DSDS DGSCKNLLKTFWKGFTI
1670	15571	A	1678	2	193	EGGRIFFNSFEVILLTL/PKPKKVVER K*SYHPISIMNGDVKILQTLNLQIQY LKRIIRYDS
1671	15572	A	1679	561	830	TLLGT/NAVVDPKLKMITY/HSVENS RGL*KSWINLGLTVFKGTNNMAGDDR HELLVTRHPTGTIP*GSLQTYCSENIFF KILLFIID
1672	15573	A	1680	415	2	TSCANLSLYPVLYKSSSLPRFIFCHPK HLWYKNIKKAAEINTNFCYINRVLIC HLGWS/ATVVS*LTVTSKLGSRDPHT LSLPSS*EGRCITPRLGDLNLFSDGG GIRGTSTLPRQVLNAPQAILLVRIT
1673	15574	A	1681	1	78	RPRIRHEVGAQLKLLTSQGTASVP* WDTREPPPCPALILSYK*NIAMGGLKCL AVSA*RHVLGPIRG/NHVECCFFPCS*A GLKLLTSQGTASVP
1674	15575	A	1682	414	162	GGPGGPIPGA/AGLRPPPPPLGNPPPP KAKICPGGAPPVPGS*KGGGESP*PP RGRGPPFIVGQPLPFGHGRGLFPKCKK KI
1675	15576	A	1683	378	129	QPFGRPNFYQIFNFPFG/PPV*HSPLEG KFPFSPGGQMGWGLGNRPFGAGGOST LRGPRTGGSGGPPGPKFFFLKQSLA L
1676	15577	A	1684	3	374	GISVLKIGICAPNKKELFEVLYNNAR KRKKYDNMAKLF/AVVCIQAKLKYLIK DCVSPSEYTAACSRLLVQYKAVFRVQ SEISSIDEFCRKFRIECLAMERIKEDR PITIKDD*GNSLS
1677	15578	A	1685	2	373	PFIRPETIKLLEIPGKILDIHIGNDL LARTPNAKINTWDHILKSFCTIKETIN TMKQPTDCEKIFSRLLIDKGLM/SQMC KELVQLN*KK/TDDSVKQWAEIDLRFHS KKDIKMANRDKVL
1678	15579	A	1686	378	201	HATCLANF/CSYG*DRVSPFCPGWS*TP ELKSTRILGLPKCWDRYCLGRSILFPGA

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1679	15580	A	1687	1	404	PPDH MCVNPGGGACSEPRSCHCTPAWYTRDS V*KINKKKVRRKKKIFHANS/KLKRVMG AVLISDKIYYKLVKVRDKBYILKGSY QEDISITNTYITNT*APKYMKDILTEIK EEDIDYAILVGDFTNLLILICRG
1680	15581	A	1688	307	33	DEGSCDHADHAGKLLDSGLPASASQSA GILGVSHGARPLISSYNTSHGGLGPAL VTSFNLHLFKDLISLQI/HVTF*GMGL GFAGAKLSL
1681	15582	A	1689	11	394	IFILEARTISSRFFPK*INHAPYNS A*LLGLFPREKK/STCPIYTNFIAS LFTVACIKKQPKCPSTGAWSSGLAN
1682	15583	A	1690	20	391	SESGKWYSCTKWCSHLZGILTFPPFP PKNPPPKSGP/OKGPT*GKGPDPWPK KRGHK/RGFFQKRRPPKPVFFLPGK RGFLLGPKGG*NPGEKRNPPWP*KGK NPGNPKGGPHLL
1683	15584	A	1691	72	392	IRMGSLFFGFAPFFFFFKTKTFFFPQK R\GGKP*IT*TPPPGN*RNQSPSPQKV GKAPPPLPK/NF*FFGKNGVTFPPGG FEPPTPKPESPVPSPKGGKTNPA
1684	15585	A	1692	389	161	HGGACLRSLGRLEDCINQGG*GCS EPCTPAWVTE*D/SSQKNGSKIKKSGL DNSFSIG*GILGLSTCDYS
1685	15586	A	1693	286	363	DGSL*PRPPGLRQSPQBS/LLSNWGR STPICLAGFFVFVETGFLHVAQACLRG FTWVAQS/ASQKIHIT*GAFETIQVLFY WGVVFGQWRFFFTESHSSVTQAVR GCSLSSLVPPG
1686	15587	A	1694	1	356	ELLPRGRGSCERRPKCPVVRABQDS VSKKRRKYL/FLRPNRSLRIPYPC */HPLQHNQISFTLQNSPGFSPRYC PSPLRIIFLPILENLGLPMKGIQNW FFGVGLF
1687	15588	A	1695	3	298	KYFETNENKIQYQMLAVLVPRENLT VVNACVKEERFOVNNALYPN*EKS LNPKGKIKVRSEKNDIE*KNDEBNQ*N *SWYFEKITYNQTL
1688	15589	A	1696	3	405	RLWCGWRNRLHGS*NRVENPETGLHRYA QLIFLTKVQKVGEGQPNK*CGGTWAP TGKT/MEQPPKASSSSSSSSSSSSSS EM*NI VFKMGNLMDH*AKSYEVRTKA *TIRGKVDKLFIRKHFCYGN
1689	15590	A	1697	6	392	LQRTLLVGLFNAAGNKLKMPILCHSEN PRALKNYAKSTLPVYKIKIAMMT*V VAMLTETPKPLFPMYCS/EKKLPKLP LITRNAPHETGLMWTNTNNGSLDAN TTSVLQPMQGRVISTEYK
1690	15591	A	1698	390	3	ALTESDFTTSREVAKLRVHPMVLNV LEPIDGVKKVKNKGW*KLK/NKQKNI EYSSSLFLCNNEPFLDGVITCDEKNILY HNW**SAQWLNRVAPK/HFLQNLHQK KUTVIVNWSAAGLQNEH
1691	15592	A	1699	1	245	GGGGEYSKILAKTALNTTYLGIYLLK /DVPDLYTQYGMLEIKYLEK*RAP CS*TERFKIVMSI/LPHLYRFNTI
1692	15593	A	1700	2	324	GNSGTSQTSQTSQTSQTSQTSQTSQTS

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1693	15594	A	1701	183	372	GRHLQCHVS KASNSNPVLSASSCSTGSP ISLGS/GSSLSNSSKNLTLPCLFSSLL S*P*ANPVDGAFKIY PGLSSVSGSL
1694	15595	A	1702	29	382	PGVLLCWPQNSAVTVHQCDHSAQPRTP RLK*SP*STWDYRYTTPLCPA GKRFFCSWEKPFPLTQGGFPLHFGQKK KPGSKKKDKRSCN*G/CREA/GTLTHY ROELMVSQFWK/TVROVLKLNVELPY DPAFLGLHPTSTQKR/DTMFMA/ATLL /ISERNKQPRCTS
1695	15596	A	1703	1	382	KKVKITGEAAVSPDPTIKKIEEKEYLP LVVVADESGLPWKKKQCTFISKEEK /SMORLTLLCKCSWVQDQSP*AKKE KGBHQLVPV*LNKKAMVTRTLFLD*FH QCFVPRVRKYVASKRL
1696	15597	A	1704	2	330	KINMLLLNS*VNTETKAEVSSSLLLEIN EYEDTTYQNLMDAAKVLKGVAPRHF LOEVKK/RLKRFQINNLTYLKEK/EKE HINKASGRK*MTKIGDLEGLYPLNG
1697	15598	A	1705	100	342	APKNSIVCPQLVGSWH*/PSRMKPNLL TRQGTMLARLVNS*RRDLPALASQSP GITGMSHRTQPLLINIMETPTLLS
1698	15599	A	1706	600	211	SCSVARLEFSDVTKACH/RTPLQKQS SHLGLSS/WD*GRVPHDLNF*IFCRD RVLPRLLOAGLEL/LASSDPPS*ASECK WNYRHEPTVPRNLGLLRTTYGWVFLKK YLLTVSVFSLMCLDCLIM
1699	15600	A	1707	409	1	RGPPFFSKGKALKLGSNSFFPIKKTRA PKKLTESPVSP/LNFPPTCTGPPFPQ MGGFF/CPRSLEFPLPPPPFFTSFP PPPPPPPPPPPPFFP*DRVSLCHPG NSAVALSQTAAALTSMDSSNSPTCV
1700	15601	A	1708	154	2	IGKPLGLTK/RYSRENTINKIRNEKGD MTADNTEIQSLIRDFVS*RTAHQ
1701	15602	A	1709	263	37	SAQLHPLNTQNHRSYLLRDFLKKQD/ G/WPGAGAHACNPSTLGGQGNITRSGD QDHGP*HISV
1702	15603	A	1710	390	42	YAGGPFRAIFFFPLPREGAKNPNFVGGP PFGGPPFFFPAPSKKKEGPFPGKKGV* GGAKGPFMARGPPFF/G*KKKKGPIKNT PGFFL/MGPPNPGGPPREGGKGIGAKK KKKSRL
1703	15604	A	1711	3	167	YTCVFCVCLCCDCMC/CVCNMYCVCV CTRVC*VCVCMCVRCVQALTVLCKSV
1704	15605	A	1712	116	391	KRNFFFGQGGGEGPKFN*RGPPPPGVK GIFPPSPPG/GKCKGAPPPGLTFNFF KKKGVPFCGPGGV*TPDGGPPPPGPPK GGAPGGL
1705	15606	A	1713	401	47	HYATKPTTHATCTCTGCTCATKCGHT QVHT/HTDTHTHTKVSQVCLIMARQE RPFCHC*GGAGAGACGVANGLSS*TW RNRKGPANTVRVVGQKQSGACHGLVFP RSYLTNT
1706	15607	A	1714	1	400	CVESCEVDIEVSCCV/CSG*SAVCSGT ASAIHCLPIPGSRDPSASACVAGT*GM PH/LYPGVPLKPREGLQTELPSSQLEI OPTCENR*HVPCL*VQLDIRN*RY QPRVAVNVHGTRRFPASRHCFS



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1707	15608	A	1715	413	3	LNTFEPQSRPFVINSSEMLILVACILVFTSGWYIYHERFLNPGREIDMATCYSETGPCPVTQDGVQMSNHGSL*PQTPRLK\HPTTSVFPVA/RQGL/NSVQAQGVQWHDIGSL*CRLPGLKSSHPRLPSSWNYRYAPPPCI
1708	15609	A	1716	421	144	RLECSQITAYCISNLPGPSSPASAS*VAETGLLHMKKIVSTGSHFIVQTAFFFLDSSDLPALAC/SWDYRSLLCPACFYNPCIFENLPC
1709	15610	A	1717	3	384	YSACVGVGVVTVSVVRGHSYGR/ARKIRVGPAAKQAQSPRPVPAQCCTSAQTTPWCSAATADPPPR*GESLPGAYPGSHSTC CPQCCLDN*HSLPSTETPACRAGAPGGG H*ANLQCGGRACORPG
1710	15611	A	1719	3	615	PVGSWARSQAQWPPSPQSVDEBAGHSIPAPRQCSKSHRABGRTARVCLSHCSFSGPRPGLVPIR*SLGRPDVAQIVPDSQEGRKTGLHAEAVMFLSGRQGVKGCGGRLCPSSPPSRCLDLGRRGMFPSSSGPAGRPSPGVGSDLGRPGAGRATSSSSSSSSSSSSSSSSSSSSSRDQBP\TGVSEAPGSLLGPNLPSQPS
1711	15612	A	1720	320	3	GLRWNLKINSLYLILAKRVDDCLDEK*YADRMQYTESVWVSRSRQCGQVGEKKQATSAAGWELRKRLVWRKGCDALRAAREBQGLADVRKAKVYVVRV
1712	15613	A	1721	44	373	KAWGQTLNKTWQFLTKKEIGPW*QSCPT/DLALVPLIGICTIDAKAYIHTETCTQNIITLLILIAONRRKASCSSVGS/NNKKLYYIRTMESYSSLR*NELSSYKKGWGGGS
1713	15614	A	1722	135	396	AQQLFCTSVRLASEQPLILFQDLKRNK\FEITYGTSG*L*SLIICQNNLQSFKQMYHHKINSLSGAVAHACNPSTLGGQQGITRSGD
1714	15615	A	1723	4	383	LNLRKATKLLEENIGHLPLDGLDLDLFLDITPSQATK/ARKGN*GFILKGFCAAKNLIKMKRQYKWKIFGNHVSDDKLVFRIYK*HLPLLIKNSSS
1715	15616	A	1724	2	405	NSRTSLILNQNL/IKLSERQTVRAKTG*KLGLQOQ\ISKIANAKEKLKVKSA TSMN*MMRE*KNFIPEMQKVLVW/I*NT/PLQSLIQNFAITLNSITAEGRBEI/KLEATRWFWFVFKSSCLINVKVQBG SGLLRKLKQNSLNPSSSKTWTSTKVS HWHKNNHWQ/VNKLNSQNLILYQ*LTANKGDEASQYSS/DLLNQCWQKQKKK\YLDPLYTPCTKLSTWTISGFL
1717	15618	A	1726	390	1	TFPPKIKKKIL*FIQGPPEPKLANFV*QNKPKIGLPIPLGFKIYYALVKTIANF*HKNPPIQQRNKVENSETNPHPPSELNFFFF\YKGAKNHWRDSEFNKWCWENWISI*RRMKLGNLTPYTK
1718	15619	A	1727	3	365	HASAKSNLRWITIKLNRKTIKLEENMGRNLDLELRSGLDRT/PKLYSIKLLRK/VNFIKIKNCPFSRDT*KS*WAGNKILSGKDYSEYLLK*CNLLTRQSKTST*MFIALFLIAKH

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1719	15620	A	1728	368	2	RNCLNSEGOGGCEPNSRIHCTPANATEPD SVSRMK*NRKINK*INFLY\EQSESTY FKLPLTLA/SRNMKPLGINSKGVQDLE TENYKILLQETIEDLNK*RNKTY*WIKL NTVRKMSILSKR
1720	15621	A	1729	326	30	NPFGGPKRGSGQREIKPPLPMPMGKPLF F*KTINKWVGAGAPPVPPS/SGVLSQKK TFTLEGGGPNKLSPPALP/ARGPKNPF FQKKKKKTQSPQREE
1721	15622	A	1730	1	374	LEKADKLA*FWKK*KPKQTSVGRKQ APGPKAGNRLLTL/L/GASAVQFWIDA ALICKAANPQVLKGRDXQLPVERLLYN KIKWTRTLLFLDCPHQCVPVEVRKYLAS EGLVFKVLLILDNGPC
1722	15623	A	1731	389	1	FPPKIFFSTLFFFRFFPPPPPL*P/ SDPIYFF/CAPKKNFFPPPPGKNFFFF KTPPPPPPPPP*P*VCLCCPGWSAVAQ SWLTTTSVFRVPVI
1723	15624	A	1732	118	422	DITTHLFRMLFKK*ENGLNLTFFKEDM QMERNLKRLCT*FVVKEIQLKMRVHYPP IQMAKI*KN/STISIANQGYRTIGTLF/ HC*EQPFW*FLSKLNMLPYNPA/IML LSIYPNALKKHVTKCN*MFIALPII TKNMKSPRCPSICEW
1724	15625	A	1733	407	1	NINGPFRGGLIQGLLIWPKDSFPILGY PFPSPKISFFFLARSCSGAPNHPFLPN QSPCFQPSFFLGRKKEKFLPGHSLAFF FN/RPGGS*RVKRGPGIPMGESLFF F*DRVLLCCPGWSAVA*SRLTATC
1725	15626	A	1734	322	362	TAIYIYIY*LTNDNTPSBRTRTYKE INIYVPANTIPVQHRNGQVICTPRTKI TVTDCDPANGSGSKLKTWKGPTILDAV KN/IRDSNEKVKIG/TIN/GVRKLIPSL KNDFKRPKT
1726	15627	A	1735	49	395	RGPGPFFFFFFFFSKRSQILFPQKRGGR EPRVNGTPPPRGKGNPPAQFPQEGGKTG PPHKPG*FLCPLKXKGVQKGG*GGPQ/A PGPKAPRPGPPKQGEKREGGPGPTRPN LYYAH
1727	15628	A	1736	417	2	FLFFFFFLFFFSFASGPAILFTCL*HT HIHFLFFYSKST*PPVTAGGMPQDQW LPETEMVNPFKKKRTTLT/YIP*KLCE CDLGNFFCF*DRLLCRPGWSAVA*SR LXTSFGQANRNG
1728	15629	A	1737	316	338	FHPLSYFFHVESYFHHB*GTIVKLSVK DIEM/LKKTARGNYQVITYKASTRLAAD PSAELSQAWRENDNNPKVLKXKTNAQPR LYKTLFVPHD
1729	15630	A	1738	197	379	QKRAQLDKAIFICRDLAL/P*PQ/MYYN ATVTKTAN*WYKNRHEQMNRSW/PPEI KSQSYSHL
1730	15631	A	1739	4	401	RGYRHAPPSLANPCTISKD/MGPTVULN S*PQ/CNLPASTS*SAGITGISHCTRPQ MATFLIGPHKIIPKSVLNPNI
1731	15632	A	1740	94	117	KDRPVVPPVQAGEDQDEFRCGHASLWS QLVASPTTPIPLPGRDVPSTRPFPAL AAQOPP*ASPYPLPGLGAGHASASVPT VPFSPISESTGS*ESAL/PAPRPGGSG

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1732	15633	A	1741	3	390	VDQPLTSHDLKSLTDEEVHNLNSSTTIG \EVRFKVKKL\*KKKSSGPDGITGKPY* TVREEVTPIL/SYLF/HLEKEETLVNS FYEARIIIL/IPKPDKNCP*TMIDAKTTS KVLNRIWQYVKII IQH*VGFV
1733	15634	A	1742	3	442	DLHSRVEPRVRSVRKQ*VLLKVLICA SKDTLKRAKRPQIGWEKIPVNHMPDKDL IPEYKINMQSGVFLFNNYSSTTDDND INKKAKDLSRHFSSEDIQANKHAKR* SVSLVIRSIKIKITGR*LTTPKCKQG*G KIIITLVH
1734	15635	A	1743	411	2	LPPKPPHPPPELITGAPKKKILTPPRFK KCISLKGPPPPPPPCRYRVLCCPGWPSF POLQSSHLGLPKWVDYRHEPYQTSSP SLSFLLQTOR*WFDLSNFFY/CYCFI YFSRDRGLTLLPELVNLSWQAILL
1735	15636	A	1744	1	393	RKGPPPKGRSGRKGGRKSRGRPRAP WASHMWGARVFSVPSFDQRPOKCKVQ SSYKQLPARARDGTGNLIRGAPLFFF* DGVLLCRPGWSAGFKQSRSLSPSR*DY RRTPPHPANT*ML/CLRSIT
1736	15637	A	1745	395	0	PSAPSSFFSTL*LGEPGPPPPPPPLKPP PRN/SIFGAPKKKFLPPPGRKKFVSLK GPPLEFF*DGVLILCCGWSAGFKQFPHL SLPSS*DYRTPPHPDNF*MF/CLRRSL T
1737	15638	A	1746	397	1	CQNPLKREKNFPAEFLQK*ARFENIR *VTEITAPCPL*HVASFLVLT/NPNT IPOLYCLPELGRSGGSGKLEPFPSTKT PNPLISVNLCPD*AIKWNFFF*DGVL LHPGWSAVAQSRPTATSTS
1738	15639	A	1747	392	2	FTKRGGRGGNLSF/LPPQKIF*KKKTLK KPFQWQVWFSSPLFFSGKQGPFFFK PFF*KRPDPDTPQPPPSIFFFLLFFFR /HLVAQAGMQWRHLSQPPPPGLTQSS QLELPHTPPHPDNFCIFGRDR
1739	15640	A	1749	33	403	IRGPKKKRGREGAPQKGGTGAKPPPPP PQGF*K*QKRGSSPPIVFFPFGGPPPP PPPPWGDKGGPPRGGAAPPGRKRNP FFFTLA/HGKKEKKK
1740	15641	A	1750	3	396	KRQTTNWEKVFA*KNADGLISLIRKRC LKVKK/W*R/DMHTQPTDKGILMTHGIM KRSSTSLIMMQHKGAGVIRPHPSDWKRC* STWNTVS*QGHEENYTLGHSW*TFDIQQ PF/SRGNL
1741	15642	A	1752	30	419	NSGTGAGHVSFAANKKSSMRGRVFLA IANRLDGELLSGLTSTQALPGNAYIAHL SHIAVRPLFLCYKRGVVLCHPGWSAVA QSQ\FELIGQVILRPHLPSS*DYRSIPP CLANFKNFRERARYACR
1742	15643	A	1753	16	410	VGPKKSLQQVAAVQATPLESYGLAHP IILKVSIAIDRAI*NLWQIPIVAS*YIP LGF/YSKAMPSSVDIYSFRRKKTHFFL TGQGGPPLYSNYLGRLGANHLTPGVKN QPQGGKPPLOKQVTLAGRG
1743	15644	A	1754	2	17	NSSLYIKRRHTHTGERPQCSGGRVFNQ NSHLIQHOKVHTR*RMYSR/CGKDF TKSTLI*H

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1744	15645	A	1755	138	380	XPXXXSPXPPPCPPXLSLFLTKCSAY* TPAHRPPPPGPPFPKPCPPPPPLRP WPPLPLINPFPPTLSFHPGALS
1745	15646	A	1756	194	3	WLCIPTRHTTSCQGPFF/LITNSQFYS PLFCLAFV*DTVSLCGPGWAGVQSGLT AASTSQAPSL
1746	15647	A	1757	2	403	RVLSPPTAYTYLLFYLGATILMSVNI KQPCPTK/GQKKIKLYIRMYYSAL KKK*ILLFAIR*VNLGDIMSEVSQ\SR KKNIVLSHWN
1747	15648	A	1758	398	65	PPPPPPPP*TEGLGCHRCCHGSPQ RTHGSSNAASLAS*VGSTGAFPHDRF TLIGSSVWVHTHLHPYSSLP
1748	15649	A	1759	456	31	PAKRTDKKLLSLTYLAT*KGSTLKALI KQ*LLQAQAQNSLKRHTTVLWML/CL ILLIHKEMQIK/STLRYHFFFTTAKI *KLGNTPCWGL*GTLHCNNECK*HNS YVGGINQ/FSNKLYVQI*YNSALSNLDG RVGRFG
1749	15650	A	1760	3	378	QQYFYVYNGSVIKAVVYNSKRR\IDQ* NRTSPDKNLHGHQLIFDKGINTPQNR KDDLPKKKNWN*TSQKKKKKKGGGP *KRNLTLPGWRIIIFGAPKNMPGAG VKTRWGGKNGFPQ
1750	15651	A	1761	69	384	YTSASNGGARYTASAAGNKLILLFLFI *DRVLCHPFRSALTPRIIAASTPQ\V KQSFVLAHIGDWDYRCMPPCANFPNF LCKKKTLRRQEVVMTPALVEV
1751	15652	A	1762	390	1	KFTSPGNKLPFLKAPPPFFCRGSEVLL CCPDWSTFGLQSP/CSLPKCDYR ESPPQAFVTFGLPSLPSPPAPSLSP SSSFF*MTHTSFAQAGVKML\LFGLS QPPPPGLK*FSCLSLPTIR
1752	15653	A	1763	2	390	PRVGRFMRKFDVSLVPTKGNLRTI DLHVRAKIDNLN*NRVHLYDRLELNG FLEMKKTKAAATTTKLPFIKFNCAQ QMS/MKVKRQSTKWKKKCSHSDKGL VSRKYVKA\NSSLRTQSH
1753	15654	A	1764	334	3	WSKRSPPPLSKNQTKKQATKPT*KNW INEIGPII/NTSPSKKTSNGDF*FY *TLKRLLSILLKLPQKTKSVIFPKSF YVKDHSSCLSGIHPKDNIMQHMQINQC
1754	15655	A	1765	259	1	KSTFLMKKKWGSFLKHFFLFRSL D/SPG/GVQWRHSSILQPRTPGLKQSPH LSLLSSWDHR*APPCPANFRFLKTRIG RDV
1755	15656	A	1766	402	386	PKKSLRLKL/KVQDSASTPLAKTI/ DKHSITQQLIHVDEAFWQMDP/R TFIRAKKSSMSPFRASYDKLTVLSGANA ADSLKLPVLTYS/SNPKAL/HYKNS TLPLEYKNNTKAMMKIQKFP*FT*1PM
1756	15657	A	1767	2	406	PRVPRVRLKLTLLVSGHSSSEKKKK KTKKKKKKKKGGGL*KKKKKKPRR RVNI.FFWGPKKSTPRVFKHGGEK/PP PPPKPRRKP/SLVGVSTVHGISPTIKH SKKTSTK
1757	15658	A	1768	14	409	IASGFLFFYFGVIGRPKRGVFFPGG GGAPHPPQGGC*KKKRGGGGGPPPPPP

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						SLGGGLGRPRPMSKIKTPPSAGGKPF/PF LRNQNTGGGGPPQ*PPLFGGPGGNFS PPRGGGGGGKTPPPPPPGGE
1758	15639	A	1769	305	1	TRTGPFPNSNRAGKKIVQKKKKKKKKIN CFVTAPFPKGIKTEATD*EKIFAKHLVK G/LVYL*YI*ISKIYKELLKNNKETTII PIKK*AKDLSRHPTRYTD
1759	15660	A	1770	148	402	FSPVSLG*GRGNIYAGMENV*EVPPFED FQHEVKRALQTSPPQVKLVIIFFKSTI* KSLAK/WLAVVAHACNPSTLGG*GGMIT RSQVKSPPGQGE
1760	15661	A	1771	250	2	KKKKKKKLCPVTDTPKGIKTEATD*EK IFAKHLVK/LVYL*YI*ISKIYKELL KNNKETTIIPIKK*AKDLSRHPTRYTD
1761	15662	A	1772	407	1	KKIRGGGCPPLPLPLGGGREGKKFFPPG KRGFY*TKAGPPFSSNAKKKKFVFKKKK KEKKIICPVTDTPKGIKTEASD*EKIFA KHLVK/LVYL*YI*ISKIYKELLKLN NEKTTIPIKK*AKDLSRHPTRYTD
1762	15663	A	1773	1	406	KKKKKKPTFFPLPLFFFLSLSPFVRPGA RGPSSFPSPKGLGC*IKKSGVSPAPKK KKPRKINPKNFPRPNPKGGGKFFNLPT HPPGGTTPFF*RRRENPPGAPQKG/EV FSPQGRNSRGEPPGPKKKKKGG
1763	15664	A	1774	2	378	ANGWLHQSLQSLPPLGLKQSAPLGVSK W*NPWHDPPPPAPRFVVVVVGVLVLRNS FFLAGAGLFFFF*IEKSEYVAQAGLE /PPRLQSS*LNLPSSWDTPVP
1764	15665	A	1775	1	431	QKRDKNLPERIK*IGRIYLNLTIGAR HEKPTVDTILSGESFSKIKTMLIGPPL FNTVLQVLA*ARKRKDI*VGK*EVKSYN FTNDM\LDNPKDSTPKKKTGYFMGGP GSKPPQRRGAFSLTRDPLEREFPKTA LFTLGQKKIKGPKFFS
1765	15666	A	1776	334	402	KGGGVGG*QGPWELAHCTOX\XREKR ERERIKRQKKERKKERKKK*MKNNK KKNDK
1766	15667	A	1777	406	3	SPSSSSSSLSFPPFFWGGPRF/SPFPF VTKPPPPFFFLGPPKKKFFPPPPAN*FF FF/LGPPPPPPPPPPFWAAGFFFTSDG* GP/SGPMAGFRSLPPPGNSLSKKKSE LGEGNSVLTRVLLSSQIPGNR
1767	15668	A	1778	70	409	LISFLVSSLIVRLYRPLCLFPDPBSKGH CIPCLPLFWILLHIIFLMHSFIYCLIN DRVLLCLPGWCAVVRPRITTAASATQ\IK RSGSHLSLSSK*\WDHRRCPGFFFFFF FF
1768	15669	A	1779	390	31	SHLSLPKWDY/RL*ATIPSQKLVTPH G*VLSLSLFLIPD*TF*DMSLARPS LQKSSLIQHDLQKVPITIFLRQSL/D S/VQARMQWDLGSLQPPGLKLSQ PQAI\SSNDYR
1769	15670	A	1780	357	1	LTLFWGAQYLPRKKGPPFFLLSLPSV WGPLPKKKKSPPLCFYFLNRVLLCHP WIAVQSWGSAHFL/VLTRFK*SSCL SLSSWNRYCTLLHPNPLFNWYRQNA VLPKLV
1770	15671	A	1781	122	254	RKNE\WSGAVAHACNPSTLPGGGQIHR

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1771	15672	A	1782	45	387	SGDQDEFG*HEPFRPTDSFFLYPSH TQTFKLRRFFHSLKSWHYRCSPL\FQ HNGYFLINLDLATSMFFFKDRVSL\LAQ AGEQWCDPPSSLHPQTPGLRR\PPASASQ EGETTGAAHHTWRNLXYFFYYTYK*GT YPMNA
1772	15673	A	1783	1	401	FATLARI/VSNS*PE/CDLPASASQSAGI TVSPAHLALSPSPAMPSSQGLSYPAY HPGLGLRCHLPVLTSPWSTDGTGPSSVL DAGALHCPPEPQHICPL\LSGWLQTP
1773	15674	A	1784	432	1	YGLPFPFFKKKTPFFGAKPKNGR*KEP EFGQT/S/CPVFLGRPKKCKFFPPE RBMGVFFFLPSQGGGARGFPFPPPLNQG EAPRNGHKKKGTPLGRTYFFFFFEMES \PSVTQAGVQNHDLGSLQPLPPFKRFS CLTHAS
1774	15675	A	1785	15	434	RLSLSCGGREHSITFGAGWRCEHLAWA DSDPDAPSPSPALSLFPVYVDVCPV LCLRGPW**MVERGLRGLSPVWLLGWPF PGGA/PHIKPE*YFLPVTILRSVFNKL GGVLAALLSLTLALIPILHISKQQSII F
1775	15676	A	1786	1	258	CWPETPVLK*SHLDLTKRGEDRREPVMNA ASTTLPFFFTGL/NSGAQAGVRVHLGS LEPLPPIPSLMTIP*GPCPLGSSWPLR EF
1776	15677	A	1787	399	63	SLHNQVVKSTPTLTKSKLISH*STWPG VVAACNSNTLGHGORTA*/SGVQDQ PGHSHSTSSQRLRNPTKRCIKYLAHSK CCINDSPVSVTSRKLIGKEVSPNNIT FR
1777	15678	A	1788	3	474	MSLSPVWNSKRGAAANRQPPSPSPWK DDSRDASPPEPASPTIG\PIRLRAESSW TWGSPCAEHPARAGRRIGATDCPWAAG SQWRGPAGQGAPRSCLFPGSRDARAQH PRVAPPPPPAPLNTASALRSQLPNPL *VMTPEPFAAAPSVPQ
1778	15679	A	1789	66	395	LVQPLDFPIWHSRLSWSGRDLLWSGKE TMNFCINHSIGVLQEWQGSVDKRRRLM ESLTGPAADVIRILKSNNPATTTAECLK ALEQVFGVSDSRDAQIKFLNTYQNP
1779	15680	A	1790	413	1	PSP*ALITDYS*EBGRFHWQ\EEKGQP LKPHPLGLSPHQSPRVGPPKRGGYNPF *KKRAKFPAGENKGPFWNGRDPTE*G KTKKKNPPKKGKGGPPKPGQGFPPF LRSLWSPRLCEASALSNCKLL
1780	15681	A	1791	314	1	KTKFWLKKTPPKKKNKKGGS*DKARY QTRKG/IVMLGH/HPSELYYLLFETE SHSVGKAGVWRNLANSLSQTPGPGQPS RHSKPSRKDYRHPKRPQRCVQ
1781	15682	A	1792	104	409	EKQSPAFDWHFDLYFONVK*KBGRSKA GKFNASTGWGPNFRKRL/RFKQVVRVIGE PASVTQEADEFPDNFKIKITEKKGYLHG KPLMYHEAAKYLNFWCPIK
1782	15683	A	1793	392	2	GERERDRL*REEREREREREGERERAR ERERARQGT*STVESRI*/HSYCRDQDVA RPAKGEVAAGRSPDGLQVGRGQ*PGP SLRPGPWRENGFATYLAAGGPITPGEVE

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1783	15684	A	1794	405	119	SGEWAQQGEWQALGPP IIRMAIVPKATVIRINTISIRVPMAPFTK \LKTIIKFI *N*KRARIKALLSKKNKA GSIPLDPFKLYYKAI VSKPTWCWYKNRP I VLVHSRTARKK
1784	15685	A	1795	455	3	CSVTQAGEQWQCNISLQPPQLKNGS/C PSQLER\WNYRHVPPRPALTATAPALTAD F*RRKEYKLMRHRGKQWHDFTLESKMKK AMRHEIHSFLTVPNGLHYLWQFFFPDT ERHSVQACQVQWHDLSLQPPPPGFKRF EVRGPGGNSGAD
1785	15686	A	1796	2	134	PRLOQCTPAMATPQDSVSKRRKDMTDP AI*KG**ATTNI YIHKFYNLDEIDQFL KKHKLPQLTWYEL/DNLNSPITRIEFPV IILNKKKYPGSDGPTGEE*D*FCLETKK RYDYRPNLKRILISDYNKHLHT
1786	15687	A	1797	1	404	PIRPLTSSASSMMVETFPPTVLISSAC WVKISKI DLKLFSPFFFGFLEGGFYFC PPNSRGGSPGKFLGLEPLPGLKGIFFP PPP KRGEFGPPPPTATVFFFLWGGGV /PP /AVGGGGKPII*GNFFPWPPQG
1787	15688	A	1798	2	383	SGWLWACRSDESEPLACFAGPRQ*GAYH PGQQLAMVR*VSQQWPTPEPALHIS\ P RP*LPFRPRAGLOTCSPP/VPESFLLPWA APAWKFP PRALPPEA/PVVGPIRPREA EECRWVRDQAAAPAP
1788	15689	A	1799	35	410	ATGSLGKVC*AESFL*KLDFKHYLF QASGFL/CHMSPSQNSCSSFGKHVM VLRVNSL*PDHPNVEFYPLATFIEYRDS /SLTILRLVSN* AQTILPLP/PKVL GLE
1789	15690	A	1800	65	415	KRGVLKGGPPPOPLGV*GPPPEKGGGPF F\GAPKEKP PLALGEPKGKPF*RGPKGF PFKKGLEPGAPPPPKPRGEKPEVFKGPH PFCKKGGGDKEINGCL*KKKPTLGNQ PPPPG
1790	15691	A	1801	417	3	NLOPNIFPPRAQNWGPAPLPLFFLKKK FTWGGGSTPLFP/LNLGLGGPPFGLGV YAPPSPHG*PRFFPKNQKLPVPVNGALY SPFFGGWEN\RKAPPGQTLFFFFFLK* GQDLPMQLLVPNVYNAQVILPWPPEV
1791	15692	A	1802	1	431	QPCTPGLK*SSCLSLSGDYRC/RTTV PS*PPFFLENGVQIPRGGIKGIDNC* LGPFWHLKNDPQNSQEGVTTQDP PG*LPFFETTFE*KAQETLAQD*HK WGLAKKT*PAPSKRGYRGGTTPNEPTHG FLKKN
1792	15693	A	1803	256	399	AIKNIHDS*EEVKSTILAGIWKILITLL IDDFDGFKTSVEEVTVD/ME
1793	15694	A	1804	407	2	FEKANLFPFLFKNSGPPNVGGRMGAVD KFCPCSKRKVPGP*IFFLRLFLFYPKCR RPLFLWFAFG*KFLLPQVFAPAF*KDS PKKKRAPVVFPPPPF/RDKVWLCHPTWS AMA*SLQVTSVSNQAQLLPQR
1794	15695	A	1805	429	116	LLTKKKKKKKPLACSSSLGGP*GVTVG V*QARDTHIV\VLSSAPSLSSEMTDS MPGHLPSKDSRYGMEMLTDKKTNDGGA WDSSPGANGKRGRAQSGFS

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1795	15695	A	1806	2	408	FVIFVFLVETGPF\SLARALACATSN* PRDLPTLASQAGITGVSHRTWPRRSCV F*EAPLTMMLVHLIPPSLLWHSVFTHLL ALSS*CYLF FLRGPWAVTQAEQGQHDLG SLQPLPLPGLKWFPSCLSLPSS*NYR
1796	15697	A	1807	1	196	FRIGASLDLGGGCGSV*PAPPLPPPPP PRAAAGLS/SSTSAAGL*SCRTAFF SFLSSFFFFFLKKINPPFLGGI*PFGK GERLV*GNI*PPQG\DFLGGTRGGKKP WGQKFGQGNFPLPKKPGPOKPPPP \PPPPPPSAASGISMAHLQLPACDRAA QLSFLSHLFFFFFF
1797	15698	A	1808	395	3	LGRKNNPKFVQGCETGFL/M/HGRV CKFVQSFNWDIY*G*AAATHDSAMLL LGMHSPACTFVHQKT*TKMFLAALFIL PLNWKQV/RCPSTV\DGVIPTMDQSTAM KMNKLIARTVMNRLNMLNKKPR
1798	15699	A	1809	7	454	IPGSTISLQPPPPFGF*PFCLLSLSSND RQPAPPR/LANLRR*T*QASA*LWR/RG PILDEMKSPMCNCSLTGKVGKRVEMMS QNGRLTLTKFCHVGQACLKTPDLK*SAKL GLLXCDWDSCEPCLTQMPFSFFLF*D RYS/PLSPMS
1799	15700	A	1810	20	355	PQCAHGSAAVAVPVCFCTCVVCSHCV SMCMGEVSAAGTLLCLLST\CSGAYA CDWGCG/CYSACVCAVCACVCAQLLTC IGMME*GQAQGEVLDDLPLCLCSWAP Q
1800	15701	A	1811	3	414	SSKNDNNSLQEFMDKTAGMKKLNGLTE LNNIV*EFHRAITSINNRIHAEERISD LENWLSEI\NRQT*KIVTRNEQKLEVV DYVKRLNL*IG\VFEREKGKAYLQNI FEDIVHENFPRFARDANSQIQEMQRT
1801	15702	A	1812	1	443	AGKSPSFRKFKGPGGRKS*FLGGAGG GVPPFRGIQGSNYRF/SPPPPLGKKK KPPFKKKKTPOKLQNGNPHYPNPRVH GCREQQPWEKAPDATRQPHYADIGHVAG EPRFPKPKHSEPLSPSPRKLFLTRST /SGNSPP
1802	15703	A	1813	411	66	WNNWFKKCLAR*TF/LIQKKLDPF LRYIKIKSK*IKDLNRLTKPKKE SVTLAKWLRSPYLSFP*QIQSQ*INS YVLIKITKERMS*TSKEQKPRERKAM YKIK
1803	15704	A	1814	369	20	QEVRPSTYLSNRRKYKDSNARPTKEA IQIANIHMKNCPTSLVGETHKTSGY HYVPINMAKILKD\CNRRCGETGTGLIHF *WNNWVQPPQKPF*WPKKKRKH*QFD LATRS
1804	15705	A	1815	2	675	GLATLGRRLRGEACTRSPFSSILIPVMS MGRWPGVP/GIKGRTTGAFAVPTRRRS SINPQTGGAGESSG/PLRGLPRQKPGS PRGPSGPQNCARWHPQAPLGACCPGS GPETSLRPLPWRQGNWCLPSTPSSA*EG WR/PVLQPGFL*SPSSLASTCPGAERGP PGSSRP/GLRGAPGG
1805	15706	A	1816	273	2	MESHIMWFTTGFPHLVQCLHGPSMLQC IAVLHSSYLFITLFI*DRVLLCHPGWS



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1819	15720	A	1830	427	107	AGCGGAHLSHLL/LRBDHNLNLEVOGCSER P*LHACTPAMATE*DPVSQTKLN*NINX LAGCGGAHLSHLLGRIT VQHQPQQRRSPSTITITQKLARGARCL *SQLPGKLLRMNRFN/SGSRSHQCTPA WVTRDCLKRTGTTRASSQRLSVGIKQS CLNPRTAQLQVSAQSPSTVSNL
1820	15721	A	1831	3	540	VQPFNKIYYKATAKTIVLQHKQR*ID E/MNKI*TFEINSYVGYLNFNCKAKAI QWGNDSF*PKKWC*DNWISACKYSQTSV SASASASSSS
1821	15722	A	1832	385	2	AGRQSETPFNSTIRKVSLLQVCDLSCL LGPQSLVQDSFNIPQAQRKFLRSGFNL PLSRFSRVQWPLPHWQVSSQSFELPR/P P*SQIPAPRSPPPAGPVPARSMVCGPRP QTRPLPAERFSPRPRRL
1822	15723	A	1833	7	399	RISRSYLSBYGSGKHEPTLGASTARIM VFG/VFIIYF*RCCLA*QWYSHSLLP QTPLKHPF/AQAS*GAGTIGTAHT*L TFAP/IFVLGCFPL*NKISVTAQGGQC NFGSLQPPFPLGKRVSLTLPR
1823	15724	A	1834	2	306	LARLVSDS*PQ/CPDPAASQAGTICV SHRAQPAEILKVFGLCLPEQRTPTD I FIIPYLC/LFMBESCSVAQAGVQWRL GSLQPLAPGVKRVSLSPFP
1824	15725	A	1835	12	400	KGMVFKQLKVKKPPFSCMGPNMKKRD SPVFHQDPIFFIPFFFFGMLFFFP/ LNGGQGNLM*PNLFWGLKEFPFPTPR GRGKKGAPPPINPFLKKGFPPLGR GSLRPPPLGDFPLPKG
1825	15726	A	1836	220	401	KGSFVFIQPEGEFPLG/LKPRFFGLK QFSLTLRLSGNYGLPPLPPVPI/C37L R
1826	15727	A	1837	12	357	GLLGGQMGSLGTOTSYEDLNSSSFKP NSPPPTPS/VKTHGLP*PLESSNGPPP PQVSHSFQGWARGHPSPPQWNTFSP PQQYTQCSKTD*FPFSPFYLQGBSNA PSLA
1827	15728	A	1838	8	380	LMKTHAKLRNKRAN*IQOYK/HH/NQ MGFLGVQIYFNP*KINLIQLNSVKKK KN/HSSSSSSSSSSSSSPVLKSLC NLGKRNKFNCLTKGIYKNTB/NSMKI TLNGEQLNAFPLRGTK
1828	15729	A	1839	2	444	VPGDARWFSVIALKDAFFFIPLVPSQY PFAPFENENPTREK/TNAVLP*GFWDSP HFFAQFLERDLGQLQEDGSILQYVDHL LVSPQIQAASQNTIKTLHPADRSYK SKKQAQITLQQVHCLGYILTPGTCK/LS PERVQAI
1829	15730	A	1840	1	642	EIKGIQIGKEEVF/SLFADDIDYLRIDS TKKLLSVICRLNKV*KINM*TVLVL IGNEHLELEI/R/ELMPCIKTSSTMYL EINKKDV*DLTYENYKVFPREIKIT*A NQ*EILCLSRRLNRM/STFPQVFCVY YALPVK/IPSRRNLVLVDKLLKFI*KY RGPRATAKTKKKKKVVRLLTLLFKSY KITVITIGWYQDRQVD*WNRIE
1830	15731	A	1841	3	423	HRITSR*DLHARLELW,SMYGLSDHKN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
1831	15732	A	1842	33	179	YDAELDRMAMPCLCAINGALPPGYVDAS SSSKAEKKATVDAGNFDPRPVETLSVI IPEKLDSPINKFASYTHEKQAF/KIQNN WSYGRNIDELIKTRPMKR\PY\KCYSEK D YMLGGRGCSDLRSHHCTPAWV/TA*LS KKQYQRQQNLQYHLEQYERKK
1832	15733	A	1843	349	10	LAGGLNSMBEGR/LR*EREECTQQQM/VH DKYCKDLMGPTKPRHITPSSPQAVQP QQSNALVGLLGYSSHQQLMGPGASTPQA KSTLVESRCRDLMBEKKDQK/QWLVK CR
1833	15734	A	1844	15	856	AARQLSTFYKLPQNPSTPTGSSLSGTH GMQIMLGSTHLPNLTMDLGLFGLVQGI PSPGCAQGRG/QGREGCCSPPGVSQGG \SAVGRGABGPQGLTRSGSGAASALVRP GEKGCWCR TASGAGPQRQRTRGPGSWG LSFSGTSEEEKCPSPAGSAGAPVQQRQ SSPAGGCGTGAGAPGST/GDAHPAQGGG GGPLRLSLPAVGGRPRPGSPFLKTSGSGSV PQGVPIILNSLT*RALAAPGSQGPAGLAV SCTGGRGYRDPQAPGTGAG*HGNSTRLR GP
1834	15735	A	1845	402	2	SKARRQGRPLRQG*ARG/AARIPEQKRI GGP/EEERRPSARGPRAIRVAGEGPKPK GQTMAGSGHDFLELPFARSRQSSTIGA ESRSGSHSQGPAPQSGSPSPQJERN LFEGTTERPPLKCSLPGQGFPPNV
1835	15736	A	1846	446	32	TSRRTS*RTGNQFLMKTESCNHSHKAAF TKKOVLT/LAUVHGNITKASETHPPFPQ SGQAKVQGGFVKEGCELINEALNLFNNV YGAMHVKTCTCMRLDLQYIMGDYARA LSNQKAVLM/TERVAGTERIP CIRPL
1836	15737	A	1847	440	4	VDGRHVEVS/KGGGVNYGAG/KTVEIWA DKLGCMNLGTADMVECLKSTRYKELIQ AITAGGAPLAFGPVIDGNVIPGDRQILM EQGEFLNYDITMLGVHQGGLKFPVDGIVH NEDGVTEND*KFSVSNFVDCMRPRRGPN YSRFQ
1837	15738	A	1848	526	0	PRRDPPPKRQIPIPTHVPVWEKSPWGP APLRFDPHSLSPCFAMG*K/PGLPRGCP QTOISPLFNRSFASPLICHIIHPPSEP/K PGDPFPPTSSISLARFTRFGSSSPL FPPTPSGP
1838	15739	A	1849	417	31	QRTQGSCHRGGPPFPQAGETKQAPL RLPGGIGIPWAGILCP*LPDPSLSLSP AARG/SGPSGAGNAPS*P/ACPS SSRSAPVPGAGSPRAGAGLFTYLPAPP WCGRGASNKI IQMPGLVC
1839	15740	A	1851	3	285	YTVBCVCVCLVCLVPSLCLSVSV CFFPSLGGFVVCVCPACVSLACALCAT IRFV/CMAACLH*ASFVSTWVNPVAVN RFRGGGSLGA
1840	15741	A	1852	128	524	KIPGLQGRSBOVGQGGDLHVTAPVPTH GWGGAASKPTVLPPPP/PDAPTVFFF FFFFWEKKYFFGPP/KGAGQIYLLGN PBGPKPFFPHQAAIGI*YIKPPWYKC PLLKRGVSTLAP/GFPKPP

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1841	15742	A	1853	1	1648	MTVPLISGLGKGVKPERKTTVRRPVSAGKKYACPFKKAETPQWRRLRMRPKAPASLALATFPISQRLIPLTPARKHCPSSESTSTWVSKAPATPRTRGAGTSPPRPTRR R\*ACSLQKLFVAVSEEFDEDFLAVED AENRPTGSLPVNAGRLRPVSRPQETVQ AQSSR/PAAVTPHCSLRGFGPARLGP/PASLPPARPVLT/AGPSCIGAPLPRPVSTSSWIWGQRRVTVTEVLRAPAPQSSALHPLTFESQCCQVKGTFBPSQDPRKVLASMELEEPOMELECGVSEATPILPAQOREGSLAKKARVVDLSGSCQKGPVPATHKNGIMSQAQDESILDVITQCRTP\DDPP*DLVLWVTVLFG/PALTVPTQQLHMEVCQRSPVQALQPLQAARGTIQSSPQNRFPQOPFQSPSSNLSGKARLPRPRTPNSSCSTPSRTSSGLFPRIPLQPAAPVSSIGSPVGTPKGPGALQCTPIVTHLVQLVLTASRTPOQPTHSTRAKTRRRPQAPILPHQSGRSLEDIMVSADQTPTHGALAKPQTE
1842	15743	A	1854	235	223	THKFTIQIWLAKITQCRTKV*KERSVLLPTSFSVPVPSQGHYTCQ/LCSSLASDLSQPOLVYKFMHIAVLHAMNSRKVSCYPMTNIVYLIANRT
1843	15744	A	1855	373	3	TKKITYRYVKALDSFICCBFHNGFFSCMDRELSQRCPFLNSAY*FPSNL*CLCYLFFFF*KKYFLTFYFLRDRVLLCCPE*SAHVHS*LTVPDLPF\VKGSSCHSLLSSNDYRHALPHLY
1844	15745	A	1856	378	1	RQRHSPAGNTRGPQVTPCG*ISWPSITKDRTSMSVSTSGALGHIAASPHARLLPLALPSVRTQHGSPPPGQEQPTIICPSNLPHPSLPLGMHPSVRASPPLCK/P/SPPSI PASVHASKHPSPPVY
1845	15746	A	1857	3	379	YMRKVIENVFLLLLLLFFFFRGGLGQGWGPPADPGFSFGKKNPQGLGSSNLRGPW*TNP*PVPGGALFLVGPPTPAEPFPKPSRGFLLV/ALADP*TRPLVSPHGG/RGAKGTPAPLESMPHWP
1846	15747	A	1858	452	1	GTHGLLLGSGFP/RQVFXPDNFVFGQSGAGNWAAGHYIIGAKLVDSVDVVGQEE*ESCCICQQLGTHSWSGWSTLPLISKIRECPKCIHNVLSVVPKSVTVVPEINITLSIHQSVENTDETICYDNEALYDICSRTLKLTTRCI
1847	15748	A	1859	1	385	NTSSDYIYFFFFLPPSISHVTPAQGGQNHQGSLLQWDSRLK\CPITASICLAMPPLANFLIFVRIIGSPYVQAQASRDPPALASQ/SAGITGMGHCTOP*VPLFFFFFSFRKKCSWPPGOGGPIF
1848	15749	A	1860	470	17	IEMDSRRVPREDLACTICKSKHIDAIKIT*NELASAD/DFFTLIYIVLKG/NPPCLQYNIQYITRFCHPSRLMTGEDGYFTNLRLGTHCSWLMMTMTCFRPRIFSSQWMSYVLRFRNGITGVSHRHP
1849	15750	A	1861	3	790	CSREPFPGRRFVAVRSKPYLSLFF*SR*SPFNVAE*TSADILASSEPIKQNDVSSLQKFMPEVK*LDHLITA*ADGWS

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						KARLERGPDGSDAPSPTFOKPAASRQPEL GELATPLGRVDPWYQSNVNTLCFALHKL ARMPPSLDTSRTVDPPFLVLTITYLRMG TQPIYFQITYTKLFSDLSQDPTEDIFL IELKVKIQDSKFPKDGSPRRRGVAEGP GAELSLCYQKALLSHRPREVTISLRATG LILKAI PASMY
1850	15751	A	1862	192	3	SSGSHSVTQA/VGQMHESSSLF/LLT* PPGRK*ASHLTLASS*DYRRAPPHFANF *IFQRECV
1851	15752	A	1863	82	370	SLCQKKAFFGELKLVHGLLVSPSGHGVPS CPDPNGCRPRFHAIVNVEKLKRVVPIE VSLPDLLEELVDLFLKVRSSCKYGRSRP *AQLSRD/DPACP
1852	15753	A	1864	2	325	IQVYSISLHLSITLYFVYHLSKSGMHVSM SLSI*SIYPCMDV*MYLSNLOMRVIVYL FYGSIYRFYLSICLSVYLSIYLSIYLSI YLI CHPSIFKTVLDEHAI FATWRH
1853	15754	A	1865	3	377	YSPWCKLRFRELCKINFDLLSPILLSGK EFNUTTHNTFDHMRKTKENEAHILLIS SVDKVMKENDELKSDNSMLQKQV\*PLK SAKTALSGSLNSCREKAEIVKCTQSLT M*VADLQRKMHVQP
1854	15755	A	1866	10	378	GMKNGEFTDAL*KVYGRKAPNKSAYVKN IT/*FKKQDDIEDHDSGRASTLRKKL HLVYALLDRD*RLTAEALANTLIDISIS LAYRLITEKLKLSKLSLSTQWVPKQLCPDQ LQRAELPMBELK
1855	15756	A	1867	346	1	DILVVLKIQKCPNGKMLAAKERKKCFAP KQVPRMNAFDSIAAKKA/RRRMNSIFS F*KEMNHCLRLLYSAVNIFP/EIKTFSFD REFUTIRSAVKEILKDVLMAEERLSHVK SRNV
1856	15757	A	1868	1	377	GTFPORTOCKKIQVYVGLIKASSTP TCVREKVKYIGKLNMLAQMLKGEWTEH WPAFLSDIVGASRTSKLQNNMVILKL VSEEVDFSSGQITQVSKHVKDMSMONE FSQI*Q/LQQF
1857	15758	A	1869	90	384	QMLLFTREYSLHYPLVLFVFFPPGGRTG PNPPAGGEONETG/PNGSPSTPGGQNP PLPPGGLGLSLMPPPPRQILIMETKRP PP*THKCCSPGYSP
1858	15759	A	1870	2	578	FVVHGHALLGLDFLPGKQAPWSGQCSL GHTEGGTSWDFAVGGASMRKVCVCKGD SHKGPATPLACKGSLRCPCLLAGSFA *GS*KRO/YAPGSP/LALGNGQ/DRIT LISQVHONQVTOIIPHS/EGETKAQRS P/SLPPEDLIRGHSWNLDSTQLLYCPLL PPPLHPAGPLVPLVPTNGRIQKNSRR
1859	15760	A	1871	1	382	SGQDAGSCILLYGAGSGAGVSGVNPYIE IIEQPRQRMRFYKCEGRSAGSIPWEH STDNRRTYPSIQIMNYGKGGK/RITLV TKNDPYKTPYHDLVGGDCRDGYEA*FG QERRPLEFFNGLIRCA
1860	15761	A	1872	490	1	ADSLSKDPGRFLHPFNIMGDRGRO*PGE TPQ*HRRSCASQDGRSQ*PGKILPSPK PGRPP/PMTGEDAGPPK/HGNPS/PNDQKK NDPPK*/PQGNRLIRHDPGRFPFQ*PRKK

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						SFFNNLGDSNDQKSRFPVA*KNLPQSSSGTRAIGRELYLPQPGSSAFPNSTT
1861	15762	A	1873	373	1	GGGVGGALESHKKSLLEFPFPPFFFRKGL*NF\KINGCGSPFLPLFLFKKSCFVP\RVKCGVVLGPCKVCLPGSPFSPASAS*VSGATGAC/RPRPGKFPSPFFFPFLVEMRFHRSQDV
1862	15763	A	1874	3	374	YMLGKBITVSKTKIGQELGLLNO/TSQVYNAKEKFL*ETKSATPMT*TKRQNSPIETETKALLVMIEDQTSNILLTQNTANMALLTNSIKAEGRRETEKLEBGRHYFMKFKKKAISIT
1863	15764	A	1875	2	364	THSGKGESLMDLGLDITFLDLPKKA*HYKQNDKLDLHK*NPFCSAK/ET*/TRKQTQAIHWRIFVNTI*NRKLVYKELKLRN\KKNTRR*ALMDRHFTK/ERMTWN*YTKGCSISLVIL
1864	15765	A	1876	41	461	GFLYLCSSEITDPPSPSKTKTSWIRTYWMKLLSENATIMLKSDLSQV\FVCNIPFVQAAGAKIEE*DYIKLWFCSAKJAI*KAQRQPTB/W/DRIFANYFCVYGLITTTCMETQLTSLITPTIITLWNPQSYHHNPT
1865	15766	A	1877	2	185	VRPTKLDPLERTQYTLFLLYKNNKAMTAHL/PTA*FTYFPKS/SVKPDB*VREIDYRMLYL
1866	15767	A	1878	1	491	IERLLWPPLSAARPPSRESGLRCAPRRPASAAAATAASP\PTA/CQFP/RKRLLIQPPLYPGLFTPCVPPL/APQSRSPS*SLT*DARTLPLPLGPRRRLIGACPAYOAEBGVDPVGLSEVLAPCKQP*TPDPACHCLDGEGRPSGVQADLEKAKLYP
1867	15768	A	1879	24	449	LQPLTWALLQPPQPKSRANPFFFFFGKKSQFLPGPPGGGGEKLG*REPPPPGTGKMPPPPPRERGKCKGGPTGRENLGI*RKGVVPPGGGGGGGTNPGGGGAK\PPKGGK*GGGRLPPQTIKPKRGRPKRKG RP
1868	15769	A	1880	190	2	PLYCHRVQGVLELLTSGDPPPLSLPKWDRY\DHBAQPSF*LFLSVQISGKFNHSVVQPCI
1869	15770	A	1881	1	458	FATRAGRNLPDKEFRYLRTVIVTAAVYGLNSKLRCLTS\LLTPQKAGVSPYTSFPGFA*TCVFAQLLEPILC/RPCHRAPLPLKNGHFA/FP*QCFFR/OALGSP/RSCTVGRHG
1870	15771	A	1882	3	392	YMRKYLLIKRAKVKTSSTNDTQ*LLKLTIC*QECRWQVPLWQV*QELIKLNI*LP*MLAILLWGYLIEWSTYER/RKICIQMFMTDIIVIAKYWTO/POCPSVAGWTKQ/TRSITHTVRYSAVKENQL
1871	15772	A	1883	2	473	TGGTAAAYRVLDQKRSNGRQGNRNLSGTNNRNNKOKGLRCKPKM/RSRGNAKVDKPRDAR*KSDRDQ/RGRTDG*RVSGGLTA*EAYRH/HBGQ/EASQSGRSRQAGRQTP*QEQAGNKAIRREKSKSRGQERE RE/KDRDADRHKG
1872	15773	A	1884	138	444	CYLTLKCRILYINDRVIVLTIVWY*HK

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1873	15774	A	1885	27	470	DRHID*WNRQSP*LNPSIIVQLILNN AKNTQWVKDITLLDKWY/ENWIYQCMRY PLGSIYTIMNQFKMNYGLS TICCYTIFLFFSFFSLPFFFFGKGVFS* PGGENTG/ANLQ*WNPFPFGKGLSPA*P PKEPGMRGAGHPGPKTS*PGKFGPGGG GPSFPYRGNKIVGKPGPIGPPGGIGYP ATIPKKQKPGKRGR/PGGPMSPYNGPP KIPIHGGKPG
1874	15775	A	1886	478	1	KNVQNSALQAANCRCMLIVCCTQCVII SBSGAGSVAKYIMVLSKVBGGGK VQVRGKQKQKLCRPELGSAPPTCTP ASV*LLPTP/PASAP/RYVDIILQSNPLL EAFGNKATVRNNNSRFSVLCRPAWSSC SLRADLSHTPTHTHTRV
1875	15776	A	1887	1	402	HSLERPHYIG*LFKNTPSRD/RVPAFLA HWSRTPLGKQSTPLSLPKCNDYRCPOH PAGSFFFFFLKNGFWGCSLGGAGGQQ *LKS*WRPNPLG*GNPPC*PSKEVGTG AHKLANREIRTRACGGNTFSL
1876	15777	A	1888	511	124	GTRQHFAGAHVPPEGP*S\MLDPKL\/ DDRPARDMWIREPGLLLPRAQAQAGKY YCHRNLTMSFHLKITARPVLWHLCLRT GGWKVSAVTLAYLIFCLCSLVGILHLQR GESCPQWVCNPTPSSG
1877	15778	A	1889	667	310	QLKP*ATKSV*QDTAFGIDVGNDFLMT PKQAMKGGKIDKGFPIYR*SICTAGETI NRVSR*PRK*EKIAPKPTWQKQIS/RI HKEFOQAN/KOKSNGLIEROTKDLNRF SKESKDL
1878	15779	A	1890	462	3	KWFFFLGPFPLPPT/PPPT*NSPQKX KLTRGGCARYFPPLKSPRPIRPFPPFK GEGSPNSKHSAPPPFWGPKETFFERTP PPPPPPPLCSFLKNNLFSYIPKGLGK GQNTFSFLPSFFFFSIKKLLG/GVHVRF YCRVNSCTGFVQMY
1879	15780	A	1891	1	455	NTCLGFGNGFLDAPRA*SMKKIINKLD FNETENFCSVKDTVKMGKQATHNR/V RKTHILYKDLILKIYNQLLKHINKTST IXQ*AKDLNREDIQMTKMKRCSGWR WFTPIIRALWACKVBSGLESSLGNTV RPHRIREREITHCY
1880	15781	A	1892	1	537	RGGIQAPKEVSPBGRQEPARKSLI*TA* ETTP*SQ*/PIPERP/TGVFMKKPVSVS LSTGLIA/VVPMVNGKELPNTPIWPK GKWLILCSKGRARFSEKSSINASVTD VELHLHG/VLGRDGYRYLYEYKATCTDS CGFNLDVEAPQDATQGLSFPQKTSKR SLYAJALEDPGM
1881	15782	A	1893	2	514	VRCQRCHC*RAQSSSLNARKLYEAL MARKVKQSLFSLDVEITDEKQOMSLQ/ CSLAYGLTLKILSEKRSAYSGNSSVRM RSAGQTSKAHLHOPRRVSVQLQVAVNL LPFRKKGOTDPAINTSLPQKVLGTTEE ISGKHTEDTISVASSLIYSPPASPGS
1882	15783	A	1894	473	2	VMGRSIRGSPPPTFGGNFVFWQGV LPCPRGFKTLCSSSPDPDPQKAGVLG SFHARDPFFFFQI*TPFFGKCP/LC

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1883	15784	A	1895	613	11	SPFF*PL*KRGIIFPVPGKIFCEMESCS VAQAGVQ*YDHGSLQWPPGF**SSYL LV*LSS*DYKCVPPHPMY
1884	15785	A	1896	20	449	FRPRSPACGLHAVSSPKLGAQALSSPG LNLVFTAGSWDAG/LRLSPRANPRVA LPRVHTGPSST/DLSPSCPLGLAQFGT SQPACL*SPFLLAPAPRSGCAWPGLP VCSLHLRGWGGADPTGCLDAWAMALAS LRPCLCPALPLSREPPSPLINDLVLFPM PRAPVPLPGRTPHSLLLCHVQSPSEQL PSKGPERL
1885	15786	A	1897	393	3	KFOYSAAARQQGLQHEAWL*YSFPLQL EPSSAQTWGPOTLRLPRALLVNVKFBGS EVS*PCVACGIAQALSMGSTSSVKLLSH QAPLPQMHQMVFAKCLCMGAQLNVPP\
1886	15787	A	1898	395	217	ESFTFQVSTKDVP/LALNACALRK/KATV FRQPL
1887	15788	A	1899	1	375	RFTAQSKNT*VRVAS/EALSPKLLDPL PGKVIANGKVDVPRPATRONLSQFEAQAR KRECVRPVPGGIP/PRAHSRSDSDADGR ATPSENLPVSSARVDKPPSVLVPFNRPP SALPVMGLPFPFIPPPPCI
1888	15789	A	1900	47	326	RER/CKSF/PPA/HQKINGAQ*QVN QAAAAQAAAPAAAMVSRDISSLLVSSQK SKVSNYM
1889	15790	A	1901	181	837	NTVLVQ*RNKAMNTVHPF/TAMFSEYFK ATVEIVCS/EKIPFKILLVFARVISHPR TLIET*KEIVAVFIPANTPSILQPMHG IILSSKPYYLKASRAQRLTPVIFALWE AEPAGSPREVSSGLA
1890	15791	A	1902	1	385	VKSLIOTFNSKNEFGHDKTSPSEKTOIV WNLGSELRSFSPSYGAAGGAEMGRSLESH RSRQRAETAPLHSSPGSGSEMLSL*RO HLTPITANAGVQWRGLCSLRPRPPGFK*/ FCPSQHIFQPPSSWDYATROQATKQFVF FLEMFG/VHFARLILTVELNN
1891	15792	A	1903	207	3	AGRVDRREPFOMOTICKLELTGSERTSR ASRWGRGRWRLQAQCRV/PQGLPLSTHLL QAQAKARGOTPLCASLHLPNSHVGLKA QRDEAMVQSGLAFAVSSTCTRW*GSEW **GLHIVAARRQQREEPPTTAAPET LCFQQTSWASSCSLEHSAOPSEVQVRAL SVPSHSPMVA/PCLSLPNDIKFPGE
1892	15793	A	1904	2	391	YWGPRKKPLTHCL*PVKLVQPLWRAA WRFSK*LRVEL*PRASLPLOYTPBNK LFYQSTCTCW*1TALF/TGKT/NNQP FRMEFLHLQAGLLETSGBDPTLASQ NVG/HYRREPLRPANTIQS*PLGLKQPS CLSLPSSWEYRHMV
1893	15794	A	1905	3	424	TQPLISQRKYKTLQNSLS/CCAHF/PP HFFFLVDSYFHSLSQLKNAPT*G*CP YWYSKGYSLIHSWSSSILPCPLTSSGF PSLPSYQPLPCPSLFL*NSLSTLCLL FFSLLSQPSFSNRNPSQVYL
						YRAGCLQSLPPPLLLFLPLCPDVFPFSS S/LP*VKASGLIRSQBNVGTI/PCLQNR KSNKPLHKLPSLRHSRAMQNRILPILR IGKFF/IFFS*DGVSCHFGWSAGVQLQ



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
1894	15795	A	1906	2	389	FTALHLL/VLKRFSCLSL IQRLGDKSCLITDNI PSSHSLTQKRGVN PSFKSMKADRGKEAAEKSEARSRSWPMR EKERSHLHN / IK*VOGKACYPEDLASI IDEGGYTQK*IFNEDY/MWKHM*FRSFL TREKLTGPKFKASIKDLITLV
1895	15796	A	1907	458	13	AKETQGVVVDFFPM/VFGGVVYVNFVSR NANLSTIKQLLWHRNQYEPFLFHMLSQPE AVYFTCLNQTAQQLLEDEQRRLCDVQF FLPVVVMVDCBGRVKNLLSSQISLFG KQVRKLSLSDPESVDFSTHMCQPCCKS AAL*DOATS
1896	15797	A	1908	409	3	EKTDGLYRASQGRDLRLCAQSPHAW KDGMAICALIHRRQ/VDLIGYAKLRKDD PIGNLNTAFPEVAEKYLDIPKMLDADIV TTPKREKAIMTYVSM/LIVLAGAEQAE TAASRICVKLAVNREKKMLMEERV
1897	15798	A	1909	116	379	HSGPREGALLLPKCLPHAKRCIALAFM CSDGATALLCCPGSSAAPS*LTQSP/AS TSQAK*PSHLGLPSCWDYRCIPPHFANC LDYY
1898	15799	A	1910	418	3	QD*YATANRWFTICMLSQACFLFSL*PAH LL*L*QLMLFSFGPTVFSYGDDEIGLDA SALPGQHMEAPVHLMDESSFPDIPGAVS AKIMVIRGQSEAPGSLSLFPR/LSVQRS KERSLHGDPLAFSAQPLKPSYIRPMY
1899	15800	A	1911	394	3	ILEAYPEVKQPAVKGASSKKEYGH*/A AQALPVAEQBOQQRHRESEKQPOKVE GNNTNKSEKIQLSNENICDSTSAAARL TQQRKIGKTYPQQFPKKLKEHEDRCTLK QENEEKTNVIMSKKGRD
1900	15801	A	1912	499	141	PGLGERDWTISKYQAGGEGSTREWASRC G/IRPGDAGQQQPRPE*SVCPGRGASHP GPGSWKASPAWHSRPEQGRCSGLGVQKE GFGHLLQPGCRTPGPIRKRERFSGYLQ
1901	15802	A	1913	127	387	ISFVFPPTLPMPQMLPBTISMTGLNLF OHLNCLARLATSAYDGCNSSEV/CDL LY*ALFLKLDYQIRFPNYPSTKYRIY LCLY
1902	15803	A	1914	504	0	PGPGQRKHSAPNCLMAYQILRLRFLA NQIYKCIKRIIHHDQVGFIPIMQSWFNI QMQ*/INLIHHNRL*/KHHMII SFDKT HILFPIKTFIKGIBGNLLNLKNI P/S KNPANI IANSEV
1903	15804	A	1915	46	415	YTSNQLDQGLKLT*YASTKCYKLLNW IKDVQDYTSNKKILLRSTKDLAK/YRD TSCSN/NIYQSNMS/KLIYRFSKPNK NLSTL*ITLTSF*PAKRYTGTGIYKVTM KNRVGRLSLNPFQNY
1904	15805	A	1916	420	1	ENADCVERRAKSPSIP*/RGQISVTM VSPNEQKAGOLAIGRVAVRYNGV/LLA IOWRKKILHILTSANLEKI IALGLFPGNF ERKPPENTFLKLTAMATHISESNLSCFAQ EDIALCRHPAIRMPEKAEQYKPLTASV
1905	15806	A	1917	384	3	TRTITSGQYSTHVRASRVPTRS*VPVF RSCTSNRRFQAI EPRVMH*KVHTRAST VRYDSGGHVAVYPANDSALVYQLKLLG ANLYVVMNLNLEESNKGHPFPCHTS/

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1906	15807	A	1918	405	105	RRAL/T*YLDITNPFMY KAEARQRREICSGPHSADSAWHPLTW WH*PPPVAKSSQEPGVHSFVE/HVCRKI LILTRPKMALANKQNYRELWFTFWSRSR *VGLCTTPGMCVKHLRCV GQREQGVTRVLNSKEPETERGK*IPFV KDQELIH\PTKFNHVAHMGPDQKQVLM DLPLSAVPPSQEESPGPAFTNLARQPEC RNKPYISWPSGSGSEPSVTVPFLNSMDP AQQDFKEDSDS\KHS\TSNSEN ADRENPLRPTFTWFGTGLRELRFPVA SACLGGTWWLALNLCSPT/PVPLTP PCS/SCVQVQFASHVANSQSKEPAKSA AVAHCECPGGTGSADPGWPGATCPESP GPATPHILGVVEPGKSSPPTMEEFPAW QGSFQWTVRQRMTHM
1907	15808	A	1919	409	3	
1908	15809	A	1920	9	470	
1909	15810	A	1921	356	1	IQMAALGQILRRVGRDPFSHRTGKEFS AMAGQAGKNGDGEQSS\GGLAAVFLP *SQHAAPHILLIGPPQQNLGDSKV*GFP SPRLLENTLENGWGSQQLHSGPSQHA GGSWNGSETSLKG/PH*ADGAGRHTMEQ SPSPPPFKHSHV*HNPEAS/PPHGSFA PSGTSPLPMASVLLPFGSL
1910	15811	A	1922	567	41	GGWGETFSRLGNLQAIR*SRFNAQAE ETSR(VLA)VSLINEALDRGSLKTLASL LLFAKGLDDVSLPVAFPHILLVAARQ KAQVTDGPVAVLLEERQGVVRAQDA NTAQMALGVAAINCAIKKGKAAQTERV LRNAVALRGVVDGANGYORDLESAMA KIQRPAAY
1911	15812	A	1923	2	405	IQQCGITSSSVLHGNVPKKEEDG/VTS VKDAKIAEYSCPPDGMITETKGVILIKT DEELMNLKSGEENLMDA*VCAIADTGAN VVVTGKVDAMALHYANKNMMLVNLNS QMDVRLCKTVGATLEKLTPECL
1912	15813	A	1924	510	37	LLGHAFIVSSSGRFLAASGSHSLKK GRCVQORTGNVGLSPNTARWOTPLQPSI SSSAPPNPSFAPGPPSGK*AAKDGFG CSLKSGLKR\RSQGLR*TRSGSPSPMP PSPSPS/ERPFGDEKGLPCTPRGSLPG PKINTACVCAADISPLGLEPV
1913	15814	A	1925	74	429	ATTPGHELLLLEFFFFFPLGKGAWPL Q*KGK\GGPIRG*GNRAPRG*RETFPT PKRGNYGQPGQGPFGPLKKGAAPG GPVVKTRGQLEPPHPSKRAGVTVNLL GPKPKV
1914	15815	A	1926	515	304	ADAAISALANGVPTNTIK\*IVGRPKP DFFYRCPP/QMG*PHSDLMCTGDKD\VV NRGPKKTSPSGHSFV
1915	15816	A	1927	1	433	NTVGSNKSCKLYFAELKESYLNPLNKL KGPO*VKILLKKSSVTKCTLIHSA*Y KV/LKIWWYWORDTH/DHWNISIKHEIV KQFEDGCTKTQWAKDCLYNNWCKE\W ISTSNRMKFNLYPT*ANINCHQDPNSK ELYRYKN
1916	15817	A	1928	316	356	GGT*PPQATPIS*LYLPTTSSL/TLPP APSLPLQIAPISDSPSRYS/TPPTPI SLGLAPPTLLIPVPSLPVSPRLNSTA

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						PP/TFLTGSCAAVTVVSLAVLSLSPAFAS AMDIAQNM
1917	15818	A	1929	490	11	PTRLTCFSGHVEGVPVTFPPYBTHSMP\ P PCHVHPLVQPPGSSHVGPVTSSSPSPS ATHIHPLVQPPGSSQLPNTWVHPSQMR TWLQHPPLFAPPQP / PPSGICSSMTH LTYELASFPAPQ / PRQAPQGGVPTSLP QW*APQPTAPCRATQSQQLDG
1918	15819	A	1930	1	552	RNPKRAFPSPFPFAPPS*NGNERSRH PQSL\PFVKSRAFPSP / LSPCSFV KSRRAFPSPFPVAPPS*NGNERSRHP QSLLLREIKWSVPVTFSPCSSVPK K*AFSPSPVEVLLRDHTEFLERPROPS TVVPGCFGRSIPRRNNTGCAFLICH SARLLCDPVSVCVVRHS
1919	15820	A	1931	414	3	RVPGESRK*ERVLDSEHKD*EGRRRONT /MGRVDYTT*TVITDVTNLSIDQGVH RSIAANMTFAEIVTFNIDRLQELVRRG NSQYPGAKYIIRDNGDRIDLRHPKHS DLHLQYGYKVKRHMCDGDIVIFNRQCI
1920	15821	A	1932	521	103	ATEPAGVRLKEGGNITSEFVTVGVNISA LAD*SQDA / SRYs*KKQVLVPYRDSVN TWLLKDSLGGNSKAINMATISADVNYG ETLSTLRYANRAINI INKPTINEDANVK LIRELRASLARKLTLAGQNGIALLDS
1921	15822	A	1933	1	490	NTGWWVRKGEGNGTLMVRRLPVCVPLCS AGGLTEDEBGLCAAGFPFLAEDFGQAL QQIQTARSAQVAP / KKGDOVLGGGTGA PPTAYTMAISIS*LSVSHVDEBGLPA VKIETLGIHILPERHALLSLVQARSGL LLHGPPATGKILLNKGTTTECLT
1922	15823	A	1934	383	151	EVAFLNLYKDDIERGRLEPLLVAAGT AAVGHs\ / S*LGRRKELCVQVNRPKMG YMRVQHPVPESHKRAKALF
1923	15824	A	1935	379	1	YVPVSKDKETFPNSQ*GLTTHQLLPYI DGRHVQKISAEADVKLNLRVIAIQILL *VGLSQYLOQHQPGKS / CRPGCEBGE GMVLES*AQLSLSTGTAL*HWCPSRKL IQFGIKNLIRRLCI
1924	15825	A	1936	376	2	GCLFTYMKPTAMSSQVARSSEVSPFTA VPA*SK / QGHGAVLGCHITSEACFAC PFPLRPGRSTCA*SGC*DVRSSSHSH GTARSP / HOTAHTPMEQHTSHSQHTHS HEQHTSHGTAHMY
1925	15826	A	1937	426	1	KHGEIIDDLLKRVYRDNAASKKSAI / YSKW ITHKKRRDDVGEVHSSRPATSVCEST IHLYCAL*ED/LAARTLAVGIERC SAYTILT/E/K/LKLSKLTAWVP/L/L LPAQQLKEKSMALIKWNOQHEAFLH IITAGLY
1926	15827	A	1938	2	469	KRPKLVSSIAATHPALSS*TRQRFLL LFLPHIVREDLVQRLKKKHTIQIGNVE VKLL*PTDNILCGKLYRFHRSTQKVLQ LI / NPSIVAAKINMHISLVFLYNDN* LENKTKQTSSTFLAKRIKIVGSKKKSK KPYFAIEKSYLDPIWN
1927	15828	A	1939	468	920	TPLSHTSPGKGTSTHLSRHHLSFWTYH ERLNPGRGTDA / IMLTRGILLMLRL

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						VSNS*ACQV\PTPTSASQASAGITGMS\HAS GHLIFNY\CSM*WLHRSNQ*KRCTGQE TOPCPVTQDGVQMSNYGSL*POTPLKQ SYHVSPLSSWDYS
1928	15829	A	1940	448	474	GIPGG*GSTTRNLYHYVMGDEVDVLT CKHGKDWQKHOSRCDRDNTEYK\YDF GEMLNATFCLVHRGRHRSFRLEAMQ AACVPVMLSGWELPFSEVINWSQAARI GDERLLQIPSTIRSHIRDKIALRLQRS QFLWESCLATAEDPNLIGVVR
1929	15830	A	1941	1	423	PTTLIFGNG*NVCPGLCARLHRLS HATPPPLLITP*LPFTFSSRCAPAP PHLICPTSCPLCSKPHWP/CSGQ
1930	15831	A	1942	48	417	RLTMYQVLYRHCHTALGELPRV*PSC LSLPSWNYMMPQCPTNF\CIPTRE PPMLP\SNWRTP
1931	15832	A	1943	450	2	VHRSNRONMDSR*RGANGSVESV\GV PY\EO*TIYDGI\NSGVWGLYAY*IEE RYPEFALRDEKYLRYPGGE\AYKVE TIKLNVEAVNTRRDKPTNIFAKNQAFVR MRNSFTPLSSNTIRRPNYSGVSRPI KPLSPLEAQECI
1932	15833	A	1944	451	3	GRITRHLPRRAEDDRERERFSPFLSRH PMFPFVTPFKASSDW/PAISSICQACH G/PPFVSLPRKPAHRSC\VFVPP\ASGG DTSIHSGKTVYVHRKQFAMFVLPFGGL *APSHGAPSPSPFQGRHCPET\R*DLL PAPAPSPSPITPLY
1933	15834	A	1945	402	3	VRLVSWKTHF*SRSSKSL/HPTLTAS LTGSCVNCIVILINFFYELISAWLAKN EIPRTYQVESSILTKMLPQFVNLVYS WFFVAPFKGKPVGYPGKTYLFNEWRSE ECDFGGCLIELNQMTIDMGDV
1934	15835	A	1947	1	405	NTGMRVFAILLCLGRFGRTERV/GGKK KKKKKPGPLGPAQKTPKTQKGGQAQG NRGKPLPFGGNFNGRIGFNPLPAFPG GGGGGR*KTR\KRENGNDLLKGGGKL VFCPMVGKLSGVPGV*QNFKGGW
1935	15836	A	1948	443	1	LTPGRANASLLG\CMEDLSVNR*ROGL WEALLTHNVAGCRLEEVDNAYGHEAF STLAPKANLSVELAEPCVPEGLPVFA NFIQLLSA/PVVVTEGGTANLEWHVQP MLALWRAELRKSQVIANVT*GAHYSDCI AALRIKIT
1936	15837	A	1949	396	2	GNRGGSVPVPSNLNEDGISCAI*/RHIN WLAN*PPTIYCI*ETHLICK/DH/HLRL VKKKKILHFNCKGRKQAPVALLTGQTD IK*KALKENKECHYELKGS/QENITVG NIYAPSTRADRYKKQLLDLQWV
1937	15838	A	1950	419	1	RMQ/PSAEPTTSGK*GASLPAEPSSGT *GAILPGCPVMKVSASSWPSRLGSEE PLCPA\PSHLGSEER\PSRPPSHIGSKE R\PARPPIA*DVGSASAPP/LPSGM*ER PAAPFSGR*GASLPGRFSPENMGVPLPR RPVWDVRAPSRAPVWEVRSVSANPPHLR REKTLRLATAPV
1938	15839	A	1951	422	3	QNHVIMSE/DAKTAFGKIQYFPFMSLN TL*MKVNFNLNLIKITQKRPANTMFTGE

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						MLE/AFLLRQGRKSC/CSLSPILFYILL EVLPS*VWQRK*/IQG*EREE*NCDFVD DMIVTVEN*KKPLYNLL*IIS*VARFKV ILDTCI
1939	15840	A	1952	2	409	CAHYSKNPQRPLRTDARLPAV/DFWSL GAILFMVGGQPPFPQANDSETLTMIMD CRYTEPSHVSKEGKDLTRTLQIDFRRR ASLQ*LENHEFWLKGVDPSPATKNILPV *YK\NLSSEEHNSIHRN\ALGDIIDTR
1940	15841	A	1953	2	367	IQCVRL*VHVCLASSCVCLCYVHATLL CVSTCL*CVAVCH/CLLCATV\ACILC /V/GCVSTCVCVCPPTXCDGVCSAC VCT/CLCVCTVSTCV\CVCLRVCTVCVR CPCICSSLNGNEWNG
1941	15842	A	1954	374	2	EAPWLLRAGRGALEPCWKSITPPSPILFV PPLLPGTLVYQVWVLEPWNRLACAVTL ST*ARAGTSNPSNHLFPVSTAPQGRHW QSPGAGTNGDPSLSPTWTHLLPGCCCHP CHCPFPHEKPTRV
1942	15843	A	1955	1	411	NTPSPLEPC*PGL/PPELSPPPQPPTW APPRSTQQKLPILCLKPSAHTDAPCT QPGSTLPLELPHPTQQAQGTAYQIHTT*A APPPGAKPG*RCPPPPPSRQPMQTEA FGNQPCPRLLTTLRVLPV\VPPELPI
1943	15844	A	1956	33	451	NGRNTFGELQSPPPRFK*FSCLSLLREW EE\RDYRCMPVPANITLASLVINS\CD LEALASQSPGITGVSHPTRPHELS*FLMP LE*GHEHLLLVLLSQPPNPP*FQRFST QOLECSSFTNLIVPSPNLNTHSDFFLT S
1944	15845	A	1957	3	399	YMQVRTTMSDHSHSISKLINTDNTECK G*GSTESLEHDERWEYKFVQLLWETVWHY VR*FTTILYNPILIKR/IFRHTYIGNVC
1945	15846	A	1958	47	399	AANPTLEAVFFFFFLETEPFPGPGRA GPQSRLETPPSGVKPIPR/PPPPGPEE KNPD\QGGGGGGDPKPPGGPP*ATGQN SNG KKKKKKIIPRGAHGDPLFPGGAGG EEWLDFA
1946	15847	A	1959	407	238	TQAFALI/KDGGVIGGICFRMFRYQGR EIVF*AVPSNQBQVKVSGSPRRQPCIAH S
1947	15848	A	1960	106	1854	NRAVKSQPNQTRNHKEKNYVHLPDAGP SQPASAGGSSSACRRSTKATLHKRWVS PAGPGVQFLSWOHPHMA*GLOQNP6 PQ AAAPPARPGLVSGHCLT*EHAQGA/GT GSLASLGRKRPILPVCE/VFL*GLC VQBSLSLQCHNPVTQSGFPGPQASD PW*GDARCCSLQASPGDRAGHSIR/RG SVGRPAGVPRGGRKPTLSGA/SGPGSV LGGFCCEPLSREARSGMVQR**GRFWT QERTPTGR*GCKVAGYLHSSATVHESG AGAGGSPGKTSATLDVQGGGGT/PSGP AWDRTNGYEKAALPLCNGKVTGNTQCG AQQPASGSP PWVWQPLLRLRQLRQSTGL *LLFPVGVGGLQPGEG/GQFPPLSPWGS LITGRKNSNKARPGCNBGTG*GARNGAS LITWMTVPNGGYCPQAGRDFWLVDSRFK PSLGLRAMV*NSRKAPLSFDGGRMTV*

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						PQGGGRASHRRKDSGLSPHSGKG*DP*G/PGGKRSISPLPRGL*GP/VGERGRNGDNPW
1948	15849	A	1961	76	427	QRQEP TPGHITSGTRHPGGGGRGPQT HSHSHLPWLETSAAGSSPPNPLCSLPPTPLLRLLSPFLCPSQTTQRMFIPAPHPSPASPCKVP*DARGAPAGAPSTL/RGHHPHP
1949	15850	A	1962	375	131	PLVGRIRLLYLKRLFPVLLRQKAKRN SQWHTLPLSSRHDAVCSPPSRNRNRGRDKRPPFLCVDA*IASPVVVIQ
1950	15851	A	1963	89	538	GLYLQKRRHGVSSWVRG*LAHSGLFPSPDPKSSVVCAGVQWHDLSLQAPASGSKRPSLSGLDIRHAPHLAHFCIP/*TQDFAMLARLGTSPFIYLPQCC\FETGSHSVAQAEVQWNNHSLQPSFRLRRSPHLSTPGSDHRRNP
1951	15852	A	1964	402	42	CCRYPGTGLQRLSASHQAS/SGPQLPAPLPLQVLPFLALGIVDDVPLAHAPT EALPGTFLQVGPCT/QSSSAAQLT*EPLGSSDLGLMNLGASCPHL*TGEIIVLCPKGYCLDQ
1952	15853	A	1965	8	14	SSHAACFPFPALSLPRFPVPTRMGPQGGGLPKPLVSAFSSRMGSFPAPSPLIIASGDHRCFPAARALPLAIEGQDS\PPGH*PPSPGGLHRCSPS*PLIL
1953	15854	A	1966	521	2	YELVGLIKRHRVSNQVRYEHSYLPDYVSVPTDPTWGPERRERSSGHFVDTGTAAAGGGGMLASPKLGATPLPPE*ADA/PPPPPPPPDPGVGSGHILNPLILEELRVLQQRQIQHQMQMTEICRQVLLLSGLGQTVGAPASPSEIHTGTASTKPLLPLTV
1954	15855	A	1968	111	395	YLMRGFLLEHNMVKGKEDERTKARLYLFFFFFFKSKSPSPRVEGRDP/NLGT*NPLPKVKIKLSRPTPEKWEFGAVFICPNNFLFPRKNGGS
1955	15856	A	1969	413	101	DVNRHFSKKNKRCQ*LVIKEMQIRTKRRYHFSPTRMGKIKN\KKNKFWQGYGTG IPTHWNCKRMVPIKKTVMQFFLKVK*LLVFGPACKKLGYSYSLVTS
1956	15857	A	1970	411	1	NLTPLACTKRVHFKWVYDIRMKRTIRLLRNTRYKYLHNKIKWGLNRT*KE*TIKKKTORFDYDITLMS*SSSKRKTQLDWE NTL\YLQYITDK*ILSGIHAKFLK/YK/KETNHPVQKWARDLNGHLIKNDHMACI
1957	15858	A	1971	3	828	GQACHFIIPSAQAGSRPLIWRAXQLGRVRCALIMPALHESFPTRLIQGNSVGGP SISLDTSL/CNRCVWGGRG*TGPGLP SLGKVLVBGIPSES PGPTASHPCSPRPDPDQ/LSCISAPSATPTVH*SHLTLPMPWPGP*GLHLSQDGPGRKP*PGCSGLAGGDMPRMEKP\PPPQLP
1958	15859	A	1972	398	3	GPQCYFSVRLOCP/RKIPANKRAVCSATLI\SLQGPSISAPHVLGLAALAVHLGESRALPEVDVGGPAPGAGLPVPALPDSLLTCRTRDSLFFCLK*ALLPQSRLLSSLSK

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1959	15860	A	1973	2	433	SDTCSFDKIRRRHADIPPLY ODPTMTKRELNALKSTGDGTGLG/RASE VEVKNEIVANVGKREILHNTKEQHTED TVKDCVDIEVFTAGENTEDQKSSSDTAP FLGTLAGATYEEQVQSQILEASLSPENT AQVESNEVMGAPDDRIRTRPLESPNCASD LNGGS
1960	15861	A	1974	373	580	TIFSRQVLRIQNALSKDKPNVSTVYSNNG SELHNTSEASV/YHWKILISTEYHKTL
1961	15862	A	1975	47	413	RWRHLRGSEHWRCENQVHQRDLALRRK GLMSQR/PABAAGQPRKSHDYLLRE MQHWATDPAQERKVKASVKNVRAQJ LQDRTRRAGARREPSRLQQTSPVLPE KSSVPGVLVLR
1962	15863	A	1976	444	3	GYSRSRGTTSGTHSSRDYDIFGQATVK NAMLQDFRMLSPCKSEVMHCPFYLKVE IMAQCEENLADIQQYSSDKRVRGRIMSRH SAAIKRRTQQRLRELLKPCPEGLDPDS GDAPEVCRAATGAETTHMDQV/QPSSS KVLPSDFQ
1963	15864	A	1977	281	567	PRSSLQGGQLSRPWRKKNFFGPPVFPPE QRMFYDSELPSGIDSPPCF/RSAPTAD QVYQGDQMHVVRKHCMDYLVKRWPLG KGQGGKISSDHRP
1964	15865	A	1978	357	2	KQILGPPHPQAGPRVVPFHPGPKDAPL WSSRAAPPGRGLGRAGPANGVAGATLR DSSPSFTWRGLHVQAKRPSHVHKG/ SQPGCLDEGFPTSLRLQAQLAETGRGN GLSVREO
1965	15866	A	1979	29	434	VQAEAGLPDTHFPQRLVSRSELEQSS DVTIKHVACDDFTACLTDRGLIINTPGS GSGNCLGHGSLTDISOPTIVEALLGYEK AQVACGASNLALATERELFALGRGDSG RTGARTKESH/YLPQQVMP
1966	15867	A	1980	3	2082	SSGGYLRGNMSENEEEISQJQSGDYE VEEIPGLPEQSPGFEPQSPPEFQSPR FEPESPGFESRPGLVPPSPPEFAPSPPE SDSQSPFESQSPRYEPQSPGYEPSPG VEPRSPGYESSRYESQNTLKTQSPPE FRAQSKFOBGABMLINPEKSPINISV GVHPLDSFTQGFGEQPTGDLPIGPPFEM PTGALLSTPGFEMLONPLGLTGALRPGG RRGRARGGQPRPNTGICGKSPGRGS TLIQHQRHITGEKPYKCBVCSAFSPQSS DLISGRTHWGRSPYKCBVCSAFSPQSS YLLHQHRTSHGQKPYKCBVCSAFSPQSS YLLHQHRTSHGQKPYKCBVCSAFSPQSS SLRSHQVHTGQRPFGSCIGKSPQSPQSS ALIPHARSHAREKPKPCGGRFGQSS VLAHARTHLPGRTYPCDGGKTFNRSS TLIQHQRSHITGERPYRCACGKGFCSRSS TLIQHQRVH/SOERPYKCDGCKAFS/R ASDLRHQRTH
1967	15868	A	1981	2	188	LPETINFAELFLPYISQHNLRKYK/WP GAVAYACNPSTLGGQGNITRSGDQDHP GLHKEWP
1968	15869	A	1982	3	424	EGQATVERINLCLKQQLQKQGENRYR TPHKOLN\ALLTLNPLSLPGRITLSAAE

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						QHLOKPAKTRABQLVWNRDLITSEWBI GKIITWGRGYAYVSPGL/NPSRHLKPYH KRMRLKRFPREDPEDPPSCSHVKTDAAED PN
1969	15870	A	1983	3	399	YSKLSFGKLTTRPRITVSSSPYKPEQGC ISDLCHP/R/TLTNCIRGELIKENLAVG AFGCHPFPFCYINKSQERNLQALRHPT TVAFGETGFNYSKTCMPVPEHHVKPKR QLRLAASLEK/PLVILCQQADE
1970	15871	A	1984	1	405	RRHTGGVRLCYITGGVEVFAKSSDAIF AQTPNCNQRVKGHPGTVCCKIPPGCNLKI FNRGFIADLDQSVNGLEADY/QLTRM CITLMSILKQGAERYKCTATPCWKE LHLNGPIQRVDKVLTDQVYPSILM
1971	15872	A	1985	27	452	QGRHEAQGGGSAGAH/GPTTFRFPQPEPQ PRPSSQAVPAGRWEPAGE/PTTRHPHRL SPASRPLGSPAPLVRSSPGRGRCHHT INSSVTGTSVEPAGSLGRPQAPLEPGTV TSSVRLQQPHMTPLGKIMPDPSKRNKGF TPT
1972	15873	A	1986	414	220	GAEQBELLSF/GSGGCSELRSCHCTPAW ATRAKLRLTQKNKTKRESYRQGNQWGR ILGELLGRL
1973	15874	A	1987	52	412	TRERCLFPACDNVWHLKRYLRKNSPGR NLWSSRNIRKKGKKKKKKKKTINFT PKNFFFKACQCMGKNTKHDPEQNFI RHALLQQLNINFSINYIEGRVF/HPGAP IESILLACH
1974	15875	A	1988	2	143	KKRGLDKRTP/AQAFKKNQEKQMER ILKKASKIPPPPVQWQSVDS
1975	15876	A	1989	3	163	TEFQPSER/NGEDLGNTWETFAIDLL CCHQWICHPLPLVGVVRGAESVGVF
1976	15877	A	1990	1	439	DKTAARDATRNHLHYLKHGVNINREAST NKSITSTKLHVNINISPTCNKELRAKFE EYGPQ/IECDILKDYAFVHMERADARE AIGKLDNTEPQGRMHQJLSTRSLRTAP GMQDQNGCYTGGKDGHWKRCSDIRSOR VADLTEQ
1977	15878	A	1991	1	145	VVAASKAMK/NGDWKTSCHSPTINERKNG KVWDLFPADPVLLKRLRESR
1978	15879	A	1992	2	425	NYSTLKKTLSESDT/VLPSQIQGGEQAQ AKVDRLCLSDLAETNFRDLQGBOLTEL NSTAIKPVQWPQINFFSVSHINVEEF NDYEANDPWVQQLILNLQQAEPFASL SPVIYDSITGLMTSLDAVELEKVKLST FN
1979	15880	A	1993	3	449	VAGAPAGAGAPGLDQTLQRPIQLKV LPPSSSQNALMPTLLCLLVALEKPD QPTCNLLYVSWRKLDEMLHLYFRDRA YYTLNVLADIDINPDQRIQDLEPFCRO LSSMASKLIIISPTLVYTYQCFILSTGL LGPVSIIPGY
1980	15881	A	1995	1	410	SSRRPFIATKTKSMEDLNPDIDDLITTY SGMVIRTYQLIPMQEAPFOCVCAHTT RVEMDRGRIAEPRVCGRCHTTISMLIH NRYLFSDEKQMIQLPESPEIDMAGOTPH VILVAHNDLDR/VQPVDRVNDSGFF
1981	15882	A	1996	1	154	LEFFRLLVRYTKKVAQVSTPTTKVSRN



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1982	15883	A	1997	2	475	LGKVGKIGKWKHPKAK\VRPGGN
1983	15884	A	1998	3	431	KKLRQKTRRRAQKR\LPDKV\RWGLVTP SETPVGIGNLSPFLGPRCL/QNPDELKP PWRFFWQAQPIGAH\ERANAGPKTPAQK KVKKIKKLKEDISQGVHISVYVRNLSN PAKPKKIRANAGQLYLTGVVVLHKDVNV VVVEGGPNPKITITMLPIRI
1984	15885	A	1999	1	400	ALDLRLQLILNGVPPKRRVITCSYPTALQ SPIRYQRKRSTAVMTWTPDSAYQASPR PYSAGPADSKKPTKGVCYNPTLP\RLBI MTLGGTTG
1985	15886	A	2000	1	372	QNTDLVISTFSSRLQAAGELSVPRVLE IIXQGVVALPKDL/RGSCAPTLGAAGR SSGGQSPCMPLGLCVCFWVLTVSWLVCQ KFPBELKFYVBEERQPEFFIFPYVMSLVY NSAVGLYNNPQDI
1986	15887	A	2001	393	1	GGTGGGGAGGGVGAAGSAGGVGRRGA GGVIADSGAPGGVGGVGAAGGWR/G RGTSGGVGGSGGACGV/GSGGGAAGGV GACGTSIDGVGRSRTIGLGGSGSAGG GVGACGASGYVIRGAGGG
1987	15888	A	2002	2	362	WVTFISLLGLPSSAYSPGVFKRDAHNS VAHLKDLGRENDAKLLLAQI/QQC PEDHVKLLNENVEPAKTVVAGSADSD DK\SL\HTLFGDKLCTVATLRETYGMA DCCAQQPE
1988	15889	A	2003	2	358	EANRGKFTIRLGRSQLYNIRKVGQMASA DVEAASYPEDLAKITDBGCAKQTFN VDK\QTAFSWMKPCRTLAREEKSVP FKL/SKNRLALLGANAGGFKLESVLI CHSENSRTF
1989	15890	A	2004	190	1	DQTCPLSPFVIAVTFNGAVVWLTPVIPA LNDYRH\RPANFFVFLVETGFHHVAQAG LKLLGS
1990	15891	A	2005	1	132	GMCHQAQLFVE/CSRDRVLHGCSQTFC LKQFSCGLGPKCWDR
1991	15892	A	2006	2	134	PMTFFTRLEKTLTKFTWNRQRIQIAKAY LTNQK\NKARGITNIC
1992	15893	A	2007	315	127	SRIAPFFCSFLKILIDTR/PSFFARAGL KLIASNDLPSSSSQAGITGVSYGTQPV CFEYNG
1993	15894	A	2008	3	325	RCSMLAVREM/QKATKRCHFLPTRIALI K/ND\GSKCRKVGHWVGLLWIKI VWQFLKKLNLRLPDDPTPLRD\YPKOL KTYVHTKTCQOMFLAVLPLNLVPHLNV
1994	15895	A	2009	369	3	VGGAGLEPLTSGEPFASASQAVTNTMS HHTQPIFCIPGPA/GCPDWSTPELKQS AHLSLPSSWDYRCMPHELANFYFCRI/R VCCPGWSQTRGLK\YPPALVSQSVAITG TSPRAWQDTILPV
1995	15896	A	2010	114	287	APLCLCLRLHLLIKRLIVLGTFRATHL\N PITTRGRGGQITWGREPETSILAMVVKP

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						CF
1996	15897	A	2011	218	346	IMKPNLLKFPYPIYLFPSRQSL/SSVAQAG VHWRRNLGSLQPLEPKF
1997	15898	A	2012	310	1	SSSSSSNTHFGIPKYLINPDTCPLA/KVN NSSLTGLLEYTETLLKPGIK
1998	15899	A	2013	3	301	SDCCASNQRDSGGVGPSEDPARKHTL/CV/ CNSLDLIE
1999	15900	A	2014	332	3	LIRDPLEKAVCPFSDIQLIAGRTTALFKA VRQGHLSLQRLLLSF/VCLCPAPRGAGY RGRQAG/SLSCGGLHIPVRASRLCLLPQ AKAMAGAPPAPWRPFCSLISDCCASNR
2000	15901	A	2015	2	325	LLHHAPPPVNLFLDRVSLCGPLCGPGC SQTGRLKQSSCLSLPKC/WDYR/ATAP GL
2001	15902	A	2016	373	3	WAHSLQPKPKVDLSLKKKKKKKKLKN TPFILRSRTROACLSPILSNIVLVLPLN EIRQ/QKKEIKGTHGRELTLSLFTDN MIIYVDIPKOSTKGNQGSYSVARGAVA HACNPSTLGGGG
2002	15903	A	2017	343	1	EPFVFGSSRATGKSSDIRATKYINRVLE YLRWPRGRORLKSS/HISLLGSHVPGA FRGDKWSCCHQKDETTGGRGEDVLLCCP GVLGSCALCRSGVRTKFGIRGKRPWKERE R
2003	15904	A	2018	139	2	NSISTRNTRNNGMVAAHAFNPSTLRGRG GQI/VRGQDFKTSLANMVKP
2004	15905	A	2019	3	322	ARELVFFFGAYREGFFHRDMKPKINLLCM GPILGKIADPGLARELSHPFYTYDGST ENR/YRGNPALLRPTPMKFFPYEGWLHI SSGSLNRLKTSQDNFIFFKESKG
2005	15906	A	2020	205	377	NIYENLVFCWQVCGVGLGCTVCINPETS DE/WPGAVAHACNPSTLGGQDQITRSG DRE
2006	15907	A	2021	3	324	KRWGR/LNRAPNRRPYETPMALREBDQ CHICKELHIKTVRPHCTPIRMAKIHTTD NPQSWPROGTVRLIHCRRGKTV/R/PL WKTVRQ/FL/RKLNIPLECDPAVLSLCI Y
2007	15908	A	2022	2	382	RVSQDGLNLLTSRSTRIGLPR/KWDYRC EPPGP
2008	15909	A	2023	1	421	RWNPGRGCSSELRLHYCTPTWVTERDSI SKIAKNK/NNKRPNNRC
2009	15910	A	2024	339	3	SWDHRVLI FVELVOTGFCIHVAGLLEL LTSQSQSAGIAGVSHRA/GQKHFRPEH RFLK/GFVFRDRVSLCCPGWQTPRLKQ SSRISLPSKSWGPATALDDSSYLEEMVL S
2010	15911	A	2025	2	146	NTFGRSRQEDHIGPQQAQCSLRSHHCT PAW/VIEQDPVSKKKPKP
2011	15912	A	2026	3	380	RLGSGGISIHNGR/LPGFRFPSCSLP PSRMDTSLR/PFVFMVGRPHLGGAG LELLTSQDPKMDYQD/DHCTWP
2012	15913	A	2027	32	296	DYMSLNI/VHSLVLAETDEGLP/TVST QSAGITGISHCARPWIPF/CFFFIQRKK TRFVAQAQGGQGNPGSLMPLPGFRGPP CLSLT
2013	15914	A	2028	2	187	FTLLPRLECSG/MILVHCSN/PGLRWS SCLSLSSWNYTCVAFPIFYFIFLTLN

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1014	15915	A	2029	197	3	GGTLNC AAGLSQAGMOWGDFGSRHLPSPRFF CLKVPNNNDYRHGPPRPVGIFFFSF/LV ETGFHHPGQ
1015	15916	A	2030	88	362	KFGINLKKKKKKGQPNQNFPTSLFFP FFETESHSTIQAGVQWRDLSPQLPLPPG FKSLPSSWDYRCLPPCANFCIF/IPDS VSLQWQW
1016	15917	A	2031	7	131	GTTFMARPQEGCGSEPRSCHCTPAWTV SETSPQKKKKGLL
1017	15918	A	2032	1	343	LCESEPLCHCTPAWV/TGDSVSKKKK KKKK
1018	15919	A	2033	243	14	OKLAPNPPQAGNRRVPPHPSMAFLT KIKETALKEIQNHKRQPIAK/TILSKNR VGSITLFSKIHMYTTVIKTI
1019	15920	A	2034	238	3	FLALPKVLGTIGCVPPHPSMAFLTTE DTALKPIONHKRPOLA/KPILSKNRAS ITLFSKIHMYPTVIKPLRVST
1020	15921	A	2035	345	2	LVKIKENYVMTANPISIPQNDQGV SSCKSYIFRNKFLYV/LAAMDID/SSNG SWQSEWKTFWKGFILDGIRNTDSDWE VKISTLTGKKKLPTSTDDFKRKTIV EDVT
1021	15922	A	2036	1	140	GRCC/HELRSRCHTPANATRAKLKKKK KKREKTKQKQGLGWAF
1022	15923	A	2037	199	348	RSSNEGGRDCVFCGDRVSLCLPWSAV AQLWLATSTSQ/VKLSLHGL
1023	15924	A	2038	3	193	NGLNAPIKELRLANWIKSQDPSVOCIQE RHLTCRDTH/RCYLKG/WYKAF
1024	15925	A	2039	116	337	SKLKLRLRLCGHWQAPVATQGEVA EHLNPG/RSPNATQRTVSIKKKII LRPANGK/CHQPSW
1025	15926	A	2040	368	252	VFFFFALFYLFYFFFFFFFFFF QFLGFYRFKE
1026	15927	A	2041	204	399	VSSHKINGLTVCSYFPFLSLLPSEES ACFPFAFCHDCKPPEAS/SVNLPPKQVE L
1027	15928	A	2042	103	356	NHFSPPQPLPPP/PLNPPPPPTPPP PPPPPPPPPPPPPPPPPPPPPPPP PPPPPLSPPPPPSTPP/PPPPPPPPPP PLPP
1028	15929	A	2043	3	344	LYNNKASLAHLFAAMPTVYFRPTVE TYC/SGKKKIPKILLIDNTPCYPRAL LEMCREISIVPAPATTISS/LKPMQGV IVTFKSNYLRNTFQAGGKKKKHERKK NIIS
1029	15930	A	2044	2	349	PRVRKSPGPGFTANFYQTKELTSL KLQPKKKIKKGRNPPNSFYGATIPRIP NNMDLSKK/ETYGPSGRNMAKIFTK FLAGHKQSGREHHDRQKFPQIQGG FHGN
1030	15931	A	2045	280	462	CXFFLVVVLVWCVLFLVUVLWLCVFG FVVCVVEFCXGCVWFVFPVWVLCQV LGNC
1031	15932	A	2046	3	284	PSPSFSLILPPSFLFPSPF/SPPPPS FSLILPPSASILLPPCTSLIHPTLSQ LPPLPSFYLLPTSIHHLPTINLPTTS IQDSTPQCSK

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2032	15933	A	2047	95	1	GRVDATLAHCKLR/LGPFTLFSCLSLFS TWDC
2033	15934	A	2048	211	1	EPTIMTGAKGSSQTTNYHMLQSLRLIN VRVDFFFFCTDR/SLSNLPLRLVNSKI PAIILPHPPQVLGLQ
2034	15935	A	2049	35	266	EVRRPSTWOPPRLRSEELRL/QPFRLG NIGFCHVGHAGLKL/TSSDLPTLASQSA GIT\GHSYRASEDEKKESSMS
2035	15936	A	2050	281	3	QSNFKRALLSILKATYRSNIPTK/VF MTFPTLI/ERVIPKFRNLKRLRIKAVI LSKNKTRIRITLSDFKLYY\IAVFVAA WYKKBLSLQMW
2036	15937	A	2051	251	12	ILKFFFLKFLTOKRPPSLEKTHFFLPAP KSLFWPPEKLGOKKVFFFFFTLRQG L/NSVSQAGVOMENLGLQLPLRLR
2037	15938	A	2052	2	325	ADHLHPQVQDQPPQGNKPTPSPLIEK \LAGCGGHPRLRENCNPGGRGCSEPR SRRCPTAM/VNDSKTARKKKKKGVE KNECGRKVMV/LQPKAKVKPWGEL
2038	15939	A	2053	3	166	SLLLEFVBCNGAISAHCLHL/HNLHLP GSSDSPASASQVAEVRGSLPRSSSLA
2039	15940	A	2054	227	3	LNENIGRTIGMSHARLILLCB/VRYS ITQAGV/QHDPGSLPLPRVFKQSFHS LOSSWDRCAPRLAIFVVC
2040	15941	A	2055	301	0	QRKSHMFLTNOKLEHKLSEEGMSRVE TGQKLDLMC/QVSQAVNAKKEFLEKIG DTSVHTQMIKQSSINVDMEKGVIVWIE DQAP/HNHIPLSHLLMKAR
2041	15942	A	2056	1	109	RPLRLHQENRLNRGSGYSEPKLC/HL CTPAMAT
2042	15943	A	2057	313	250	PPPPPPPPPPPPPPPPPPPPPPPPSP/ PPP
2043	15944	A	2058	134	2	EKKRSVA/RLKSGAISA/HCLN/CLP GSSNPPSASRVAGSSGA
2044	15945	A	2059	120	326	NSLVADME/KVLVNTTSDTSHNPLSQ S/LIQSKALTLFNSIKAKRSZAAEKI EASRDWMRFKIKQK
2045	15946	A	2060	102	413	ERTGFRHVGKSLFFWTSGDPTLASQS VGIT/VHEPRTRPG
2046	15947	A	2061	311	1	FFKQRFCKSGCKTPGKRGPKGLGANO FSGPTPLKNGVGSFGPKGGFFPPPGG FPAGRPKWLITLKGKGLLRG/RYPKK GFLKPLIGDSSPQAPKRG
2047	15948	A	2062	229	380	WYDLSGLQPMPLRFQASRVNLPKSNWY RHPPLSLN\IVFIVDTGILHW
2048	15949	A	2063	142	383	POSFSTHWQLLQKESAGAVSCVCT S\VCVCVCVCVCVCAGMVCVGA/CPC VCVCAGA/CLVCVGA/CLVC
2049	15950	A	2064	408	200	NLTQIKALTFFSSIKERGDKSTE/EKF EGRGMFVRFKRGHLNIRVKHRAANA YAEACSLSRSS
2050	15951	A	2065	348	3	WSPSPSCVCVCVCVCVCVCVCWNSP CCPVCVCVCVCVCVCW/CFTM/CAGVC VCVCVCWNSPCCPGVCKEWSPCCTS WSLKLLSSGNPTTVSSQANITGRSH ANPAPA
2051	15952	A	2066	73	286	NLTIRGLLESHTLIMRYGYCKSYTLMSR DIPSAINKWS/IPMPCSSRRLLVMSA

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2052	15953	A	2067	329	0	VLKSLINRFNAKDVGH PSSTFLLPFRPPPPPPPPPPPPPPPP /PSSSSPASSPH
2053	15954	A	2068	221	3	ELKVLHCLARDFSLQSSIMKVLKILKILI LSVCVCV/VCCVCVCAVCVCV/VCSVCVC /VCSVCCLCVLCVCVCLSC
2054	15955	A	2069	1	167	GTRENPINPGGGGCSERP(SCHT)PAMA TKSETT.SQKKKKKKKISNYKTPFKSYRI
2055	15956	A	2070	2	354	ARACLGLPSSWDF/SVNRFRHVGQAGL ELATSGDPPTSASPECHDCRH/DHRTWPL LL
2056	15957	A	2071	20	341	CIVTVNTRGENINICWSPDGTITAVGNK DDVVTIFDAKTHK/LKONSSSS/SEVN EISWNRDNNMLYFDNGCINLLSYPTT ESKAIYKRPPIFHVHVUCLDPROVLS
2057	15958	A	2072	353	58	LQLLTTSDDPASASKGAGTADGVWTFQ/ SLNGAQGVQWRDLGSLQPHPPSRL/LL ASQSARIASARPPPLRSGSEERLCLAAH RLGCEERLCLAAQSGK
2058	15959	A	2073	1	338	GSRLGRVCINLYRL PFFFLSGQWINTFW LFLCLVCFLDRVSLCCPGWFSSTGFRK SSCPSSLRSRWDYRHPQHLASHTLFKKL /TILPR
2059	15960	A	2074	1	322	GGGRKAGRARGGGGGQSGSRKKRRKGG PRTGGABGGRGAGETPGGARPEREQGR GRHSERQGP/ROTGRPKTKIKQLSQNK NT
2060	15961	A	2075	450	225	TPVVRGCS ELRS CNCTPAWVTD/ETLSQ KEIRGGVKIGWKRRRTRIISLHLPQSH KFNNLETVKNCVNHFCRLAT
2061	15962	A	2076	2	470	TPGRKPHEPTTKNTQPPFTLKK/PVTVLP /TTKPKTKNTTPPAPPMQKQNHHTK PTTCNPKTKQKNTKNTVTKQKQNTN QNPKTOTQOKTTTOTKP2KKKKKTADT TSPNPTS2KKIKKLAEP
2062	15963	A	2077	304	1	NSATTPCSPTA/XPHPTPTTPPTTFTFP TCQHSPPPTKICQAPRPTPPVAHPPCP RKIIPKRRKHP LAPQARRDNLNYPHI INRGRVCCVCCVCCVCA
2063	15964	A	2078	167	1	TILQTNSTWNVLLMGAVAQAC/NSST LOGQGRITRSGDRDHGGHGBTLRA
2064	15965	A	2079	3	364	HETRSRHSCAWCSANMRAAVASRCPS /IPVTPPOCLYWP/WKVPLOCPDPL
2065	15966	A	2080	303	2	SRKGRPSGHECPFLGTS5SCRHVASCTT RTPRRLCKS QLDRC5 PLKERHEKFLGSR5 VLSAMTQSGIY/WQPPPEFFKCTCSCLN LLSSWDYRHAPPRARA
2066	15967	A	2081	4	326	AGITGSHRAWLFLYFLANKFAFTYGLV LNFFLAKIQEPSLG/SGSGP/LSCNS
2067	15968	A	2082	1	343	PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPSSSSPPPPPHTHP
2068	15969	A	2083	330	88	ACTDSIISRTHGELHOLCKQKSNPNPI KKWPKDMIRYPSKQDVTKTKMNKCS LIIIRMQIRSTMRYLLTVTRTPHS
2069	15970	A	2084	1	340	RVRSHQTHLQALIFVLLVQGFRRHDGQ DGPDLL/NLVIIRPPQPPKVL

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2070	15971	A	2085	2	348	ARALSLGANAAGNFKLRPLLRYSQNPRALEKNYAKYTLPLVLRHMESELETAFTETCFTYFVKPTVETVCSERD/1/SYKALLIERALGHPRALRMEYKDISIVEMPVNTISILQPMQ
2071	15972	A	2086	369	2	KGLPPSPANLEFLSVY/NGFPMPTLRLLISCPCYPPSPASPSAGIRGLNPPGMPPFFYFQKFRVRFVLAARNTTFGVDFYSILYLYGCSNLYRLLSALYFVSVVFVLTGTEAMVRA
2072	15973	A	2087	314	3	LLESVGPTRRSRPFKGLIGAILLDPFYPGLSYSDLLPASASPNAGRLPFTFETGSSIS\TQAGVQRHHSGLQ\LRSSYLSLTSSNVYRITPHIPANICITFSRA
2073	15974	A	2088	330	16	CPCFFLSALSIVNGCFAPVVGCV/NNCVCVFVVVVCVCLGCVNLCLCFV/VCLVGVCVVFFGGLCCVCC
2074	15975	A	2089	1	337	GTRTFLPFSYKDFCEV/TWAILPDNFGSSSNOMLNFTSD/PVHSSGNKWLSSPNNRPPYYSTATPHITDPTPLHSPNPNSSPSPSYPLSDSTICQTPTTPTTTSHTL LTS
2075	15976	A	2090	350	84	QRKSNRKRTERATERRDESREEKAGRKSGENQEKRNKQOQRQRSDRT/EEBKEBAKRREHKNPKKKRTKPPKQKKRKBKKTDMLSN
2076	15977	A	2091	1	355	SDPPTSASQAGITYVSHRWFLLEFSGTSIRLAGKPGVGLVETGK/SVCGGGVTKTMHRECHGVPECCSSQAGSSLPFPGEKRFESCLSLPSSNDYRLLP\QNFCTPSRDL
2077	15978	A	2092	27	345	ASTPCLKRRKKKKKKTKGKPPV/GGPKPKRGSGGGFPPTKRLTGGPPQGNTPGGVS/GPPKGGDPFSP/PPCQRKSPPFEKGGKKGPPPNRGVREKGFELKIFQOK
2078	15979	A	2093	3	301	REHVAQAGRLKLSLSDLP/LASPKMDCKR/DYCANPHILFISGLYVFFPLPMSPHTHTKYTRTFPHYAHRGCACTLNLLLRQFQCHFFRGVVPDP
2079	15980	A	2094	76	342	WFXXF FFLLEVFVVFVFCFVCGGFFFCFPCCVNVPVFGCLFCLFVNFPCFVFGFEGFNFFVFLVCLFVFCFPGCFFLFPCFF
2080	15981	A	2095	115	325	MDRKKIRGGGRQGGKECKIHCKKLSPGTRSYPVEN/F/VDTMYDIQPAYYKLNLDLTNADPCAYRLLFDQN
2081	15982	A	2096	80	227	SLGLW/CHLYSHSPILSFTHHTHTHTHRRRRRRRRRRTCTCGVDA
2082	15983	A	2097	308	1	NSTVIMBSVATHVYTRTFTEAQPTLAKSNWPKPCPSLLEWIKRIWLYTYCYVYICVVCICVCVCVCVCVCVCYIYIMSYYSALKRNEIAAFAVWIRA
2083	15984	A	2098	2	361	ARACLGLPSSNDV/SVETRPHRVGQAGLEIATSRDPPTASPECRDCH/DHHTWPLL
2084	15985	A	2099	1	221	LLWRIRHSHNLNGLGGRCSEPRLIHICTPSWMTR/GKTPSQKKTKQPMNQNLCLKVFGNIGVREITNGIKLS

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2085	15986	A	2100	186	2	ERVYVCVCVCVCVCVYQCLPQIRSL/V ASSLKANARVCVCVCVCVCVCVCVCV SLWHPLTA
2086	15987	A	2101	305	2	HNILLQSILQSKALTIGNSMKA/E/RG EBAARKEASRGWLMRPKE/RSHLCN/ TKVQGEVASADTEAAPSYYTDSHSKI TDE GGYTKQQIFNVDKKASYNNMS
2087	15988	A	2102	6	166	EQTALSTLARARQKEKIGIQIRKEV KLCPFVND/VVLVLENSKDFLKVDA EIRNNKPGHVMUKY/NPSTLGGGRQIS WQGEFTSLVNRVK
2088	15989	A	2103	53	176	FAIVQGEHAKLTSGDFPALVSGQMYYT GVSHCAQFIYGDFTPLSIL/D/RSTQ KINKIQDLSALDEADLLDITYRTLHPK /STEYTFP
2089	15990	A	2104	3	267	PPKHEGSSPATQSWMENDPDLRESGPF RRSNYSB/LREDIQTIGKEVENFENKLE ECITRIINTEKCLKELMELKIKARELRP ECISLR
2091	15992	A	2106	3	170	GFHHVDAQLELLTPQVIHP/LGLPKCW DYRREPPCLASPHPHQIATSQRRHREAK SARGPDGPTAEPTQYFKEELVQILLQF QRIKGRILL/KHNVKPSITLIPK/PG/ RDI TKLLTRSPCVSLCPVLSPLQSLQ RPSSLGMSILSHVCFPSVLSASAHPHVHL CPTCPTLVLSGSHCVCCVSLFFP
2093	15994	A	2108	3	370	HNWNNKGGWGSTIYSKYLTPKPMRLP Y/C/SQKKI PPKILLLFDMAPGHFVIM EIMKMEV/VMPVYTFP/ILQPDQRV ILTPSYTLRNTFPHKTIAINSDYSQGS QSQSLKTFWKGIVL
2094	15995	A	2109	1	213	HFFVENESAPG/PAAGQLTLLGQNA AGDFK/KALLVYPSNPCLPKGSPKNL PLVNCSHKAWQLG
2095	15996	A	2110	391	3	KKKKPNPHKKIKKRWKKIPNABNKKR AGVILHILDRIDFKQQTIRDRK/GYTT MINGTIQOEVIITLNIHAANTEAVRYIK QVLLKLTTELGPNTIITGDINTLLSL NRSSRQKIQQTLLDLCNI
2096	15997	A	2111	188	363	PONTHTICVVCVCVCVCVCVCL/CVCPCV FPFCILGGFMCGCWDCFILPCFYGVG FFFL
2097	15998	A	2112	3	340	RMSALDELKQPTLVGDTGDFHAYDEY KPHDATTNPSILAVAMPAYQELEBEA IAYGRKIGGSQEDQIINAIKISVILIGA ELLKMTGRVSTVDARLSFD/SDAMVA TA
2098	15999	A	2113	11	305	PLPDPCLPFWHLLGKHNVTIN/CGRN VIT/GYPSHRRITLKISIRKISRSGS NTWKLNNELIYPTKDEVSRETRIKYLE LNINENTNF/QHLNDHK
2099	16000	A	2114	3	387	QTNH/NIFLSQHLQSKALT/NMCKAE RSEDAAGKFRASRGWPMFKKSSY/KV QGEAASAGVRAVAIYPLAELIDE/GCY TT/QIPSVFOTAFWKKKPSRCTM/REB KLIPGLKASKDSSLLRLVIAAGD
2100	16001	A	2115	152	393	VYCFICWLVFFFCFCSVLILFPMV/V/CL CPSFCFLGPFVVVSSFPLICVFFPIV

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2101	16002	A	2116	2	373	IGCLGLCVVFDLFLVLVLVLCFFVS ARACGLGLPSSMDP/SVENRPHRVGQAGG RIATSGDPPTASAPRCWDCRH/DHHTW LL
2102	16003	A	2117	3	449	HEFDHMLQAHRAHHLAIDAYHRPERTY IPKDKYSFLHDSQTSFCFSDSITPTFN MEETQKQSNLELLRISLLLESWLEPVR VLRSMFANNLVYDTSDDYHFLKDLSE GQTLMGRARKKHCKRTVQNLKQTYRR/ DTWS/SHNDALL
2103	16004	A	2118	146	15	FFFYFIFLFFFFFIPLFFFFFLFFFF FFFYFIFLFFIYSLLVF
2104	16005	A	2119	406	3	LFSVNRITGFYSKMLRRTTATRETSIPG PKVSKOKLTL/LGANAAGDKPLKPMILY HG/ENPRALQNYAKFTPEVLYKWKHAKL MTHLPTARYTEYFKPTVETV/IILLID NAPTHQORALMEMYKKNVMPRANTTSI
2105	16006	A	2120	109	396	YFYFYFLVLFYFFIFLFFYFFFFFLILL FYFFFSFIFFFLFVYFIPLCYFFLFF FFFFYLFYFFFFFIPLFFFFFFFF SYIILFFLSYII
2106	16007	A	2121	15	413	IVLARNNTFWLSPLFFVALGILVILKGV KIYFWPLEYQRLKMPVSYSFHY/PFLG SLLFLKYGFHMLILL/CIFIIIMCFP IKYSFFFCCLYHFFFSYLFYFLIF/ CTVILFFFSFLGLFLSSYCFPF
2107	16008	A	2122	1306	429	SSSSSSSHVLRITIKORDFKILEQRQVV LSKBAQALCKEYENEDFPLKLENTS QPSLALVLLRDNGLOYNKOLLSPRTVE ATEYFPESLCAQFAMDSLFWNLQYGSDS LETARREIQHFPLQSTLGLTKPHATSE /HKRGPSMVMILTKNNVAERNRLMGPT DPERAKLLS PDSITRAQGISLKNIVHG ASNAYEAKEVNRLFDPEEN
2108	16009	A	2123	3	206	LRLROENHLNWRGGGSEPSRQHCAA W/VSNSETPQKKKKKKKKKKKKNL PMS ALKKTYSQRGKLF
2109	16010	A	2124	23	401	IASGRPPFFFFF FFWPPPPQGVPHFS FLKKKKKRGGGGKSLPPGKGNPK/ WGFLPFPPLPFPKTPPPPPFFYKTPPI FPQGPFGGFLKFTPPGGGGNPPITLLD KRGVLGPPPPFWTH
2110	16011	A	2125	3	439	MFVSLTLTTHSLFHSFOPHRCKELST LCDGGLRDHLILPTSICPITR/DKSC PBGIC
2111	16012	A	2126	1	213	HPFVNRSAFG/FICNGDLATLLGLGNA AGDFKLKALLVYPSNPFCFLKGSFKNL PLVWCSSHKGMVQLG
2112	16013	A	2127	104	419	NSFFFRKELNDFRLGKKTFPGGGRFF GHTPPNKALGQGNKFTFGRGQTFSNN GRKKSVSFWISIRKILHRAILL/ALACK NCVVELNFGQKRPFPFPPKRF
2113	16014	A	2128	399	140	PPPPKIFFPPPKGKFG/EG/VGPXFPFP PKKRVFSQKPPRGFFYPPLKKNNPFP PGNPGPPRGFFKPPPPPPPPPPPPPP FFFFF
2114	16015	A	2129	10	457	KTSWTCVPPVVPATQKAR/AGGSPBFG RSRL



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2115	16016	A	2130	409	0	PPPPSPSPPPPPPPS/PSPPPPPPPPSP PSSPPPPPPPPPPPP/PPPPPPPPPPS PPPPSPPPPPPPPPPPPPPPPPPPSSSS SSPPPL
2116	16017	A	2131	317	177	PPPPPPPPPPPPPPPPPPPPFLRLQIFFF FLPILIFLFLFLFLFLFLFLFLFLFL
2117	16018	A	2132	3	542	EPWSVAQAGVQWRDLSLQQLPFRPRFR SRLSLPSSWDYRRLFAHPANF\QFLVET VFRHVQAGLELLTSQHLFALTSQSAGI TQMSRTS, R, QGLFFKV
2118	16019	A	2133	146	439	LKSVTLAKTQTQK/CPITNSGVDKCPS TVKMKKQWY/FTMEYGAJK
2119	16020	A	2134	95	1	QRVDATLAKCKLR/LPGFTLFCSLSLPS SNDC
2120	16021	A	2135	2	380	THTHHTH/THTHHTHTHTSLS
2121	16022	A	2136	4	337	KRNKKAMTVHLPTAMPBYPRPTVET CSEKKIPPKIL/LLVDNAGQPRVLVEM HKEMNVVTRPANTASILQPMNQGISTF NGYYLRNTTFHKAIVADISNSSDGFQNK
2122	16023	A	2137	2	356	PVSSSQVRASVYLKKKKKKGPPPBSTN TAGKKPQCSFSGKG/PPFLISPKKEP I\SLFNPGPCTIGKKKPPHFAJNGGP LQ/RPPTQGGGRGKKKKNNRPLSLGL GNRSPPKPPF
2123	16024	A	2138	2	357	PLGSSDPPPSASPVGRATG/RVFFFFFL VEVVSHYVAQNGLELLDTSNPPAVASO VRITCVSHRTWLLSPLYLKIQVCVSK/S PELQSEDKSLKK
2124	16025	A	2139	379	16	LLQVRCFVSTVNRGSSCQRTIQVYYQBE ALPSEFLSLPFL/PTTKNSRWKDSN VKDKTLK\TLLENLQMLNIFFTYQLLN LYLHPSQLELONSFRALQEGNLIITFI QRVGRPTDGL
2125	16026	A	2140	73	411	NYLLNNLPPFFFLERGLTFAPRACGKG NLT\SNRLGPPGNKPPPPPKRP\QTPK PTLKEGLGFFFKTIGFPPGAQKPELEG LRGPPGLAPPNGNKGNNPPGPKLTFN G
2126	16027	A	2141	46	421	AGVSWRDHSSIQCLTSRARAV\SHLSF LSSRDYGPMPPPPKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKQ
2127	16028	A	2142	26	479	LAYLLPSVMYKQNNRTLLQSTSNKGL ICRIYKEITLQNHKKTNPIFFKQVKKK KHPTREGAIQVANK\HIKKKLNILSVYGN AQKNTMRHYHTPIKMKGGCALMLTPVM CQEGYILKMYRGWTPYGRVVGRTAP ALPFGKTPPD
2128	16029	A	2143	9	166	QNKLLRLTKKKKGQNGQNP/IYNDKGD ITADPTQASIRVHKL
2129	16030	A	2144	1	328	LEKESRPFPFPFPFPFPFPFPFPFP LPKPLAGLQLEPPEVSLTYLPLKLGAC RGGGVRLAAPSPPRIYLMGMCQDRIQ KIDIVVQKSRKEDCLFAGVKALKKA
2130	16031	A	2145	1	440	KTLFRLSNQWVR/CYISSGLIDDERFEM ALTTRHPRSGITAPRPPQPPGRVGIPE PTALSPPGPPPPCSTPGRCQVPSLER RRKRGRETPSVGRGCGGHGISDSDIFF HLNFCLAHPPDLFVFCISLNQLYIPE

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2131	16032	A	2146	23	422	KKKKKKGR IASGRPFFFFWGAFGGBEGKKNFPGWR GGKKKIRGAPTPRGKGNFPKPKWKKKGG APPKXNLGLFGKKGAQRGPFPGWFKTPGKK KSPDPGPKKGIKGRGRPGPPQIPFPKP FPSTGEKNPLGKKIPNWRLLFN
2132	16033	A	2147	3	372	KKNTFFFLTPRGFPFPPGRLSPPPKRA TPPPPPPKKKKGFPFKKKNFPFPPGGG PFP/LPGKKGGYF/W
2133	16034	A	2148	363	1	FNCRWFETKSHSVPAQAGQWHSFGLQPL LPPGFK\EPSCLSL
2134	16035	A	2149	2	361	FFFFLVETGFGVGGQGLEHLTSDPPTF GLPGWGYR
2135	16036	A	2150	387	2	KKSFYVSPARVQWQDPNPPFGSNNF PSTTPPKGVIRGPPPAKKLVFPITKG \FQIQRGVKLKSLPQ/CDSPDPAPPKGG VSGGNPPAPFFFFFPMESHVSQGVV QWRNLGSLQPPSPGFKQ
2136	16037	A	2151	23	421	IASGRPFFFFFFFPLGLGRVFPFP PCGGGCPNFPYKTFPPPGKKCFPPPS KGGFLTPPPPPPPFFFLKKGVLNGGG GGVKISPPGGTFFLPQKGG/KKKGPP PFRKKLPLFFPDGAIQRPP
2137	16038	A	2152	3	366	VIWAHCIFHLLGYTDRCIKKKKKRFP GERMOLKNFPPLGKCKPPPLPMPWS IEKPPRGFYLGAAAPPKYFLLKP/GPP FFKPPPKKKGASPLKCKFFKGGKS PPFFSDFTS
2138	16039	A	2153	423	253	FWGGGAPLFFPPPKKFPFKNPPGVFFS PKKKKLFFFP/HEVNFPGPKDFFKAPP P
2139	16040	A	2154	287	1	KBNKKKQPKKKKSKKISTAFYNYKLN NINTF\FAFTFTFTFTFTFTFTFTFT FTFTFTFTFTFTFTFTFTFTFTFTFT QLMQHSA\TRD
2140	16041	A	2155	433	2	RRVLFFPPL/HFSPDPLPSPFPFPFP PMKFPSPFPFTFYFKSPHPP/HDPQV VTSPPTPMPFTITPPDHTSPSPFPFP FTFTFTFTFTFTFTFTFTFTFTFTFT FTFTFTFTFTFTFTFTFTFTFTFTFT VMSRTRG
2141	16042	A	2156	69	606	LWNPPLSRHAYRWGPGPTAPRGLGHV KGPASPA\PCGAAGSTAQG\GGGAAC LPGPAAGAVTVVPAGGGGATGVLQR PAGAGQPTQQGQHDHAGRVLWGHGIRP GAHRGPGCAP/DSAPRAGGCG
2142	16043	A	2157	449	0	SSGSSSSSCSPPPPGGGVGFPL/YKPPQ KKPFPFVGGGFPQKKLKSFFLPPPP FFLGCGGPPPPDKLGFDPKKK/SF PPDPKAZLPPPPPLPPPPSPQPP LF
2143	16044	A	2158	241	5	KKFSFPFGSGGGFSGSLQNPFGTTP FFCLNLGKKWQGRGPPPRNPF/SPFP FFFFLVETGTHHLSQDGLDLTS
2144	16045	A	2159	434	2	LGSASQAGSQRDPLEAVCFPSDQL CARRT\TALFKAVRGHLSLQRLLSF\V CLCPVPSGAYRGQASISOGGLHPVOA SRLCLCPQAWAMAGAP/PPASLQPCSL

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						ISDCCASNQDSSVGVGPSEPRAGYNLLV RCFLSP
2145	16046	A	2160	448	84	FLAGFFFFFWPPPPSPKQKAL\QKKI FFVFFSPSPSNQKFFFSFSGGGPPNPL FKGGGR\FSPWFLFFFFFWFFLVVFF FFFFFFFFFFFVFFVFFVFFVFFVFF FFLGKCPCKYT
2146	16047	A	2161	3	156	RGCSFRLRHCTPAMV\KSTVSQKKK KFLTLGGKT\KINFFPNRAGPTFP
2147	16048	A	2162	412	37	PHSPFPFPFPFGAVFPFKKKKSPFP PTPLL/RGGGPPPPFKGPPQKQK KGGFFSPFKKKKFFGGGPPGPPQK PPPPPPPPPPPPPPPPPPPPPPPPPP FLRTLNRKGRGRI
2148	16049	A	2163	5	370	QSSCVQVWLVVPTTQAEAGGFLEPRS ERLQ/CSHCTPAMA
2149	16050	A	2164	437	36	FFFFFSBAESCSVAQGVQNHARSLPQ LPPG\SSDSCLSLSSYMCLSPRTROS
2150	16051	A	2165	3	623	RGQPTLVAVAGVQWYDLQSPPTGPK RFSCLSLPSSMNYRHAPCPANFVLEE TGFLVQAGLELPTSGDLPASASQAG ITGMSHCA/RPKVCSVHLFF
2151	16052	A	2166	337	0	PPPPPPPPPPPP/SPPPPPPPSPS\PS PPP
2152	16053	A	2167	350	156	ABATSKIRCKQCYIMLAGEISGRFLQPL LQRLQENHNLNPA/RGCSNPSRSHRTN PTWYISKSFIA
2153	16054	A	2168	1	337	DERSLSQRSKSWSYNGYISDLSTARHSG HHKKR\TKKK/TKKKKKKKRGPFPKKKG PLKTRKKPRGILLKARPPWGGPPPGFFL TSGGAPPVFFVKKKKKPLGGGGFLM G
2154	16055	A	2169	2	606	RVLRAVAHSEPDKEGKRPAGVSPRG VKRQRSSSGSGKGRPSQEPPIAPP HRRRSQPP\HPGPIPTNAPTVGVPE PLLLPPPPPSIAPAGBAVAPLPAFST SALFTFSPLTVAAGPKHGKEREKHH HH\PAPMVIAPAPEI
2155	16056	A	2170	311	2	GLQPIGLSGVKQCMACVPETVCVCVC VCVCARAHPTVCQGVPESTQCVCQMV C/VCVWACTCVPVCMITCVGVGASVCMQ RNLGRWAWENDATRQRC
2156	16057	A	2171	78	337	NTPNSTYKAVSLKGPITGTFLPNTPGKH VCVCDTYLCVYQHTHTHTHTHTQAFP HT/HIYHT
2157	16058	A	2172	2	278	KNRLNPGGGGCKLRSCHTLAWAT\SE TFSQKKKKRGRKGRKKKKTIVYTKI EKGNLHPTGSEFIHPCKSSSVQVALS ASYKCSST
2158	16059	A	2173	2	365	FWHVOGGLKLLTSSDDPALGLPKCMY RRE\DCAQPRVKS
2159	16060	A	2174	195	389	FRVFSKLKYTYDFRRLSLSCRWSTT PGFKRLSLSLSSWYKRRPPCPAN\F CTFSRDGVSP
2160	16061	A	2175	23	374	IASGRPLIFFFFFFFFLFCRGGGDPF NPRGRKGGFLKFGPPPGGKGNFWAPP PGGGEIKRTPPPPGVFFFLKKGFSFG GGGGKK/PPPPGPPPPPKGGGKKKK

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						TRGFLF
2161	16062	A	2176	2	158	FFFLKQSLSVTQAGVQW/PVDSLQPLEP RFRKFSCLSPSSWDYRCVFPQCFAN
2162	16063	A	2177	340	120	PRFHFLLASPSEMSQMTVLRKTTVPASEC AYPKLEPFFPPF\DPGRGSE\FDKLGVNH HPLFPLSGEPLMLHONTH
2163	16064	A	2178	3	256	YLKRDENVNQKTLTLE/ERQKG/HLHD MRLCKBFLNRTSKAQYLAKKISQY/LIK VQFNFAVKDEPVKMRQASD/WENIFI
2164	16065	A	2179	95	1	GRVDAILAHCKLR/LGFTLPSCLSPS SWDC
2165	16066	A	2180	1	143	ARGERERERERERERERERERERERER RERVVV/REAAALSRWDKRGERSLFP
2166	16067	A	2181	1	304	ARGQGHLSLQRLSLSFVCLCFPTGGA YRGQASLSQGLHPRVRSWMLCLFNCA MALAGAPPALLPPCSLSISDCCASNQRD SVGVGPSKPCVGVNLLVM
2167	16068	A	2182	3	163	FORRSTSCGWDKARSQSRSPRQQA GHHS/HTHTHTHTHTHTHTHTHTP
2168	16069	A	2183	3	205	NFKLFCCKGFFFLRQSL/DSVSQAGVQRH NLGSLQLPLPAGFLQLGFPFPGSKDTHP GVQRHDHNSLQP
2169	16070	A	2184	228	88	WFRRIYDSFFLVZLFVFFFFFFFFFFF FFCVPTFPFVVFIQVYVYI
2170	16071	A	2185	287	3	SLFLATPQWFFQRTYLRKQKIVMLAQ PSKGLSIQVVVRGQLNSPVLKSQDPTP/ PRFKRFLCINFLSRWSYRIVPPRPDSFV FLVETGFLHLV
2171	16072	A	2186	252	105	VSISCHVQ/PCLITYCY/HIDGYSNIHL CTHTHTHTHTHTHTHTVRLQQA
2172	16073	A	2187	267	459	KRVPSSTWLV/IFFRGRFLKKGANFV PGCVLKGRMTLSLNPFPPLKQYSCITL LRIGNYRA
2173	16074	A	2188	170	15	RSVMKDINSFHSKENTQANKRTKCSA LVVFREIK/TMRCHLTPIRATIKK
2174	16075	A	2189	2	304	DVTISTCHASAKVGRVLPFDHYGRTIKQ TPYPHPRGMTVSVKQLFSTLVVRKHEFQ RNKKGLG/RRSCFCDF
2175	16076	A	2190	1	565	FPETESLSPRLCSGSAHSCHNLHPS SDSPASASRVAGTGTGACHTW/IFFVF PVETRFEHVSQDGLDFL/NLVIRPPRP KVLG
2176	16077	A	2191	142	382	NTPPLFFFFVIRDRVSLCPRNSGVAQF WLSATYASRV/KRFSCLSLP/SNWDYRC VP
2177	16078	A	2192	138	365	KQYHHOC/LLKKKKKKKKKKKKKKK KKKIKNKKGGGPFKNQW/BGQPRNWA GGV
2178	16079	A	2193	385	21	RGEIFFFXTRRKKFSPQGRGGVFPSP PKNFFFPQGGKFFGG/EGGPKVFPKKKG GPKKKQGGKFPVPPKKKKKILSPGGVIG GPPCNELKGAAPPPPPPPPPPPPPPP FETLVAVKLG
2179	16080	A	2194	415	56	PPPPPTAVVPSPPPPRFFSPPPPPVFF FRSFPADPPPLFFPPPSPP\DSFPP PPPTRCPDPPPTI\VPDPPVPSPPPPF FFFFFVFSLDPPFFFFPPPPFFFL FLFFPSRLM



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
2195	16096	A	2210	248	417	GILANCSIKDLISRIYKLLKQIN/KQK TNDPLKKQAJOMNRYFSQELQGVNKH KK
2196	16097	A	2211	213	493	GKGFYFACPGKIGALQSPFKGGPFFFF FFFLTPPPNTNYLNLKLIKSPICLPYF SNILGFYPSITHRTIPDAWVTA/SQSGP VLMRSIS
2197	16098	A	2212	159	413	LAPRVI FGPPKPPPPPLP FFFFTES SSVTQAGVQMHNLSS\PPRFKRFY/CIS LPSNRUYKRPHPANPCTFSRDGVS
2198	16099	A	2213	455	60	NPRREVGICPPPKLIVPPKQGVGFLS PPLKKKTFSAPWNLGPRDFPKGPP FFFFFLDPFFFFYTYIKTSAACRSP AQRVARRELPVPS\PPIPSICLAPAPR GPGSLCPRGSLGDNSSPG
2199	16100	A	2214	2	243	LTLSPRLXKQMVNACNFCILSSSDS/ RLR/QENCLNLGGGCSLRLRHCTPAN TTERDSVSKINKJSLKIFTCFFVDA
2200	16101	A		1	286	FSQRLRLPFC/SQGGRLCCESCPASPH PECLSIEMPGCWNNQDCAGKGLHYQ IVWVGLGNYEQVFPRTKRYSIIVQTSF ILWQSDLEIDR
2201	16102	A	2216	173	2	ITIFFFVRQGLTQAGVQNR/DLSGETLV ILPLPAPCSLQSSNDYRRLPHLENPC IV
2202	16103	A	2217	216	4	VYFSPMVFQVFLSSTHLSLSPFFWN YLFYLYFLYLYLRLKSL/DSVTQAGVK WBLGSLQPLLPFK
2203	16104	A	2218	14	228	KSSHLFDDILHRENTKSTK/NLLE LKESISKVTS/YQKSVAFILVNNKQAIK KTIPLTLASKRLIGSGQA
2204	16105	A	2219	244	3	EVLNQSGLPRAFTLRAKSLRVPRGC SRGVVPSANGAGTTRYLYAKEWGLGG GCSKLRSCHCTPVWAT/SETLSQKK
2205	16106	A	2220	162	2	INWVGNLFFFGDRVSLCHAGWAVAFSW PTVASTSL/VKQSSFLSPSSWNRH
2206	16107	A	2221	146	3	GRVDGVWRNPGSLQPPSP/GSSDPTPS ASQSGTGAHHHRLIEVF
2207	16108	A	2222	239	2	SYISKPDKFPDSDSPKIPVTVNRNRSF SFIFPFFFLPEKESHSVTQAGVQNRNL GVSSYWP/AGLKLITSGDPFALAS
2208	16109	A	2223	2	159	LNRLGGGCSLRSCHCTPAWAT/SES PSQKKKKKKKKKKGGGRNRSKI
2209	16110	A	2224	3	345	RPLFSLCSLSPSSNDYRVPFPPRA/NFF VFLIKT/GPALLTSSKTERQRLRCIPG FYGLPCREKRASERRSVG/HERKILFS FDFFFGGTSCFVTQAGVGCCYLGSPQ PPPPG
2210	16111	A	2225	103	319	FSSEYRNVTNFMMLTMSCSCLTLVE/C/ WBSYNAFTCLILLFFQRRCHLTLSPG GQWCSHSLQPTQPTGK
2211	16112	A	2226	2	110	FHHVQAGLELLTQNSIHLSPKCDP/ RIEPPHPA
2212	16113	A	2227	2	178	IFLIFTFLESMSHYVQAGLEFPQ/PKL TSRLSLSSWDYRPPRPLANTFAFALG GDA
2213	16114	A	2228	173	3	FIFIFISLFFIFPLRQSVLSPSAVQSR LQPPPPRFQFS/CILSLSSWDYKRVDP

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2214	16115	A	2229	333	1	HTPPPPPTFHSLCTEGAPFPQNT/PNP PRNPPIIPLSRSHTRANEPSSLTPRTHP HSRPPPIIHTHPNPASAPPGSRYPPR ARHRERPRERPTQERERERESVVCVV
2215	16116	A	2230	350	3	KKKDIFFUNYAPNTGAHKYITQILLDL NRDGP/HTITAGDFTTPLSVLNSSAESR CSRFPPIISPLSVGLRE
2216	16117	A	2231	277	1	QMHFARGHLFOALIPVOKPALISQCHSA SGSTQVSPFLSPCFWVENCNTRVLT/ PFCGAGTGSRSFAQAGAENCRGSLQHP PQIFKL
2217	16118	A	2232	3	335	ETRFHIVGQAGLEPLTSDPPASASQSV /GITGVSLRARPGE/SWSKTVCCNMS EPT
2218	16119	A	2233	29	448	CPSLEQAMHEAAIDEVKGTGYRLPHPE QLITGKEDANNYARGHYITGKEIIDLV LDRIRKLADQCTGLQ/GFLVPHSPGGT GSCFTSLIMERLSVDYQKSKLEFSIYP APQVFTAVVEPYNFILTHTTLEHSDCA
2219	16120	A	2234	1	365	GARLILVLEETGFHYVGOAGLELLTSS DPPASA/FPKCN
2220	16121	A	2235	28	460	DRLDIHSIKLGTGLQGLVFPSCGNLG /TGFGFTSLIMERLSLDYQKKALEFSI YPAPQVSTAGVEPYNSILTHTTLEHSD CAPMWDEAIYDICKRNLIERPTYTNL NRVISQIVSSITASLRFDGALNVLTDF QTNLV
2221	16122	A	2236	614	84	LAASLAACAQLSALAASRRMALQRLRK LITTEPGGSINIMRLGECETALSF TGSALAAVKGLEALQROFVEEDP/IV ROGKQLH/SPHFPKVIVASRLVTLKAG HPCPCCASTEIKH/AMFRVYCMASRVAVA LDKRTPLPRVFLDEVAVRVCGHIIQLG DTELQGHICHL
2222	16123	A	2237	1	393	GPWLQQLSVFRGSGTSAANDLWYHFIEL PYGHESIIMLIALPTESSTPLSALIIPM STKTIDRNMISIMVKKQVILPKFTAVA QTDLKEPLKDLGITDIVSSQGHFCQIT KARNLLV/SHILQKQK
2223	16124	A	2238	3	402	HVGQGVQIGKACWELVLEHGIQPEQG MPSDKTIGGNDSPNTFSETGAGKHVP RAVFDVLEPTVIDEGRTGYRQLPHEPQ LITGKEDANNYARGHYITGKEIIDLV /DIRIKLA/DOCTGSGQLGFP
2224	16125	A	2239	2	478	GRUGLHRIPVVTPLTSPFARGLVFSLAR GVENRNGAGPIKSYRPGSRLEHGNOSK GSLQKRTFIMETIDNR/MSKQLKQ/H ISSRUKHNRVAGKPLKPYRPTKLLRS PSILAAKLAQKDMNPLAPAFSSPLA AARAVSSALTLPPLPFCFV
2225	16126	A	2240	255	2	FLFVKPHQITSCPTKGIKSPFLVLCPLNF FLFWRODLAHPGSAVTQSWLTAASN/Y GLKQSSYFSLSSNDYRCIIPPHLOGKRP L
2226	16127	A	2241	365	11	EPPIPPGGKKKKRKPFPKTPKCKGQFK KSAAPFGG/GKIKKKGAFRKKKKGGG PPPKKKPPPKKKKKKNSPLPPPKHTP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SLFQKPPTKIPLFSPPLLFNLIFFFPPLSPFIF
2227	16128	A	2242	3	143	PNFLSPRLDCRGITINGHGLYLPGSCDPS/CLSPSPSSWNYRSTPP
2228	16129	A	2243	132	2	MSAHONLHLPSSSDSPASVSQVAGIMGACHIF/VFLVQTKPHHI
2229	16130	A	2244	334	43	TSKHKRCSISLATREMQNRRTTIGGHFVPTRIANIQPENAKYRQGLMC/MCMVCNLASPLWKTINHYLVKCLPYSSAIFTLG\IYPEEVLAASSVPGT
2230	16131	A	2245	312	2	PPSKLPKRNFPFFFFFFLQSL/SSVAHSVQWRDLGFLKPPPPESQZPSCPTLLSIWETQALSGDCATLHPGQRETSKHICVCVCVCVCVCVCVCICIYN
2231	16132	A	2246	3	230	RQAMVETSRECLLRPPQETKTRHVAQAGLKLASSDPPTSASQAGITG/SHHTWPQPLTFCPHAKSLPPTINOI
2232	16133	A	2247	2	214	GRVDLVTAQGVQMDGLSLHPPPL/SSDLP/ASDQVAGTAGRPHYANLIFF/VFVETGTS/HTQVNSGYDL
2233	16134	A	2248	3	139	EGVQGCCHNSLQPTPG/SSDPPPTSASIEAGTAGSHYHWWLIFFLIF
2234	16135	A	2249	3	160	EGVQGCCHSSLQPTPG/SSDPPPTSASIVAGTAGSHYHWWLIFFLIFCFEGDAA
2235	16136	A	2250	319	3	GQKRYRIFLCFFLPGMLVFLRWSLTSPLRLRESVSKKPSQKPPIKKPKFTPREFKEVLAKYGTKEFFVFPGLFVWFFLRWSL/NSVQAQGVQMRDPGSLQASPRP
2236	16137	A	2251	15	394	FVSFSFFSPFSLHFFSSSSFFPPLPSFHPSFLPSDRPSVVPS/FLPSFLP
2237	16138	A	2252	60	306	GREKILEIMADFLNLRDLNISIQVAQQIPKMSKPEPHYGRSSQORILKATREKOLATYKGSSTV/VSPSPQPTNS
2238	16139	A	2253	3	351	GSHVQDANLKLTTSSDLFASTSQTGTGTI\DHCTOPNPII
2239	16140	A	2254	150	2	RPRPDRSRIGAGDOPGCHSKTPPS/HQKKTKTSQANRHAPAIAGTQAEAA
2240	16141	A	2255	357	1	LNINLSLTLYAKINLKWITGTNVRHRTKFLGGKNGANLMDTRLDNAPLDTLSKALTKEKIDKLNFIKIQT/CSIKDLLGNLKRQAPSEKKILRNHISNKELVSRHKKEVPKLNKK
2241	16142	A	2256	397	1	FSLPPPVGQGGFFSSCKSPPPRFRAPFCPNPFRKGGNRPDPHKGKTLGFFFFFRQSFALSPRVEYNLCLGSSDPPASASQVGGAGLPPPAWVNFGIFFF/CFFLRQSRSAVQARMOWRILGSLQAMP
2242	16143	A	2257	2	132	TLTLTPRLECSGTIS/AHCKLHLPGRSHSPASAPRVAGCGGHH
2243	16144	A	2258	214	347	KISLITGVHRICEE/CFEHNKSRSTVQAGVQGHDSLQPPPPGL
2244	16145	A	2259	347	2	FFSFFFFSSASSRSVA/RLECSDTVSAHCLMLPS
2245	16146	A	2260	333	1	SDQWTHAIAFVLELDGACPSFSE/LRSTPSTSGEEVENFEKLDECIIRITWTEKCLKKLMELKAKAREPRESCSLSRHNLQKRRSVMDQNMNMRREKKPREKRT
2246	16147	A	2261	2	357	SPHSCSVYGIALLILFLYFLYKLAFAALLY



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2247	16148	A	2262	355	0	GLA LNS PLHE TQEP /SLASGSGPLSRNS
2248	16149	A	2263	348	35	PPLPSPSPPLSLSPFFSLPPPPFFFPF PLF /CPSPSPFFPSPFPF
2249	16150	A	2264	270	92	YFLKKGPSPPRGGGRKDRSLKQLTF GFKKP /SCPSFLRKW \ETRLCPAQKIF FFFFFLLMGFCYIAQDLKSSSQSGI TGVSYHIWPTFIHGLTMCLAKC
2250	16151	A	2265	1	417	DRPARRKMPFTYSRLFPFFPPFFFPF FFFFR /FFFFFPFFFPFFFLSRMSLM IFIS
2251	16152	A	2266	344	427	FPPAGVQWRNLISLQSLPPGFKRL SLSS /WDRQNPQLA /NRPVPTFDV VYVYVPLVHRRLRLRLDLTVLICI SLANGMEYLFCLSPATHLPLSKRPT YPAHCLPLYTPLETGSHSVETGQWCI I
2252	16153	A	2267	310	417	LIGLCEINLGAIRAKRVTLAODLOLA RVPTGTLSGLPLATAGFDKDKPHEG AAPILVR
2253	16154	A	2268	186	464	NSCLSHNQQLFLRLKMGVPTSAQEL VLHITLSGFSGLV /VGLVPRMESCVVO AGVQWRVHPFRFPKQPSMIS FPGSWDYG HVPPCPANF
2254	16155	A	2269	1	427	PEPSPLPDGAQRKQTKSKKWRICPLR KKKKKKKKRKKKKKKKKGGGSKKSRR GPKLTETNIIILIKGLIKMYRETEK KLLFGGGVIGPTPTQDIKREEINYLE AVGREKQRPISLVK /TNVA /HEATRTDI FRGYL
2255	16156	A	2270	399	44	ISFQLLLPTVLNGHVR/LMSYKEHV VFVA /STTFPLQMSQGVPLTFSKYV LENTFNKAVRALTSDSSESSQSLKPV WAPPSLNAKNI /RDSWEAVKIPALKG VVKWNLKM
2256	16157	A	2271	19	420	AAGTHERERERERERE /QREERERE RERERERARNYIYTYRPPRVVFFFPF FFFPKKRGRGLVPTPPGGGAQKKKTS LEGGKGVFFGGGKKTPLEN PGWGEPP QKQNGGGGPPRPDPFPPLF
2257	16158	A	2272	463	20	SYNIPLSQSLYQ /SRALTFDSTKAERN RRGX /RSGKLQWBSRGMLRPFKERSHL HNIKQDEAVSYPEDLDMDALNTKQOI FSVHKIALYSKKMDSRIFIAVERESMPG FQASHDL /LLIG /ATAAGDLKLPMLI YNSKNRPVPAEF
2258	16159	A	2273	474	82	VGVAIDFLKNTSQQAQTKARMDKNDPIK LKSPTAKETISKARQPTGEKIPANY TSDKGL /SRIDKELKQYKRNPNNEVL KWAGNACMLTPTVLALAEKAGRTQQQ ETBATLALFSLFCOVFLC
2259	16160	A	2274	152	3	ABGRNDGITYQKST /VTLISNDKNPN IHRPRTPLTMLYQNNLCHGL
2260	16161	A	2275	32	361	LGASARYEKKPTVNLINERLINIPTR / SKTRIGYLLSLLLFNIGLATLASAINQK KRIQIQIVKKKIKTQKKKKNTKKKK ALFKFGGPEKKEGPPKPNFKTPEVPV
2261	16162	A	2276	329	487	EFVNITIKATSLHYKALVIRA /AMWV YWHKNRHIQDQWRTESEINPHCNK

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2262	16163	A	2277	2	466	AHHSCSHLLTTAAHYSCSPQLLTAAH TYSPPQLLTAAHHSCSHLLTTAAHHS CSPQVLTAHH/HAHTCSQ/LTPAHH SSPQLLTAAHSCPHLLTTAAHHS CSP PQLANSYRG/S PYCSWSQ/TPGFRSSH VGLPEWIPFHGLQVV
2263	16164	A	2278	4	467	ENVTQGGKIHRDKLDEMGNTSVFCIN HMRQINFNARKGNVFKSGK/TACNFP LQYQISHANQKPYECQSKPFRKRAH LQHNRIHTGKPYECLCSGVFCST LIQHKRTHTESEKPYECLCRKTFRRSAH FLHRQIHTGEKPYK
2264	16165	A	2279	383	3	LICVRCVCVYVCMCHCAC/CCHMCG CVCVCVCVGLRGGLGWAVVCRSWGPP LCFLLGLPLKSRLLWLPRT/ISITL PSAQGLPAPGFGKASNTTGVKSSSV FSLLSRITALSHLHW
2265	16166	A	2280	47	219	VCSELKSCHTPAWAT/SVTLQRQNK KQRRTLGSIFFOATFMHLKKEKSLILQK W
2266	16167	A	2281	294	160	NKIFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFLFLF
2267	16168	A	2282	68	490	RTFAYPKPPVFGSHSGKITIPKARGSF PS/PPLFPFPCSPSPGSPVSCLPFPLP SPSPSPSLSPISRLPSP/SRSPSPSL
2268	16169	A	2283	3	454	QSAFLGASQLGYSGVADTLEAAVCFP SDIMLCAQRTTLTAVRQSHLSLQPR LFPWLCAPRGVYRGQASLSGGLH QVRASRFLCLPTQASAGVAPPASLPP CSLISDCCASNGRGTGMD/SEPTG
2269	16170	A	2285	1	452	LKDSGRDVSQFEGCLQKQNLCLLDN WDSETSTFSKLREQLPVTOEFWNLEK DTEGLRQEMSKDEEEKAKVQPYLDDFO KKWQEMELYRQKEEPIRAELQEGARQK LHEL/QBELSP/LGQEMLDRAHVDAL RTHMAPYSDELQ
2270	16171	A	2286	3	266	NSSFPSSGHSITPLAPPSPAREGTD/AV SALKSPQPNRGMQRQ/PGLPS/DTAT ITPHTSGFPKQPOLSLKVQTORAKGLSL HWDLEP
2271	16172	A	2287	274	453	IYTPVKSSSKTLRPRHIDQNNRIENPEI KP/EYSQLIFDKANKRIKWKDTLLNKN CWDN
2272	16173	A	2288	81	487	TVYERFVETV/CMDKKITPFKGLLRD NTPCYPSLLMCKIKINVPATPSS /LKWMDQGVTVFSSHYLKTFAVLGEG RKKKKKCKRKS/HKALAAINSDSDEGA GQSKQNT/PWKGPSINAIKNTQDWE
2273	16174	A	2289	75	469	SRGVAGAPPKSPSTPSIGFLDTPSP SSHHASDGP/PPPPEPTASSMASAP/P PAPQPTPL/PPATLGPSSAGPE/PSPGS CTSTGWGYSFCCPCRRIMRWQPDQGP AHHWNPREFP/PPPRVSGS
2274	16175	A	2290	256	55	PTQPLRVELTITVLCDINWDYITKLKS FCTA/KKQPTERKIFPNHVSINRLIS KIYKELIHTI
2275	16176	A	2291	497	29	SLTHRVAGGAVTPLAGAGARQIFFLGD PHPTSSLLGWGPANDPCAFVSDHPASS



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2291	16192	A	2307	133	2	RVTHVVVRSHPALPVTTRAEAFGESPEP GGGGCNEPRSCHCTPAW
2292	16193	A	2308	3	369	LITAPPDFPGSTHPLTSASQVWATGAH HHSWLTVFVFVETGTGFL/SELSSSSPL ASASQSGITG/REFPCLTSPFFF
2293	16194	A	2309	253	365	TDYFLVLYTLRQSL/SSVAQAGVQWQDL GSLQPPPSGFK
2294	16195	A	2310	362	0	TKAQCCVHENHFLLKIDANTLIVIKVRNFI CHSSPNQKICYGLALINI DKSSPFRSKDT GDEB/HPIKIKKSVIQEAILIINIYA
2295	16196	A	2311	167	2	LCYCVLPVFFPIFWRQSLTSLSCGQWCD HGSLOPLPP/GLKRSSTLSLPSNWDYR
2296	16197	A	2312	67	482	DELIPGGGCSLEQSHCTPAWVTA/ET LSQKKKKKKK
2297	16198	A	2313	188	437	AQFFPEANGLDNKVRKSNESDPGRQVNP ESDSESTHGSLSLSLSPVLPFTFLRQSL /NSVIQAGVQWRNLSLQRTSP
2298	16199	A	2314	41	325	TTTLFXRVQGYSSLLVFLLEFVCLCPA GRGGVYGRQSSLSCSRLLPVRASPLC LPTOASAIAGAPPALLPFCSLISVCCA SNEQSGV*DP
2299	16200	A	2315	417	0	SPFNWDYRCVPPRPAFVFLVEMGP/Y HVARPEFGLLEPTSGEPPLA/PSKCKD YR
2300	16201	A	2316	98	288	LMAVVPATWEAAQSELEPGGWSGSEEG CSELRSCHCTPAWVT/SETLSHITHKKK KKGGAAL
2301	16202	A	2317	1	410	LNHIPLNLSLTRKPKPSHSLNLRKKKKKK KKKKKKKKKKKKGGGVKKKPRGGQKKK GGKKKNPSKGGKKKKRGEHGRKNFPG QKKRKETPKKKSPKKKKKNLR/EEEG EKPKRGGEKKSSSPNDNLNLRGKK
2302	16203	A	2318	249	3	PLKASSPKAKNFCREVGICPEPKKV PARKIKLVPIPPFIKGLLPCPPPIPL APPRVPLKRP
2303	16204	A	2319	2	393	AHLGLPKNDYRHEPPRAPPLFLNLSVF GLDLT/S/GDPALASQSAEITGVSHC AQ/PEYVY
2304	16205	A	2320	389	2	RGRNHTGGGFLRGGKKSPPPPLKNWGT KLGPDPDPDPDPDPFG/KGPGWSLPKPI LKFKGPKKDPFRAPKNGKSQPGWFFF FLSNFTQLPGIILSRGGKXNFASPPPPF FFFVHYKTGYPSATDDAW
2305	16206	A	2321	389	206	PQWRGF/NEVGQANLELLTNDPSPAS SRSGTTGMSHHAQLKNYFLMVQWRNWN IAGVM
2306	16207	A	2322	371	42	SFFPQSGFFSPDPDHEFFFPDPSPFSW VGVRQIPPPPKIFSSDPDGGFFSPDPE R/VDFFSPDPDPDPSPFLSPDPDPFF VFFFFFPDPDPDPDPSPFPGVKKKK
2307	16208	A	2323	82	386	PPLTKYVFFFPREGFLKKRRRRGGPS PTDPLPNNMGGIVTKAPPIIFMGGG IANTSGVPTKAPPRPLRPNMLRQG FDLLTKAS\WGSASWY
2308	16209	A	2324	1	413	RGSGRNRHGFPCRNVFPLVETGPLAVG RSGLEPSTS PALASQSWGITGVSC/RPP PQASY
2309	16210	A	2325	58	400	SETLVSKKKKKKKKTPPPPNPKKKKNP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
						PPFPFGAKGGGKGF/PPFPITPKKRGG FKK/SPPKPKPKKKKTPPPLGKKGGPPP RGGPLGGFPFPFPQKXNGFPFPKKKPPF FFPPPK
2310	16211	A	2326	462	506	AHHNLRLPSSSDSPASAGVAGTT/GMC HHARPILVYLGSDASALLHCTSSAQLF
2311	16212	A	2327	1	393	SRPPSRTEKIRNFFVETGSCYVQAAL KLLSSDPPTSASQSAQ/ITQMSHRAQP TS
2312	16213	A	2328	391	2	AWFKETKAGMIIPRSWDRGWSVQPYSA LTSSPESGFHSVINGDSMTCLDQKISL VAPHGIPQRGSSLQDGVSPCAPATKPKY LASTK\KLHREARLQFPFLSLRQGLA LSPOLECSGATLAHCSNL
2313	16214	A	2329	2	115	GCSELRERFCTPAMAT\SKTASKKKRG KKKKGGVYF
2314	16215	A	2330	2	406	AAAPSAALARDGNA/VRPELDLLEPGRE VAPGAHCLGCGSPCLFLVPSHTRQSP APTSSPGLSTSPPLVPTIVSAPHSSKGP PSIPGAQALRGCGLGWDR\SSSPSLP/ PDVSPKPLNFAP
2315	16216	A	2332	226	377	KRKSKHITFLFKTLSMETVAHACNPSI LGGQGGRI/TPRSGVRDQPDQHS
2316	16217	A	2333	3	191	CLSPGGGGCGGLRLCYCPAWIT/NETV SQRKCKERRKEREKIKERKCKKCKEK KEKKKG
2317	16218	A	2334	295	81	FFKFPFPFKKTCPEFS\FFWEKRGFP FLRSFTQNPFPKGGPPIILKGGPPFP GWPPPPPLVFFFFFLR
2318	16219	A	2335	375	8	TQIVPLPSNLGKNTLRLLKKKKRNEQGN ITPTIDNRKQILQ/TYYEGLCRANK/N LDMDKALESHNFPKLRGSLNI/HSA KRTHFI/ILNISTKKTPTPTGTGKFLQ YFKEKIMAGHSGSHL
2319	16220	A	2336	399	97	FFFFFFFFQNLA/SVTVQGVQGGYFRL QPLPRVRKPFSPFNLSNRGYRGPLGR VRQENCPKLKSKRPQLNRIPRLGCKKL RFPKKKKKEKEKIVKT
2320	16221	A	2337	411	57	KKPRSFSSCSSPPFFFFFPFKKKTIF PPQIQFWGPPFPFPFPFKFPFPFPF PQKKKKI\SPFPFKKGFPTFPFPFPF FPFPFPFPFPFPFPFPFPFPFPFPF
2321	16222	A	2338	97	354	AKAPSLSLVLVFSFTFFLIGIQLALP LECRGAI TAYCSNLNLDSSGPPTSADSP TPY/RIAGATGTHNRALLKFFFSRDL PL
2322	16223	A	2339	391	45	LMFPHLSHIGRSGEAPSIIHKSIIYLSIHP SIHPSLYHSSIHLSIHSTIYPTCLSIH /CISIHPSIYPSICPSVILLASFIHST ICPSMILP.IHVSIOHFLSAQILPVS VFG EVSDI
2323	16224	A	2340	506	0	REHSQIGIVADKKKKKKKKKKKKKK KKKSSSSSSPGTFPRG/VPLKDPVG
2324	16225	A	2341	203	1	VELRVATEPGEFNLFLGIYCTSRVDWIK KMVIYIMYHAAIKG/DRIMSFVAIWM ELEAIFSLKLMQ
2325	16226	A	2342	402	40	PYPKKKASPTDA\FSSSSSSPPFPFPF SPPPKKGFSSKPPFPFSPRFFSPPFPFK

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2326	16227	A	2343	181	1	PPDPFFFFGGLKKNFFFTDPALKFFFFFK SPPLPFFFFFFFFFFVAGVLLCYSG OLKDOASDLLGKNGDEVKRTIPSLPSS LPPF/LPLFLHQPLPSFLPSFFPSSLPL FLS
2327	16228	A	2344	2	407	FVASOLGCSGV\RVDPLEHACVCPSSDL OLRAGRRTTALFKAVRQCHLSLORLLSLF VFLCPAPRGAYRGQAFLSOGGLHPV GASRLCLCPKQAWVGGAPPASLPFCS LISDCCASHQRDSVGARSPSPGAGH
2328	16229	A	2345	405	178	IKFIYERATA/LLAG/EKLAFFPLKLG TRQCHLSLVCVLEVLGTLRQKE IKGIIIRKKEVLSLPADRL
2329	16230	A	2346	2	412	FKASKASLSPILGANTGKFKLPGULTY HSLH/LKNYADSLILVCONKNAWIA HLFTAMFTETYPSPPLRPAOKKISFQMLL FIDSAPSQPGVLMENYKINNVFMPANT TSILOPMDQGVILTLKSNVLRDTPH
2330	16231	A	2347	2	397	ESLSPGRRLQGARIMPLHSSLDNRVRL CLKERRKKEIGVILRCWQCKIVQPLWE IVWVFLKKN\ESPYEPAVPLNITYPRE MKIHVYTTCTQIFIVALFTIAKSGKWN QTVACACKPSSES\NLRWVDYL
2331	16232	A	2348	3	423	BGCSLGSHTCPAWAT/ASVSQRKKK PKKK
2332	16233	A	2349	49	262	QMKGSNNRRGRGRVGRSQISKKKTNAPI KMAKMDNRBF/DIQANKHMEKCSLSL IIRWQLKSTMYHLY
2333	16234	A	2350	356	2	FVTPALHSSLGHPARYSGEKKKQVAA KAVLRQKFIATVTPKKRKLNSNLSTLS LKTLEKEHETTTADGAQYVTKI\RAKI NKIETANETKRSLEKSTVSGKCLRD ILLSAQT
2334	16235	A	2351	360	19	LDAQFLEVLGELLFASIVPTLPQPPGCG ASFVPLNTLPF/SLSPSQSSSSPASLVR PNVAPPFLLCPHGEPDGPDSTTSLPFPG PAATGPAARLIQHPASROPRPASHTHCG V
2335	16236	A	2352	360	0	NTFLAAPRLVFCOVTYSYLLSLNKLAL MPLNLSDLTRNTHCMGELFFLDLTLAQ NPFTFTVFLGHPEWGESRFVQAVVOW PDLRQLQPS\PPGSMRFCSLSLPSNWS PSYGRLL
2336	16237	A	2353	34	474	BGRPCKELAARQVGCPCSCFSPHWQLL QKQKTAGAVSVVCVISTLCVCVCVCVC VCQAMCVCAQA/CFVCVCVCAQA/CLCV CVQA/CLVCASAVSVQV/VAVSMVCV RS/VSLCYWQWQSLCVCAQA/CLCVVC CSIPPPVLCN
2337	16238	A	2354	297	16	KFFFLKSSFFFFSFFFLTPDPRFFFFPKK KKLFFFPDKLFFFLDPPDPKFFFFFF FFFFFFFFFFFVFFVFFFPKXHG WFEEITLTV
2338	16239	A	2355	3	315	PVTPATRETAGETL\HDLGEPGRGCG ELRSGCHTAPWVTQDSVSKKKKKRGA RFKESNFTTGLQRNIFPLGALKLISGA GVLRKRDGKTLGFPQPNRPWG
2339	16240	A	2356	399	154	PGORGEIPLPKTIQ/ELAGCG/GHINFG

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						GRIFQEPFRSRHCTFPAWATEQDSICKSHS RSLGLWCYKSSSVYLSTRGVVVRGIASV
2340	16241	A	2357	416	2	FFFFFFSETESRSVAQAGLRTQWRNLGS LQAPPPGPTFF
2341	16242	A	2358	209	2	KRNILVFWERGGYFRSLQPPPPGV/SCFN PPKKLEYRVLFPQPSNPFFFFCFISRDG VSPCCPGWSRTED
2342	16243	A	2359	279	380	RGYNF/WFGAVAHTCNPSTLGGRGRIIT RSGDQDH
2343	16244	A	2360	415	224	FFFFFFFFFFLLITFILMLNLLPCHKFLFL QFLQLGLLLYL\CAFFLLVALNIFITS FQGLDYFF
2344	16245	A	2361	278	2	LSDFPRFMITYRTHGLSLTQISENCV SCOKFQILEHFRFQIRDAQSVLRK/RKA WTGAVAHACNPSPLGGRGKVISRSGDLV HPGQHSPT
2345	16246	A	2362	139	282	KKKKGGRGGGGGGGGGGXGGTGGKKK GGKIKQLMGGGKGGGKGGGS
2346	16247	A	2363	19	409	PKFPSVLGGGGPARYPSFLGGPNRPVFL PGVGAPPPGPPGKTFPFLKKIKIYPARG GPPVIPASPGGEGKSELPFRPRVPLTQ IFFP/PPPPGGENQG
2347	16248	A	2364	159	383	HSHFNLSSLIKKLHNNNTFTEHFSLS SLNQCFNLITVFYSHLGNFNGN/SWPG AVAHTCNPTLGGRGQITR
2348	16249	A	2365	400	221	GRLRQENCLNSGGRESEPR/S/HLHCAF AWAT\SDQSVSNKKKNQKQTHIYTVL LCARH
2349	16250	A	2366	383	14	GGRCGNAPFSCHCTPFWVTERASPOKTK KQNTHTKKRISSCCHREDFPLRQAATF LCQFPAAGPSQKARMBLMEKQEKNGP ARHRRQEQFLTSPCPDHLGVLSQVSS TPAQGLSLICK
2350	16251	A	2367	274	1	PRKILKARGKEHLASRGTMIMTSDPYL QIMQARRWSKIL/NVLEEKIHQHRLL/ PVKSSFKSEEEKTFSDQKLRGLVTSR SDLGHDVK
2351	16252	A	2368	161	2	FFFFFFSETESOC\VTQARVQNRHLSGLP GSSDSPASASQVAMITGRHYANLIF
2352	16253	A	2369	361	198	NGRLIFVFLVWGF\TMLARLASCDFFA SASQSTGIRGNHNSQLKCFPTSDSFC
2353	16254	A	2370	116	300	HLNGDAVEEDFMKCTVSGITVAICNLE FLG/SSDSPSASAPRVAGTTGMCHINLI FVILVEM
2354	16255	A	2371	2	192	MKLDPHLSPTFYKNSRNKOLNLRPKT KILEPNIR/ITLGLGLGDSMTNPEA IAIKTKLAR
2355	16256	A	2372	1	133	AGRLLEPGVGRGCSKPRSCHCTTAWATE QDSSPEKKKKKKGGG
2356	16257	A	2373	43	403	LHDSPLASQGGTGTGVSHHAPPAAGIN SRICQARDRLSELDESEIRLRQSDRN MDGRMMKQHLQELRDYVETKSN/WR LLOVDERVGVGNSNLENIFQDLITHENYK GKPIRLMVDL
2357	16258	A	2374	404	215	GOGGRITRAQKPTSLGRVWVPGSEIQE LLE\PDDRGCSEPRSCHSTPAWTTEDQS VSKRRKC
2358	16259	A	2375	3	397	SKOLEFTQLYTKLNQNTKTKSBLKKK

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						YPIRLPSKRNITQMASRVIRKYSWLIIR EMQIKTTTFRHKLAAALSSKCLLGL <sup>3</sup> AT SAHCCTVGAPLW
2359	16260	A	2376	413	1	PKKGLFPKPIIWTVGFFFFPRKKKPP KKIPGAPKKKKSPPPAKKFFFKGAP PPPPPPPPPPPPPPSGDSQERVRAM PVAGGP\PRPHLSAPSPAGGTAWPMH PVQTHKAQSPKLPASECCPPTTFLS
2360	16261	A	2377	398	247	RPFHHAQAGLELLTSSDLPALASQ\SA GLTWSHHAQASATAFGLHVS
2361	16262	A	2378	2	143	QENLNFGGUCSBLGCHCTS\AWVT AKLCLKKKKKKKFPKGG
2362	16263	A	2379	417	90	FFFFFPFGGRQVCPPKGLLFCFLY KGGSPPGSGTIFPPPPPGVGVPPGPPP GGFFFFLE/QGGVSDPGGFFVLPTPK KPPPPAPQGGGE\KFKPQWGPWPTF
2363	16264	A	2380	36	427	VHPLNMHDQKGQASSTQKKKKKKKK KKKKKKKKK/KKGGAF
2364	16265	A	2381	402	2	NFFLKGKRGWGLPPLPRGPPPRGSPK /RGLGSPPPPPFSGSKTPAGGSRTPMG QKKKGPPLPESPLFGGAGQAPFLPPVP RGVPSPKKKKG/APPPPPPPPPPPPP PPPPFFFLRYNLALLPRLGCSGT
2365	16266	A	2382	166	5	THGHVYVDQEQMMIENM/WPGTVALA CRSTLGSRGWLTASGLMVKRLY
2366	16267	A	2383	2	457	TSQPSLLSSHDYRSTSLRPLNF\ILPYF IYFFAFPSVETGPHRVSQGLNLLTS/S /IPSIPRIPIKMDYRHPDRTWP
2367	16268	A	2384	2	417	GRVPSQSNKNPSLSFTLLKVLPEVIT PGEKRLIFKVSIKVALVSWRLHEAL VSGQIVPLEV/QALDVMRLASWRY
2368	16269	A	2385	318	32	TNEIHLDKKQIQVTF/FFPMGREAVET THINITYSGPETQWRFKCKCKGDESLE DIECSGRPEVGNDQLRAITAHASADANV DRDSGRCCACAP
2369	16270	A	2386	409	3	ISQAPSTPPRKRGR/PPQKTSFLGPPF YAAFYQEKKLFFSSDPRETGDKGQK GFPPPKVAPKKGFPGGPPPGKKDPP SFFKHKSQPTPRAPALEGPRSR/SA LQPGRRR/PSQKKPTRPPTRPPTRP
2370	16271	A	2387	415	10	KGFFFFPGPTPLPPPPGLPPPPPPF WFGPCPPPPPLTFYFFRGGPK/HLLVF PLFLPPPPPPPPPPFAKESPPKGGPGP LNFFFFGPKEN/SPPPPPPPPFCMBETH SCRPGWSAKMHLGSLQPPPPVFK
2371	16272	A	2388	410	95	KATMDKSDHILKKSFTYAKETPTKVKQ PPEWVKFANYPSDKGLIPILYKBLKQP YQVKENNSLKWAQDLNAPPSKDQMA NACMKKCSRGQNAVITVAPST
2372	16273	A	2389	362	92	RLEFFSSDPKGGPPPKGPPPSRVPF PPFLAPPPKLLF\GPPKKLFFPPAGG KKLFLKGGPPPPPPPPPPPPPPPPF PVNTFY
2373	16274	A	2390	131	487	ATRHKKTRKSSLSFSSISKKKKMKELH DIGPSSNFLG/RPKAQATKGKTDWTSAK LKICSSRDITSRMKQPKQEWAKTFANKS CNNKKPEKIDKNKKKKKKKFLQGLAKK TNLSPRG



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2374	16275	A	2391	408	145	RWSLALSPRLSCSVSSA/CCKVPPPGVT PFSCLSLSPNWEDRCESPPPAQ/IVFVIG EGFYLLHGFF/RKGFPLRCPISGCPFPV LSFPT
2375	16276	A	2392	1	203	LFFFAFSVETGFLHVQGAGLEPPTSGDP PVSA/FPMCDYRHD
2376	16277	A	2393	386	16	TPSAGGRHIEI/SLSTCPSCAQHQKEHL EGBGGGGAQSLITAPSSATSSQDPISAH AVEDKLSIRLETDLKTKS/WPGA/VGHT CNPSTLGRRRQANHLRPGVRDQPLVIC RRDPKVMGLQA
2377	16278	A	2394	3	396	QLLEKLBQRLSTGSGQCSLELRSHICT PAWATEP\DSVK
2378	16279	A	2395	273	416	FFYFSFLIKTRKKQPGWAAQANPSTLS GGQGRJ/LTRTGVRDQPGQG
2379	16280	A	2396	329	76	FTPIESACSCQECIKPNLRQEW/YIPTGL KLIFFTESHVPTQ/DWSAGELL/DPRG RGCSLELRSHICTPAWATEP/LCLGITHK IKK
2380	16281	A	2397	210	7	GGKRMVCRKPGGGGFFAAVMSPKGLFS/ RLWKEAPILSPQKKKKNNPFLKNNAND ANRHFSKEGTQQ
2381	16282	A	2398	48	393	SILKTRKPTLKKRRGRKKKEKESVRTHV FFSYQSNAPSPKPLNNMTLGRLLSPSF FLVHFFFTYDGLLCCPGWGRTPGLKGS SHLSPFKCWDYIHEPPIPAVHS/LFCR
2382	16283	A	2399	128	383	BEAPKHPFKPNLH/QKKVLVTAWAARAG LIHCSFLNPWETITPEKYAQQTINWAGK LQCLQLALVNRKGPILLHNVRLHITTH AS
2383	16284	A	2400	54	384	LFTFPLNSVPHITMCLYFNT/FFSVNPF VSMPTPOCLDSSFLISLDSLEINPNYIS QLIPDKKTORGKNSLPORNCNENCIPT KRMKNDP/L/SPYTKILSNMMDLNLIK
2384	16285	A	2401	393	1	HRGENTHQGGGLSRGRHSRQGTSRW IRTRQMGPSRMITPSRQGGSSRWGKS RAGDIEVRKTOQSGALVIRIRSRQGT SRWSFSRQVRSFRWICSRQCS/XV RRRSRQGTSRWRHSRGR
2385	16286	A	2402	1	330	RPPFPFHCDYR/HSPR/QPTLWVIFK LSVETRLCYVAQTGLKELGSSKSSRLD LPKCDYRHELHCVIFQEKLV/SGPL FKIPRPFKAGMEIFQIGEPFWSSHPLAT
2386	16287	A	2403	3	407	ADANGLKGTGHPWEQAGISGLSPNSFL FVCFRQSVAVLSQAGQWRRLGSLQPPP PGCGRESCL/PSFQGGITPSCFVFLKCM GLHVRVQAGLQLLMSGEPPALCSQRGR ITGVSHDARFSPSKFIMHTARM
2387	16288	A	2404	239	573	VCPVFSLSIFPESSESSITQAGVQMLN LGSLLQPPSGFQKPLCLSLSPS/YWFTG TPPLVGGSGAGLGG
2388	16289	A	2405	1	122	PTKRGKRGRLSCHSTLAK/VNSETTS QKKQKKEKCLPLL
2389	16290	A	2406	417	130	QALRVKIVQLVPSDFLAKTRAQSVNNL LHHSSSSSSSSSSSS/SSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSFLFLFFFG LRGAFIRGFCPIRR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
						QAGVQWCDNSSLPFPSSGLKML/STSAFQSL/WDYRCEPQHP IHY
2405	16306	A	2422	90	444	YCFSSSECEKCRCPGHDLQLSPGLCHHG VSGLAKLPLLCFMPWIKPQPLCSPTTSL PFLPLPFPSCQCPQGPAMVLEGRPSLMX OGGLQSLAIKR/RBGSRAQMLTPVIPAL WEAEAGG
2406	16307	A	2423	1	444	PGPGPGCGPVATLGSFSPSPARTDPSLP PHSQLEAEARNRDIEAVVQLQERMEEL LQAGATYGESLMCPLPKRT/WEBVGRLL
2407	16308	A	2424	189	418	SRRLRPSFSGCLRGVPSCTCV/SLNV CVCVKQ/VCVVCVVCVCA/CLCLCA NVSL/CSHVSLLCLSLSL
2408	16309	A	2425	30	895	LDEQCTSETHRRKJENTAPRAPHEHPAP ATAVRGRDAASQMLKRRPGSGTDGLRLQ GABPSRLRLTYAGGAVIPRGTPERAOPP PPQDPLGRRLWLSRNTWGPWPGTTPQPS PQLLENDWGSCGFMPENARJGVFQDSQ EGAIHRET VSKSVCAEPWRHQRARDPA PTNFFLKQKQRGASTSSGQHDRVNLV FFIIDDYSPPSKR/ PKTNEPQQPPVPEP ANAGERKMRFNPSGPHNVETKILCLC PSGHASCQVHLATGAMILGFPQSWRLKG SGLKARILQ
2409	16310	A	2426	494	154	SSRVRCQA/LLGGASQLGCSGVVRDPLE EAVCPFSDLQPRAGRTTALFKQMSEMQK SPVFCVAHAGSCRLSLFLPHGLSSSLHG LNH
2410	16311	A	2427	416	1	PQRQPLALEPGRQGAAPVEDLQPGPD KPPPPPLPQPFARTRVTAAPVRHPPV ACHPPQPLAASKPW/SVAGGDLPLPG PIERPVHAFIFIGFIVHLGLGVSGRGAV APARSGPVPRPPSSSTSRFSLFLHE
2411	16312	A	2428	84	409	DYKHAPTMPCNFVTHSPQPCREHNTFTPKKKKKKKKKKKKKKKKK/KTF WGG
2412	16313	A	2429	1	389	LRDLSSDRSNFGRFLSTNSSLY/EXDK RNKAYFTK/RPSVNDIIST
2413	16314	A	2430	456	0	PGWPGRGAP/PSQTGMVPGRGAPHIPDDG QPORGAP/PSQTGMVPGRGAP/PSQTGMV GRGAPHLPDNMPGPGAPYIPDDGQPGR GTP/PSQTGMVPGRGAPHIPDDGPGRGD/ GSLLPRRGGSRAEALITSGTMVPGRGAP P
2414	16315	A	2431	3	344	CRRRRSCHCTPAWAT/SETFSPQKKKKKI FRRGPPPGQAGLKLRAWGFFQKRGSTM GPTTMDPQRSEPDLLCKKKKIKRPG QDGPAPPQGGAGKSVNPGGGMFQGG EIP
2415	16316	A	2432	1	109	RPLRLRLQENRNLNRSRGCEPEKLC/HL CTPAWAT
2416	16317	A	2433	1	239	QSFVAVLPLRLVSNSNAKVICL/PSVSNQA RIT
2417	16318	A	2434	3	464	DWLQLENGQETVALVHS/HGGILPWLS EARRLQVQSDLFNNLVCRGTIHKFRCPVH LTGRRPRHGVIDCYTLFRDAYHLAGIEM PDHRENDWWRNGQNLVLDILQAPGLYP VPLSAAQPGVIMCCPGSSVPNHAAY/Y

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, = possible nucleotide insertion)
2418	16319	A	2435	3	427	CGDGLPHIPK EGARTSSRRHPCNKYLLHLSLAHLEINA LNLVLKGLSPSPFPALPISFFIFFSPH FLGTPTTLAGGRADLPFLQPPGAPG/QPA PLNYGPGPYRNP/CP/RLQQLKPNAGPHG LLKS PPPNPGRNWPLLQSLDFPFKRTS IPLP
2419	16320	A	2436	238	400	QFRMKRGKAIPIFFFLRQSPSVIHAGMQ WSNLSSVQPPPPGQKQFLC/PSVPS
2420	16321	A	2437	11	442	LGTFRPAHMGVRLGSLRACFVLGHPAK HPRPQRWCKNVSYSPEQADKLQAGE IVEMIKG/CNPNKPSVSGPQPPPKT TDEKMGWBGCCQRRRGVFNFLPPP IKDAQPLLLFGIDQAGPTESGIGSIRF RRLGC
2421	16322	A	2438	411	80	POAEAGAPTPGSENFPPPPGGQAPPP PQKNFFPPRGVNPFGGGQKRPKPKGG /SPKKNPGGDKNPFPKKKNIGGGGFI GAPRGTPKKTPPPRDGYFVQVFFIVSLK
2422	16323	A	2439	290	1	QLNKIKTKTLLFLP/ANKEVLEIPNYP PGPKKKGYPPSIFFFFLRQQL/NSVTR AGVQWRDLSSLPQPPPGKRFPSQKPNIS AFPHASADAWDP
2423	16324	A	2440	440	213	PFSRLPFFFPPTPKGRASPPFFFCFPR VFFPPPPF/SKPPPKFFPPPPKKKIS PPPPKKIFFFPFPP
2424	16325	A	2441	131	408	GCVPFPAFLFCVLVLSSVAGQAGVQR NLSLQPSPPGLKRTYRPLPS/QDYR RAPPLA
2425	16326	A	2442	102	351	QSSSVLLKLCVCRRLCV/CAQVCAQV CVC/VCV/CBVCVCV
2426	16327	A	2443	190	3	PQARREKSHRFGPIGRKL/DPPFLSP HVKINPRMIGDLNFKPTTIKLENLGN TLLDTCPG
2427	16328	A	2444	410	30	VCVAPPLVCVIGLVCVTHQFCVCVHT HSLCVCV/CQFLCVCVQ/VAVSVVCVRA SLCVCV/ALCVCVCV/TVCV/HTVCV CVCVRSFCVCVAGAVCVCVCVCV/C LCVCVSAQLLGRGFCSSVNIKGAP
2428	16329	A	2445	243	1	KVMVQNGKPPSNLFFPGPTINFFTPQPK QGGQGNPNPL/FFFFMQGL/LSVTQA GMQWCHAGSLQHLPPGLQFSCLLP
2429	16330	A	2446	276	408	MLKNCAFPWGTVAHNCNSTLGGQGR /TLRSGVRDQPDQHG
2430	16331	A	2447	24	405	LQDVCAFFFFFYLNQLNPGGKLLPVG PAGRNQRWQFDKLQKGIKMNPLRGT SVPLTKKNG/WARG
2431	16332	A	2448	239	3	SPLCGRNVYKPTVETKINQKPPSKO IMLCLVRLWQ/SNKGIGSCAHACNPG TLQCCWRLMDSQDRDPGQGETP
2432	16333	A	2449	406	144	GCSEPRSPCTPAVTSITSL/RKKRKR RKKKSCLLRAILSLTPELTHPTLTLPL SRYNDYPHPRDEKTEARRVYATCSGSHS WKRLG
2433	16334	A	2450	349	1	GGATFLTPRPKVP/LTPTPLP/NPGHQ EIP/LPKKKKIVRAIYDKPTANILHQ KVEVFLKTTSTRGCCPLSLLYQKTRM PSL/PLLFNIVLDVLRALQKKEIKGI

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2434	16335	A	2451	382	19	QIR DLGRMTAGSGDQRCAVGVKLLSFS/LGAA GKGPKHSEAEASLPNPGSYNRQAQNPQ SSLHLKVTIPDITS LINTPNRMLSSLKVP SWQGAVAHDCNHS TLGG\RGGMITRSRV RDQPGQH
2435	16336	A	2452	3	396	FKLKMLTYHSENPFRALRNYTKSTLSML YKGNHKAAMAHVFTTWFTYFKPIAET YFWGKKITLKLPLVDNAGHPRALME WYKSLNV/VQLCILQPHQDGVISTLRSY RANWIFCKDLAALDGGSSRT
2436	16337	A	2453	115	411	KGNFPFGPGGGEKKIIV/PNGGPPPRK RKP PPPPPGGGGKGGHPPPGPIFFPK KKKOLFGG/PGGAPNSHPKRNPPWFPE GGELTNPPTFFFEQGA
2437	16338	A	2454	3	114	HRV/GQAGLELLTSDPSPASVTFQAGIT GVSHRIRSVS
2438	16339	A	2455	397	1	WSWQK\NRRIQDRENTSEFPMNPRMYQ VIFDKIAKNTSEWEKSLFNKWCNMI/ LKRMLDHPHLP\KQKSKWMDLIRPE TEKLPSESTGGNPHD IGLSNDF\LDLTPK AQAKVNTDKNDMILKLNFPTRP
2439	16340	A	2456	424	3	PKKKIIFPPPPGFKLFFFLKAPPPFFFL CLSHFLNLRNSLSCTTSCCVSTIPTSL CNKSSGV\OGLHCSILAI/CSLHLTLIC PFCVLLVCMCDTVCVCVCVCVCDTVCVC PCPYGLDIAFKHFFSRMSLTLVAGGV QR
2440	16341	A	2457	266	379	HNPGMAHTCNFSTLRGQSRI/TLRSQ VRDQPDQHG
2441	16342	A	2458	10	409	SRTGFNFRACRDPVVCVAPACFELPLN RSVDSATREAEAGGL/DPGGRCCSELQ LCHCTPANV/TSETL
2442	16343	A	2459	184	387	IIVHFMHRMINVAYIIPQYSFTLEIQS HSVTQAAVQNHSHSSLPLPLPLGQSSH /LSLPSNDY
2443	16344	A	2460	110	1	KNRVSTFF/CSPETESRSVIQAGVQWVN LGLSQPPTP
2444	16345	A	2461	380	2	FFFFFSETESRSVAQGLRT/CWNCNLS LQAPLPG
2445	16346	A	2462	382	29	NGPCHGPPVIGTWGGQGGGFRF/GS KPGFTWGNPPFLKNHKNYPGGGPPVVI PFLGGKPGNFYPPGGGPG/SGPGAVFP PPPGQRRESIFLPPKKKKERKILIFTSLEQ RTQNCDA
2446	16347	A	2463	228	1	KRGTLKPPPPGGRFFFFFSETQSRSA VQATVQ/WMPGSLTANFTERTQGILLP PLGKGSCSLGSDWYDRV
2447	16348	A	2464	395	1	RLAKENMLNPGQFGCSERS/HRAWQGS ETTSQKTKTKQKALASDITLSFRQGS ESRHLSLPHSSSVITPTGLTSLTSPH PILPVNLAPALPAICYGDSVKSHPQL WLSKRLQSSLSRLLTWQAFS
2448	16349	A	2465	29	299	ETPNRASPKTSWDYRVLPCLANFFIFF VKTGL/HRAGLELLTSDLLCFKPCNDY RH\DRSTWPLSSVPGSIFLVYVWPLLYL ETNMLTTL
2449	16350	A	2466	1266	1473	YFVPOSTQNHAAVFRVGSLLQSGGRTS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
2483	16384	A	2500	80	404	RTAAAVSTVSFPQDFEQSPKCTQGVRE ALRQIK/RLVPTGSLRH/WPAGSLA/LC QPLSDKDLTLQLFMFARNAPTALAMNDY PYPTDFLGLPLFANPVKGRRLPRGRERP
2484	16385	A	2501	215	1	AAIQGGLSACSHSVPAITTPRAYTPVPV QLLVNRF\YPKTLELSQLRCARRFPRE TGAQRHAGAGQTK
2485	16386	A	2502	423	214	WQAVGGLLFPVGGRGCLRSCHCTPA WVT\GEILSQNNPKRQQNKTKQMGPGV PGSWGSPRAGGLTV
2486	16387	A	2503	294	1	LHWNRQRCPFPFPFPLFPFPPLFPPL PLR\HRDAGAQGTAKIRVVRVVRVGA GLGVAAA/DSRESCPDGAAGGGGGGD SAATAGPGGGGGGK
2487	16388	A	2504	331	411	PFLRTGNKGAPPPPTKFFLFFKKKG/W PGAVAHACNPSTLGGRGRTIRSGDRER
2488	16389	A	2505	407	195	GGRGSELRSCTPFAWVT\GEVLSQKK RKSSNNKSRCLCDAQVGGGRQI\QVSV PSTQRRVGAWFTYL
2489	16390	A	2506	1	468	EQGSMNKLETERQIKKAPARNPERERER ERESKKGEDRHTDTCRP/RERERQNYRD RQ
2490	16391	A	2507	27	380	FVCLCFAPRGGAYRGRQASLSQGLHPV RASWLLCLPQAWAMAGAPPASLLPCS LISDCASNRDSVGVGSEPGVGNLM VRRFLSRSEKRNIRVGTRFSRCVCHFP L*LGGK
2491	16392	A	2508	396	234	RQENCLNPGQASSEPRERLCTPMATE RDSISN/QNKQTNKSHILRAAFSRPSCY
2492	16393	A	2509	1	421	AKKTKPPTFLKKKKKPGRGPPPPPPF/ AKFGRETPPLNPGGKSGIKPLGPPPPPP GGPNLPPKKKKKKALPK/PLVPSHVKS TGFPFPCS/RSALLRAFTQ
2493	16394	A	2510	197	3	TGPPDFNFTFFFLEMKSHSVAGQGVWRD LGLSLQPPSPQKQFYWGQGA/LPCL NKICIFSRGGV
2494	16395	A	2511	114	454	QGPLEKKGAPFENKFFKIGVLFPGSQNI PWWFKKGFSRTPEIKKQNPGLLGG PKKFFFFFFFEMVLLHHGWSALAQSL TTASDF/LRLQSSHLSSLSS
2495	16396	A	2512	3	495	FFLSRGLFIHLESAPATQCLLFVVFLV FVATGSHYVPOAGLKLASNEPPASN KCVIRHSEYPAKCLCLCFCLF/AFPLP
2496	16397	A	2513	25	437	PLLFSPPAGHAMEDLLPPAFSFLPYFF FWLWVVKLTYLVLAQNTTYHRLSG LANKLFLTLSPRMO/SIVPA
2497	16398	A	2514	2	256	QAPSAGENTSIVLLAYLTQAQAPTS LTSATNLAKNTKHS\WAGGGFYNYQDN LPYSLCSGRNESTAFGTNGQQLTHPVHS S
2498	16399	A	2515	2	284	KQCDELCSYYSQCCDTTARCKPQVTR GDVFTMPDEYTDYDGEENNAIRHEQ A\GFTSVISDLQQLIWSISQKHAMSFV EEMTVLEVIL
2499	16400	A	2516	2	432	RDCRESSRAAYTASLASCWMDLAR PSPLDDQVAMTTPAGCGWSVGRSQP FPRGSRGPGCCVSPPSWTPEGTGQ/CG EGGGRWSQVPP



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2500	16401	A	2517	401	2	GGEAATRGQTKFQLEKRAPECSECEKKI VRS\PLRLRRQRTPTGEKPYECECGKS FSRRYRLAQHQR\TRAGEKTYECNECGR GPSERSDLINHYRVHTGERPKCDECGK NFSQNSDLVRHHRHAHTGEKCE
2501	16402	A	2518	398	1	ETFGK\SGGRSIVGGQFLAVGPKGRAVM ISAIEKQKLVYILNRDAAARLTISFVE AHGASALVYIIVGVVDVGFENMFACLEM DYEAADNGSTGEANGNTQQTLTYELDL GLAHVRYKYKPLEERHCL
2502	16403	A	2519	384	3	QSGZLD\SDASDY\KGVRLDEGRYRCEL INGIRDESVALTGLLEGZLPLPFSVCV AAGPPLRLGLPLGLPSISSAPLGTSPSP RPRRFPSSPSAPIRNPSPGSPPPRCGVS VPTQGPVPV\OLLRGVY
2503	16404	A	2520	1	426	GDROMITALLEKLEKQSGRESVEENRPL LKALKEIGDFYLELHNDQSWVFLLSRI LPSDACKIKYKGINIRLDTLLIDFTDMK CQRGDLSPFNGDAAPSESVVLDNEPK VYQRLRHES/QERNRTQVDCLT/P
2504	16405	A	2521	2	425	ALPTGRMPIMVRSR/CVLIGRTPEAFA KLNRCPDLPDGGYFIVGVKVLILIQBL SKNRIIVEADRKAGVASVTSSTHEKKS RTNMAVQGRFYLRIINTLSEDPIVLIIS KPMGVESAQEKIKTVSPQPEWR
2505	16406	A	2522	2	376	IQSFVVIGYHLCSQGLSERVSASKFP LLFPFFPKGGPFWP/QGKTRGPLEPK GDQSGPLKQFPCLAIPMKKGGGPPPP RGNFLGFKKKRFPQVGGGSKPREGK FPFLAPQGGGNRG
2506	16407	A	2523	403	3	GAPRSLSEKERGLMGLNQSSPFEQLL HAHYEQKLAASQIEKQRHMKLGKQ/Q QEQIARQQRLIQQHKINLQQIQVQ GHLPLPILMIPVFPDRQQLDALAQGGFL PPGFSYKAGCSDPYFVQVILY
2507	16408	A	2524	2	369	NARCLTLEAARYAACVTVVISVPACMC FCVRVCVPVSGGCLCVCVSMVHLSLC /VEQACLNMVCSLHVCLYICACLCVSV CEAVCLHLESHCRGSGRFPVVGPAFSL SSCLITAPPSVT
2508	16409	A	2525	59	380	RNRNFNKKSSFFFFFKGPGGGEGGK GPKQRQGEF\NHWGQKTFGQTRKPRKP TPGPPPPKIPFFPKLEKKQPGQGPQGG QPGQKQKPGGAPKRGKKGGET
2509	16410	A	2526	1	371	VHPLSRKIKPFFSNTLVILIVASBMD KRRFQATRKSSP/CIVVLRHPT
2510	16411	A	2527	445	3	RHLGLALIAKRELKQDLPEMHWDS SITFWG\VDITETPEKRDYGLANLVE HPAQLMPPVNDTPTVLGVVITKKEQK LRQTRRAQKETQKRVGLMPPPEPK VRISNLMRVLTGAQDPTKVAZIVRAQ MAIKQKAHV
2511	16412	A	2528	1	478	RPTPRKRLKSHRLQSRQESKKVRL/T NAXDNEMEETDDGPLLVRVYVAGDS IILDRSLTVEVLRTPKCVVERNDPIF ERGSTTTYSFRQNYTSKPSNKETDMF PLAISMGTDPSMTQQLPFRHARIEIKH KPKREVYASALDQATSVIT

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2512	16413	A	2529	385	1	OKKCEDLX\,DODNP\IVR\PEPTPSQSHG GVVNI\SKPYVVLQNRGFYLYGAWGRD YSPQH\PNKGLYWVA\PLNTDGRLLLEYRL CNTLDDFLLY\INAREIRITYVQSGSIAY NYNKNYVSMHNTVNV
2513	16414	A	2530	1	1228	FRATLRPE\TMFGQTN\GVRLPMKYIGFE TVWGD\FTCTQKFAARNMSYQGFKNQGV VPVVKELMGEEILLGASLSA\PLTSYKVIY VLPML\TTIKEDKOTGVVTSVPSDS\PDIL ALRDLKKQALRAKYGV\IRDDMVL\PFEPV PVIEI\POPONLSA\VTICDELKIQSGNDR EKLAKAKEKI\YKGFYEGINLVDG\FKGO EKVDVKKT\QKKMIDAGDALIY\I\EPK QVM\SRSSD\ECVVAI\CDQWYLDYGEENK KOTSQCLKNL\TFCESTRNFEATL\GWL OEHA\CSRTYGLGTHLPWDEQWL\IESLSD STIYMA\PTVAHLLQGGNLIQQAES\PLG IRPQ\QMTKEVWG\YVFFKEAP\FFKTLQIA KEKLDQLKQEFEPFWY\PDVLRVSGKDLPV NHLSYLLYHNVAM\WPEQR
2514	16415	A	2531	335	2	KKKAL\FTHP\PPVNGR\PHKNPKIK\STIG SP\TFSSL\PLKKKECFVNGQGVNWL\YFG SLQSL\SRFP\FFCLNLLSHEWLL\FP RQKY\FFP\FFFLVDM\GFTVLA\WY
2515	16416	A	2532	3	380	AINSYIR\DDSSSY\PEWQ\SA\SSK\W SPL\PRALH\TD\AK
2516	16417	A	2533	3	2083	SS\EGYLRGNMS\NEEEES\SQE\GSQDY VREI\PPGLE\SPG\PFQSP\PEF\QSPFR FE\PE\SPGFES\SR\PGLV\PPSP\EFAP\ESPE SD\QS\PEFES\QSPRY\EPQSP\GYZ\PRSPG YE\PR\SPGYE\SS\RYES\QNTL\KTQ\SP FEAQ\SSK\FOEGAKMLLN\PEEKS\PLNI\SV GVH\PLDS\FTQGF\GEQ\PTGDL\PIGPPFEM PTGALL\STPOFEM\QN\PLGLTGALRGPG RRGGR\ARGGQ\PRPNICIG\CKRS\FGRS TLIQHQR\IHTGEKPYK\ECVCS\KAF\SQSS DLIXHQ\RTHTGERPYK\CPRG\KAFAD\SS YLLRHQR\THSGQKPYK\CPHG\KAFQD\SS YLLRHQR\THSHERPYK\CTCKKYS\QNS RSH\SHQRVHTGQRP\PS\CGI\CKSP\QRS ALIPHAR\SHAREK\PFK\CEQ\CKR\FOQSS VLA\IHA\MTL\PGRTY\SCPDCGK\TFN\SS TLIQHQR\SHTGERPYK\CAVCG\KGF\CRSS TLIQHARVH\SGHERPYK\DDCG\KAF\SR ASD\LI\RHQR\TH
2517	16418	A	2534	434	3	APLHSGKRS\PTKCN\BOG\GAWNR\SSLL DRHKI\IHSEENPNK\CEG\KAF\KQA\SKL TIHKI\IHAG\KPKYK\RECGKVF\SQSSHL TTQKILHSGENLYKCKKCGKACNL\SSNL TNHNR\IHAGEKPYKCKR\CGRAFNI\SSNL NRQECI
2518	16419	A	2535	46	454	PST\SSKVM\DKOTL\SSSQAT\SNTRYAA ALYRQGS\IYK\EMKTCV\TKPYTVVHSS I\PM\AKONKQ\PCPSA\DSWNRHMS\IH AMG\CYLTMKRNBAVHL\PRR\WSLENIVL SER\SH
2519	16420	A	2536	13	476	RLKYTYK\SHKKA\PNKKY\GKCSQ\QDF PINHCL\PTKLIH\CDKIG\GV\GKVP\QPT

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						IADHTPVAIKLIAIGGPDIVNGSHQKTF EELIPRIIISKELSLSGKVCNRTGGI GLNSVHCVOGSGYPPILLKAWDHYNSTKG SANDRP / DFFKDDQLY
2520	16421	A	2537	162	296	YVCQRYKLINPFLPSTYKINCKWVDIN VKPTSVKLLQEKRRSL
2521	16422	A	2538	495	348	FGWHAFTVKEPRVEKLCKASARAKPQP PALIAKTFKAGGTTQYAGAL
2522	16423	A	2539	480	63	ARSEAMISLADATNAGSERLQGLLLLP YIKVGNSEIKKGTGPGSTDPKTAAYWA SRVSENRPACKALIQKQFGLVTGTAD VSIIALNWQ / PDKWPKLKAATGLVSVGT ASEVYQGSTVILHCLGPKNDNRNTHSYST R
2523	16424	A	2540	2	509	NVDADDVRLAIQCRAGDSPTSPPPRDFL LDIARQKNOTPLPLIKPYAGPRLPPDRY CLTAPNRYRLKSLIKGPNQGRVLRPSV GAVSSKPTTPTIATQTVSVENKATPM SVTSQRFTVQIPPSQSTPVKPVATTAV QNVLINPSMIGHNILLI / TTNMVSQNT A
2524	16425	A	2541	501	1	QMQUVEDPGPGPREBASSYKCELRQ /LPQYVRDFPRKKAESGMDSSRNLEKL AERFLAKTCSTSDQFKKQDNVLSFVNC CHLLLTQVKRESRAHTLSDIYNNILIP RFQVSDSSSLFKVQRYFFTE/RGWS NDTIFKILLDMLITWVTOISVHOTPV
2525	16426	A	2542	473	287	EKDPNLEPKDLRL/KTSDV/TSTRENEF EDYCLKRELLMGLCEGMSKPSPIQVC
2526	16427	A	2543	268	482	KKKKNGIQRGGKPNPAPLRLPTHTQIT NSCSVRL / VDIKKKFPKSLKVEGGAQA RTHINRAFDIIVLTRGG
2527	16428	A	2544	407	1	CKKICYLLHYWWEYKMIQPLNKTWQFL /KKLINILYDPVILYDIYPEELY
2528	16429	A	2545	28	399	FRHSSFORSGRGSQIWHFSL / SVNPK IGSVAGINYLGVAPATTGTETLDVQ / K GEADTEH
2529	16430	A	2546	2	365	FUVNVDEVGGEALGRLLVVPWTORPYE SFGDLSTPDVAMGNHRVKARGKVLGAF SDGLAILDNLKGSFATLSLHCDKLVHD PENFRLLGNVLVLCVLAHH / FDKFAPP
2530	16431	A	2547	375	1	GFACRHWKRVREVSAAEASAASKVR AMSGKQKNGMNVWTIATLALQAVISS ATTQNGPHSLQIQQQQIHLQKQVVIQ QQIATHHQQQPHRQSLHATHLQGA \QKQKQQQSWR
2531	16432	A	2548	3	376	ELGSDVA/GARALVDRGRKGEIDAE DSFKSADESGQALLAAGQYASDEVREKL AVLSEERAALIKLWKLRRQYKQCMDLQ LFFRDTQEVNMMSKQBAFLNEDLGDA VDS / IKBILKKIE
2532	16433	A	2549	360	1	RGEMLWTVNNRFLYNFVPGKLEFPKSH SLYPCCYVHDVSPWIDQKGFDELEHT VGRAVSQDTIISIQFLSRFQHPKTVQS LCYRITCOTCDKALTQQQVASMRSQIRK EIQQHQY
2533	16434	A	2550	2	403	VVAREDTLRDLVQLTLENSGVILNRKA ELRAGVFLALEBQKVENKPTLVNBSLK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2546	16447	A	2563	407	1	KVLPPPLQCLSETAS/SIN/VGGQHEW KWDHPLSKCEVPQGGSIITSSNGPVSYPG FPSPY\TSSQDCVMMITVP SGHGVRNLNL SLAQTEPSGDFTATWGXQQTAPRLGVF LRSMVKKSQSSSIQVLLKFHRDAATGG IFAIALSAYPNTKCPPTIHPCI
2547	16448	A	2564	382	1	TOEVEVAVSLDRAPAFQSGQCSSETLSON SNSNKTWILDHFGSLDFLDQRFSACTV FTPREQVSSHTRMFLALFTLAKTWGQP /KTPPVIGWIK\WHLVYMEYYAALKK DEPMSFACTWKLXAM
2548	16449	A	2565	429	0	PLQSSQTSCHQNSRKRISLHFFGDVLA TPEQVGGSPQAPVP/PIYLLDIPLEVBQ EPVSLRLGDVSLVSVSREGLQPASITGS RGHLIVQLQELLLHMMVLSAVKSRNVIV GLFVSLILLSLVAIRLR\ SASEAPVLL RP
2549	16450	A	2566	464	1	VIHGVI\NPFVGGDQYKKKFLK\FYQE IYESPFVTETGEYYQEBANLLQESNCS QYMEKVLGRLKDEIRCCKYLHPSSYTK VIHECHQRMVADHLQFLHARCHNIIHQE KKNDMANMPVLLRAVSKGLLHMIQEHVL RALGRIPTSYVRMS
2550	16451	A	2567	3	178	YNGGGVCSDLISSHCTPVWVT\SETLS QKKKKKKKKKGNLPETRERALPGKKG GGG
2551	16452	A	2568	215	411	ILHIFILHVFIDYLSVRHSSKILGYISE QIRKNS/WLYYVAHTCNPTLGGGGGQ ITRSGVODQG
2552	16453	A	2569	170	430	TSSQLAQCLAV/VSGFLAACPELTSA SPWLQVRTNMAASPLKFSAEOLFLKAA LSQFCVIMLNAKLSVQKYEK\LI SAFP SDSR
2553	16454	A	2570	3	463	CRFFGYSTAAAPMTSSSGSTLSGITAP AVPNIPIGVNGFTGLPQANGQPAE AVFANGMHPYPAQSPITVADPQQAYAGV QQYAGPAAYPAAYGQISQAFPPQPMV QQREWPEGCNLSIYHLQEFQGS\ELM QMVLPFGNVSSK
2554	16455	A	2571	3	424	LKTMKGGTGNGLEIMLDIQQDEYLPVWG ETGTSPTSGAPLHGSRPQ/PARGFLGF TVRPG
2555	16456	A	2572	1667	2046	YIFFPTAFLMAALTFQVTTTFLAPLALLV RSKMMRASHDIGPTANITLN\GKTGRAS KQRREBRNQBKLSLPTDMFLYLSPP IVLAPKLLILNPKVLAYKINVQKLLA VLYIKSSKSENSEHH
2556	16457	A	2573	1	399	FAISQDHVLPSPSPSLHKKQTITAPH PDLPHQATCSRPIRHQRTWEDAPLAKA DTVS PARHPAAATKAP/TR/PAPDKPG GTSDPQTGPAP\ PASPPCSGP/APQVP RKPSRAAPSKSVTVPRVRPTFPF
2557	16458	A	2574	2	452	AKVNEMKSPMRKHTLLNKEEKNQLE SSLWEASDEGLGSPTKKAVTFDLS MDLSSESSESFSPPHLDSTPSLTSRKI HGLSHSLRQISSQMSVSLSDLSNPQS PTPLASMPAQLPP\ RDPKSTPTP/SYC GRGRGFSLTS

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2558	16459	A	2575	2	369	TLVYPATITFILLISICICYNIVTAVELTT SGVPVYKVIAPGGHCIRKQKCDPEIFN TPETAKACPGALCNFAFYGEKSLYHQYI PTPHVYNLFVFLWLNLFVIALGOCALV\ GAFATITVYA
2559	16460	A	2576	406	1	RQEGTGPSYLLLVGITPRSPWGFSPPLG PSGKNPIKTPQGPQLQGFPRVQMGVLLP LPSPSGN/CSIKVSALNSSFSPSGVNPQ EASLPWF/CFFNESPVAQVQVQPP PQGFKPSCLSLGSLGKVRPLV
2560	16461	A	2577	3	410	YISPFYITTHRENTNLEGPFF/RLNQRAD ALVSAAPADAQTFHSITHLNAGLRKRY GLSKQVKQELVHKPSAGEVLHLPHQAG VNPRLGSPNSINQMDITHTPTFGKLSFV HVSVDIYSHFIMATYQTGEATVHK
2561	16462	A	2578	386	1	TERIRQQRQRETERKRYTERQRKTER IRESDRERQNKQIERDRKAT\REDRK KQRESDRERYRERENQIETERDRKQSD RDRSTQRRTGRIRYRERERQQTESDRD RERESDRERQREKCI
2562	16463	A	2579	2	432	LILYFAKRYGARGECQQRADKAACLPK LDELREDEGSSAKQRLKCRSLQKPGER AFIKWAAARLSQRFPKA*FAEVSRLVTD LT*VHTBECCHGDLLECADRSDLAHYIC KQSDNPSKINRECKEPILKPHCIAEV END
2563	16464	A	2580	3	426	NLLANDALIREKTLGKDHAPAGAAITANL AVLYOKRGKYKAKPMSKRALIEIRKVL GKHDPDVKQLANLALLQNGKTEQGE YYYPRALHIYHTKLGPDPDPAANTKNDL VACYLKGSTVKQA*SLNKENLTSAREWD V
2564	16465	A	2581	10	389	KLGA*GLMGHTLITNPLTEPLTYFPLGL YL*SIITTSICLLQTDL*ALLAYSSTI HIALVITAILIQTP*SPFGAVILILHAG LTSSLLFCLTNSNYERTHSRIILFQGL QTLRPLIAL**LLA
2565	16466	A	2582	1	192	LIPTLAITR*GGQPERINAGTYFLFYT LVGSLPLLIILYITNTLGLSLNIIILTL TAQELSNS*ANNLI*LAYTIAFVIKPL YGLHL*LPKMHVEAPTAGSIVLAVALLK LGCGYITLRLTLINPLTSHIAPFLGLS LA*GGPRLKANTFLFVFLVGLSLPLI ALITYHTVLSGAILLILTAQKLSNS
2566	16467	A	2583	2	438	QNHGSLGSLRLEFSPSPVFWRRRRRW RQRHKKKFTAPAAAGVAGWTKACGL RELINILRLNVSYNHIDLSGLIPLHG I KHKLRYIDLHNRNIDSIEHL*CVWGJH FLTNLILEKGDNDNPVCRLEQGYRASIFQ TFAQL
2567	16468	A	2584	3	415	GRATLLERAYQLSGTEIDLIDDRGE WDSLTPQARR*KEAGLMFVOLARFINI VCKEAPGTFLAFLTSEIKSLPHHPFLAER IISMLNYFLOHLIGPMGALEVKDFSRF DF*POQHVSDSGATYLDLGDENFC
2568	16469	A	2585	2	453	DAKMYLSKYATVIRNLREGTCPEAPSD ECKPEKRCALSHHQRKCDNDSDISVGK IKCVSAETTYECLA*IMNG*ADAMSLDG

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						GFVYISGKCGMLPVLASNYNKGSDNCEDT PEAGYFAVAVVKKASDLTWDNLGKKKS CHTAVGRNAC
2569	16470	A	2586	3	413	MAVESRVQREIGKEP*KPDIR*KTCPFL MLRVFTTNNGRHHRMDEYSR*NVPSSEL QIYTWDADTLKELTSLVREVP*ARKKG THFNFAIDFTDVKRPGVVKIGSTMSG RKGTDSDMTLQSQKFPQIGDYLDLAI
2570	16471	A	2587	1	798	LEVMLMLKAGADQRAKQDGMNALHFA TQSHVLVVEYLQCHLLEDLNQPDDEG RKPFLLAQRGRVHMLKLTNLNLTSE KDKGNTALHLAANGHSBAVQVLLAQW QDINEMNEINISLQIATRNHGLASLVNF LLSENVDLHQKAEKPSPLHLVDINNH TVVNSLLSAQHDIDILNQKQQTPLHVAA DRGNVELVETLLKAGCDLQAVDKQG*TA LAVASRSNHSVLVUMLKAEYYAWREE HEESIRDPSTGFTL
2571	16472	A	2588	2	285	AWSLAPSHPHSKVPVPPGRKKAEGRFGA AAQAQAQAEVHPSSSGPSPLEARQFPVW QIPPTPSLKTTTRGAQPHSRICLA*S RSVSLFRKM
2572	16473	A	2589	11	438	AYYGLNHLGATLSQKKKKKKKKRNF RGGGPPRNPFWHVGIGGRPTGTPRGEKN GLKQKKEKFLAPR*KKSTGKPLKPPQG KQWGGPKFPKPKRPPRAGGSLKPKGK NEBFFLALKSLPGVFLGPGGNFGMLK NQ
2573	16474	A	2590	313	391	VHLVRVKGLL*SRIYKELLQNNNTT*DN PI*KWATDLDRFSTKYTQNVDRLMEK STS
2574	16475	A	2591	62	616	EVHQTSVRDSEVRERFQARGPLMFAER AGRQRMVLPALQPRRGLR*RGAVRQH GAHPGLLLQDQKIPALPGRKQAGSLHA PGTEGEFDHGGDPVLDAGIQEHRQGRHP TADHILNPGHRRGBAHVRAAV*RAAGAE GAACKERRAHQANTALQVHR*LGSTFAEL RLLRKPGRTSVWPSM
2575	16476	A	2592	345	438	HKRWLPVPIYLQHLF*VFGEHPEVYLIL PGF
2576	16477	A	2593	479	313	QDGLDLLTS*STRFLPKCWDRREPPFL KLINLQSSGVGLHVQLFPPSPCFDQLL
2577	16478	A	2594	3	419	LTLHSNTLPPPEMSGLT*FPATNAYTF LPSAIRLFPPEIFFIAYLVSLFDETE LSDHSHLTFKYERDANHLNQAQR LERLPOLHGTPIVPTADHFTGSLGAS DTDIAHSLAYTGRSARQIMRTAKY
2578	16479	A	2595	1	419	HKCDERYRGRTYGGYWSLCATVNDLDE RIPITSASYATVTLDRVNLILGSDTGV SMPLL*ERRHILNETGKFLVDKPGGSP NCVR*RDNIHKLMLHVVESSFPYRDVT LFEGN*VAFYTRAQILLVTDTGTVLEK
2579	16480	A	2596	199	397	SPTALNTDDNVFPMGSSSRGHRQFOTG IVSDHPASAGPIS*DEQELPYAVLHFEK VQPLEFKVTD
2580	16481	A	2597	154	3	MLSIRGFPCLFVCFETGS*YAAQGLKL LGSGSPPISSFSQARITGVSHL
2581	16482	A	2598	425	223	QITGHGGRCL*SQLGKPGQRNFMNLGS

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						RSPN*PKLLPOTSGWVIMLNSLGRGKKV TAYLNKMMPTP
2582	16483	A	2599	3	441	OGPSRDIVSELYQINAPDTPESLLMIGK DHSDDPIHHTFDHMRWTKENHAGWLLLR SVDKVMKNEDELGDSTISQLQKQILSLKY AKIALTERLISCPV*TEIVLNYT*SLIM LLTDLL*KVHAQSHHAHQASNCNVMT LIGLQH
2583	16484	A	2600	131	423	GFAPNVLFLHGTQFLAFLPISHLTYSY LVPWILSGTDGHTFRSACLERMLAEAWI FGGVKIQYGGQGBK*CFFTG*SVYVNG SSGKVPWETSRT
2584	16485	A	2601	222	447	SGTSPFGL*VVQKQNRFGRLNAQLKDLG VSPGSDYQKLNKNGISSGLDNGVTTSDHD VLNMAIVGRKTIWLGDSG
2585	16486	A	2602	2	457	FYCDPLYKATGTEDTDVLSSEIMSPAK SIEVMGDGCLNDEHLEELGILKAKLBG HFQVQELRQVKRQEDNYDQVQVMSLQDE DECDVYILTQVSDILHSLFSTYKQILP WFEQLLPLIVNLICSSRPWPY*QWGLCI FDDIVKHCSPSL
2586	16487	A	2603	1	297	DHRQKLYAHTECGKALLKWSVICVHQKI LEEEKFCRGTKYDNI*FSNRGCPVPRMV HAVEIPCK*TECEKATGVHGPRGASEFTL PERFTGMNMAKCESR
2587	16488	A	2604	1	405	RFDVSDGLELRPKYNGIAHLRTTIWYLD GLRGLYKGVTP*IIWSAGLSWGLYFVFN AKSYITTEGSSERLKASEYLAETAEPPG MILCITMPLAVTKGLMLQDAVWNSPH *QYKMSDELVKIYHGQVQGLY
2588	16489	A	2605	165	3	FEELLVFFPVLKNTGIRFGAVATCNF STLGRITRTGD*DHPOGGETLSL
2589	16490	A	2606	3	455	KRYGCFSEKMRKRSATNTFFCARKEVTL GLLGHNGAGKSSSIKVTGDT*PTAGQV LLKSGSGNDALFGLGYCPHENALWNLIT VRQHL*VYAAVKGLRKGDARVAITRLVD ALKLHDQLNSPVTLSQGLKIKLGFCLS ILGKPSGGLA
2590	16491	A	2607	1	429	VDYIVRKFCIQGSDMNRKFORLITQF HFTSWFDLGVPTPIGMKILKQKKAEN PQYNGAIVDHCKA*VGRGTGFDIEAML DMOHT*RKVDVNGFESRNRQSCQKQVT DMQYVFITQALLHLYGDETELEVTCLE TPW
2591	16492	A	2608	166	435	KFLSNHYVHFQKQNFVKVLKPIKHLVLNY FKNIVLQGV*RTATGIPALWBAETGESL EPSSRPTWAMWRNSISTNAQIKNLVL RLIDPG
2592	16493	A	2609	228	431	IFSXCILFNCFNYPFVCHGIGRI*LTPE TGSCHVTPAQGVQWCDYGLQP*TPGLK* SSHLELPSNNQH
2593	16494	A	2610	439	175	RNGGLRLWSQLRLRLRWYHFPSSGSGC SKS*SYHCTPAMVTVQDSSLLKQKRLIS TYTSLSVLNETVIYIVYTYTKLDTSPK RKLL
2594	16495	A	2611	1	439	LLGSILSSMOKPRGLVDQETLRKAR*QA ARINKLQEHKQKVEFRIRMEKEVSHV V*DSGHITT*VQSNMNSIERLHVEVVEV



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						DGLTSFYFGEDDDCRYGMIFTKDAAPSD EELDSYRRASEWDPHMADDKRKLRLAQ RPDDDA
2595	16496	A	2612	1	439	VIRKVTGTGSSSTVLDYTPSTSGMP VRKSEDQTDTKRTVIKTMEDYNNNTAP ARDVIMIQVPSIWDQDDFESRDQDDK STQPISSVGRPATVIKNVTKPSAIVKY PEKESFPKALIKFTMDVSHVPIVHEVK SS*YSA
2596	16497	A	2613	2	453	EXPEKEECNLWTEWQENVPGSFGGIRL YQLQELMTITQKALHSQPMKKAQGAIA ASMALQTSNLVPPGLMILTAIVGELAG RTWALKEELKATACVETASAEI*KSV PNQPSITHRIQADLKRCSENGPYKI*P VICAAIDILHA
2597	16498	A	2614	2	441	LEPALPGRWGRSASPSFGSVEKTRON KQKTPNGNDGGST*APQPEKKRARD PTVSEEAFAKNIMEVKVIPEELKRWLD EDWDLVTRQKQLFQPAKKNVDAIL*EY ANCKKSHGNVDNTEYAVNEDVAGIKEYF NEMIGT
2598	16499	A	2615	1	430	RGRDLHCETESQSEASTSEGHDSLSVGT FEEDSQLEFILOPKSKPPANLNGIMTC *DFELLNPRVRFLLEVQDLALTRRQIL LHKGLSDYKSTTLQRLVLKSSRSRGGP LSIEDGLNFQL*PSSRVYGFATAEELK SSE
2599	16500	A	2616	373	352	YCKIKYELFNSAALFPROGLALPMEFC SGAIKVCSDLDPLGSSNPL*RKIKESTL NLEKSLCTRIGIFLCKYEEVPPKFLKICF QITPLETGRSRSVQAQVQWQDQSLQPR PGLKSFSCNLNPKCWYRCEPPERALS
2600	16501	A	2617	498	157	OLIGSSTHQAALESRLSPPPAGPGTHF HYQGAHWVVGSGTSPDSLPSILGRGVS OLHPRGKRGASDT*HKCFVPLWTIGG KYRVSETSRIFSLPPTTLQRAGLDSGSG SL
2601	16502	A	2618	255	389	LSEFYTYEOPSRIRPPIGS*GTNLPLPLS YIPRSPSAVDENLLOE
2602	16503	A	2619	3	207	QHSSLIITRAITAKLGIAPPHF*VP*VA QGTPLTSLGLLIT*HKLAPISIIYQIS SLNVSLLLSGT
2603	16504	A	2620	3	207	QYSSLIIMVSGIKLGIAPPHF*VPEVA QGTPLTSLGLLIT*QTLTPISMIIQISA SLNVSLLLSGT
2604	16505	A	2621	45	447	WRRLDCLNLKCYTITASLKHFFSIAHRFH LHNSILQSQSCRAQGTATCTLNL PIGSSQSWPTLTLEAHLAWLTITNN WKDNRVSDQVSMFDRSSEMNIIYV* RSIDNLPHLICSTLINTNSFL
2605	16506	A	2622	3	142	GNQATPKTAPATWASTPTTLVATVHAYR **VARKRHPLKFGGRACS
2606	16507	A	2623	2	453	HGPGGLLDVTDKRRIRDFPLGECPCRP DGLVLPKSLRYTA*DLRNEDLKLWTDI YQASVPKGAPEHILIQIVDASTVITWD YHVKGDVIFNTIYHSKPSLPPKDYLI AHSITFPDGRNVHLNKKVWMLGPDYIMW ITTLITNNRN

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2607	16508	A	2624	1	315	EEKQAPGFTTGRGKLTPLFCNAHVRFTI STSLYIKGAYP*ALKGKXY*LA VFWVY NKKGLNNNLFIDGVHLCFVPEVRKYLA GRGLPFSIGLYHLTIJLFFFF
2608	16509	A	2625	232	478	LDQGNYPYTV*MYIKTSHCIP*TYITLNF HLYNFRYNLGDYNGEIVSEVMAQRQPHK PTYAIPIPIITNSQFKIQEAMDVKE
2609	16510	A	2626	3	430	TSTPNVHMGSTSLPGDSTTIEDAQSHS ESASPALSSHPNNLSPTGWSQPKTPVP AGRRAPIVSGIPDRDKLRPCGQRD*GYI WEIEASEVMAKTRIVSGSPGTVIQKNH GDVALATLQVVDSTPQTFQGFNDVAGL RI
2610	16511	A	2627	2	341	ALQRHEDTDCPCVVVSCPHKCSVQTLIR SE*SAHLSESRVIASTCSFKRYGCVFKQ TYQQIKAHESFVQHVNLKKWNSLKL KKGSSFDKCEVCNKNKSIHCWHIQCSSV I
2611	16512	A	2628	2	179	RHTGLMVTSLBAVFPFGQVRRITLFTGLP RDARKETVESHFRA*AHNLVGDSPCCIS RTGEADPVHRTPORQCGEDCGEPLPVS RWVGSFLIHVIOEHL
2612	16513	A	2629	1	418	GFSPCHPVPVKRHRDSQP*TPGLK*S CLGLPCWDYRHEPLRPNTISY
2613	16514	A	2630	3	442	FTOGTIIITAPNGVKEPT*LATLHGSNM K*SAAVL*ALGYI*FLFTVGLGTGLVLSN SSLDIVLHDTYYMVAHFYALSIRAVFA ILDSFTH*FLPSGYTLQAAYA*ITFTI ITFGVNLTLFPQHFVSLFGMPROYSDF DATTTR
2614	16515	A	2631	2	454	NAPNELICNSGGWGLFSVLDLSLAVITY ARFTGAPLKVHKINPWS*PSGTLPALR TSHGEVIVSPHKIITHLLKEKYNADYDL SARQGADTLAFMSILLEKLLPLGVHTFW IDTRNLYLEVTRWEYAEAMPFSLNFFLP RMORQYM*RLP
2615	16516	A	2632	131	410	WMWSSKAPICFRLPSIGDADTVHQCAM FQKHSALEGVHLVFKPDVLVYQLLQM PPRKCLNPGAVTHACNSMTLOGRSR*F TRSGVDQDP
2616	16517	A	2633	2	230	FFSETSSLEITQIGARHGGTWRLQOENN LNPGGGCSILRSCSCAPAWTVRLDLR KKRRNRP*KILKNYLIKIVI
2617	16518	A	2634	2	370	GTSSSDPAQPGDDKEFIDASKRLVYDGIR DIRKAVIMIKTPELDDSDFETEDFDR SETSVOTEDQQLAGQSARATMAQLPQE QKAKIARQVNSPQEE*SKLDREVSKND SGNDITVLVAQ
2618	16519	A	2635	2	376	MTITDALY*RELFPDADKDKMHSRRT ALVFNHERF*FWHLSLPERECTCSDRNL TRRFSDLGFEKCFNDLKABELLLKHE VSTVIHSDADCFVCVFLSHGERNHVAY DAKIEIQTLTALF
2619	16520	A	2636	1	461	DMAFLILTERKITLGYGQGRIGPWACPY GILQPGDAI*LFTEKPLKPTVSTITLY ITAPTALTALLL*TLPIPNPLGNLN LGLLFIATSSSLAVYSIL*SR*ASNRY ALIGALRAVAQTI SYEVTLTITLLSTLL

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2620	16521	A	2637	2	384	IRGSENLRLSLTT ENFRALAMIAFGQYRQKRPFEDHVKLAN D*LNFAKTCVADESARENCDKSLHTLPGD KLFP*ATLRRETYLAKLADCAKQ*PDIEH CFLQLKYDNPYLPRLVKPNVDVMCTAFH DTETFLK*YLYEIA
2621	16522	A	2638	1	373	TFIYLLFLFSSAYSRGVGRDAHKSEVA HRFDLGDENFICALVLAFAPYLQCCFP EDHVKLANEVTFAKTCVADESFPEN*DK SLYTLGKGLCTVATLRKETYGMALDCA KQFDRNKECLQ
2622	16523	A	2639	2	375	KGFYCVRLSTGTQRHFGAVLNKHL* CNVGA*GPHCEKCTLCTPTEEPKAL TFFREHGP*VSDPEVATPTEKRPISLD QETTKLEPGQPLSPGISTHILHPQFPV VIEKTSPPVPEI
2623	16524	A	2640	215	478	KYFLASHTSLFICYTAHLCTTAEKPK IESHFGKRLDADLVF*KSDSTVVDVP SKPV*TSGLFSGKCL*HIVEGIIIRAVDP RLKY
2624	16525	A	2641	208	376	ILRNLIKNHFWPGVVAHACDPNLEAM* GGITRSRDWDHPRHGEAPSVLRILRLA
2625	16526	A	2642	424	2	KGEPLPLPGGWT*GPRAFPQAQIPHAG FKTRGCPFPLPQGRNKAQVNPPECPER FLPGKSGKRVAPLKNQAQLGGPFPYPHP FGGPPPRVPLGPGVQTHLGNKPKPFPFP KKKKGTYGCSVGNWGPSSQTLPSPPQAS
2626	16527	A	2643	190	3	ELSTKPGCGPHRRITAGLKQCLVMPFLE RSGLSER*HLHLPGSSDSRASAS*TAG ITSVCH
2627	16528	A	2644	2	339	CCEKPLERKSHCTAIVENDEPADLPSL AADPVESKDVRRNYAEAKDVFLNPLYE YARRHPDYSVULLRLAKTY*TTLEKCC AAADPHKCYAKCFHEFKPLVERPQNLK
2628	16529	A	2645	81	369	VEVTGQPCNASPVKRNWLLPLIALA SGSFVWRFTDG*TSVVR*IHNNMTQLI NNHLRA*YSVYRDIYFLMIAL*SS*PA SVLLFTADYCE
2629	16530	A	2646	1	348	DMDNPLRPNRYRFG*ELKADIDYHFK DNEDDQHLQSLRTVSLWAGAKDD*HIVE SEAMMYEGCEIKVTLATLKNVQVATVTL GGFETTPGDLRNNKSGSPVHIMGLHLV AGES
2630	16531	A	2647	1	178	GYYDTTLDVRSQRVRSLLGLSENSEPNGS VETRNL*QILINGGESPCKGQBIKRYDL YIT
2631	16532	A	2648	181	244	TKRYIVNMIPIYFNFPP*GLNLSAQA AQQWNGHSLQNPGLKSSCLSLPCS *GYTIFYLSIHQILDIWIVSTFSLFLH VSAYSSIKNS
2632	16533	A	2649	2	369	KNITFISILLFHSVYGFEEFLDAPKN DVAHRPFDGQHQFKALAEIAPDHYFLH CPFEDIVTLNNS*TEPAATCLADESA*N CDKSLHTLFGDKLCTVATLR*TYGEMAD CCAKLEPERI
2633	16534	A	2650	1	349	VTFISLLFLFSSGYSRGVRLDAHKSEV AHRFDLGEENFICALVLIAPFAYLQCCP FEDHVKLVNEVTEFA*TCVADESARENCD

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, N=Methionine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						RSLSHTLFGDITLCIVATLRSTYGETADCC AKQD
2634	16535	A	2651	21	403	CVCCVCVRESRTESLPQDNEDFNKNAS VKDVRCVHPDCDSQNDPPHEATGPTAQV TIYSLINLHRLKYFETLDLH*IAIFPS KVSILNHGQIADYAPALDCHCHICAC KYABLKBMDRRSVK
2635	16536	A	2652	1	355	ARMSITDTYGOHLIAGGLMTQEDVSEIK SSIYAKSNHDLNMAHYRPTALNQAHW HSLAQAEQITTWSSGVFEDLLMVQNM TVQVVP*BLQASHLLKTHQSRKNNMY GKLDW
2636	16537	A	2653	2	360	LFPHLG*YKFNALLRYTMKVQVLTPT TLVKVSRNL*KVGIKCHPEAKRMPACA QDYLVSVINQLCVLHETPVSORVAKCC TESLVNRRPCFSALVQETVYPKEFAE TPTPHAD
2637	16538	A	2654	360	314	YTCATVPCRLFWCCQDRVSLCCLVWSQ TPELK*SSCLSPFKC*NYGHEHTWPAKI IFILNLYKSG*ATATKCPPTKVTTPSSHQ Q*HCTWPFYFYK
2638	16539	A	2655	1	353	NWTL*TLKKIPSLAKDAERIKIQSVRWK KIPAKHTSDKGVEKYY*RTLLNQ*ENN SIKNWSKNLNRPTKDIQKANKMLSAT SLVR*ESKLR*Q*YHTSIRVAANKTID YVTSW
2639	16540	A	2656	340	10	GREKDEKCYLKPGRSQDGRGAPKSSPG VP*PPAPALPGGRSSPTQSLAGRD LRPPOPSQPGGPOLIFPVTKKKKKKE RKTLLAWTRSNTERPELAQREGGCLRQ
2640	16541	A	2657	509	261	IYPFKTHCLHSALGVAETEKETAHEL DL AGASSRPKDSQRNSPQIPPPSPDSKKK SRGIMKLPK*VKQ*TSQMGVPLHVA
2641	16542	A	2658	345	3	SAHLSHPKCMQYREPLHARTISPLPKA SSPLYGRATFYLSPTPLNDGRWVLSIFW LL*IVLP*AWVKYLSSETPLSIF*KTGS LSVAAQAVQWHHGSIQPOTPLGRSSH L
2642	16543	A	2659	271	56	VILYIVMPIPRCPHPHYIHTHTHTHT HTHHTRLGKREF*LYSN*LPGYSTNGN KIFLEIYLLPILKFM
2643	16544	A	2660	366	68	PQQSKIMPQTERKKGRKEEREREKE EREGKKEGRKNEGTETVEGSSSKIQEQ TRIKAS*LNSLYTTVPQRRLKGKKHP KDSNPKD*RNISPHR
2644	16545	A	2661	351	199	LRLRLQENLLNPEGRGFSEPRSHYSP DNAT*DFMSKK*QKQVSKY
2645	16546	A	2662	1	160	ERAMLHLSQKDGVCSEERSHCCTPTVVT E*DSVANQPGHVRVCLCKPTWYTE
2646	16547	A	2663	233	3	GRDNWLKIVAKESLSGRGFSLLRRVFP NDFPVVILFLPQAPKGGKLSFPFPFFFF FFFLRGLAM*PGCSAVAQS
2647	16548	A	2664	96	349	QMPSSVLTRVANAYISGFFFWFLKQKFC FVYQAEVQGRSIS*PGLVPGFKRFLGL TLLSTWNCRRAPPGHVIACGFKMSLLT
2648	16549	A	2665	322	74	DTYTLPRINQVESLNRPTGSETEATIN RPPTKKS PGDRPFKAFQYRKERLVSF LLKLFQ*IEKGIGIWARLMPVIVPL

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2649	16550	A	2666	2	228	NLALSPLRECKSQGPFIMLIRLVSVS*PC DLPASASQSGASIMGVSHHAQPFPLHSYLR PILILKGDQFKYAFNLFSC
2650	16551	A	2667	129	301	VRPLAGLGSPLIFFFFEKSLAPVADAG GQRHNLG*LLPLPLGKGFSCINLPSTW D
2651	16552	A	2668	318	21	FSLLVKKDQNDLAVNSSSIFPSTFLFLV RS*LDPVNANFPNPFYLFERDEFSLCPCPN TRIPRLKQSSRIJLLSSNGYKCVPLHPA INRFL*CDFISGGY
2652	16553	A	2669	2	322	QGGDLTTS*STRGLPLPKM4DYRREPPR PAFINKCLLSLHGGPGLGTGEGKQD YTPALKQLTQQRRLTGWGCVCAAVRSD SMGVWVPLLDGYEAKKGRFRF
2653	16554	A	2670	29	261	EFTNLSKQVMY*LFSLSLSLSLCVVC VVCVVCVCLCVSVCLFYGSPICLHFMHP DTLSSESFHFLOIISKELKC
2654	16555	A	2671	5	224	GSANWLLTPVIALMECHGGRSPFVGLR PA*PRDPALASESAGITGVKKNLAL NEVKSICILLIFISLDK
2655	16556	A	2672	126	321	WGRGARARRRSHRLRVSPFLALLER PSTMAHICNPSSALGGRGWT*DOREFET NLANLEKPC
2656	16557	A	2673	360	74	SRLLKRTQRQVGLNLDGRGCSQPRLLHC TLAWATERDPSKINKINQKQKR*TL PETNSLLAWEPDVCVTNKLATRLLEMA OKSCSORPQYH
2657	16558	A	2674	192	357	RIRKGLYYYYYLLRNLALSPLRECRG TILAQCNFIL*SSSRSPASAPVAGITF
2658	16559	A	2675	236	375	EEVLYSRKDRHVASYSEK*W*RGSAEAH ACNPSTLGGRGWITRSG
2659	16560	A	2676	236	2	AKVYSINSIGTLVKGVGLLEORRLRPG PKQSSCLGLQSSWDR*VQHPGNPTL FVETRSMLARLVNS*PQAIPO
2660	16561	A	2677	164	389	LTVQHLRGLRLTVVVESSGQASHLLH KNAGRRSRKQCGNQMLIKSSYQPCAEA HACNPSTVG*GRITRSG
2661	16562	A	2678	208	1	CSVYEGSCFCLLREVERVCVVCVCLVC VCARSCIVYRSENH*KQLPSSSILT*RF *IQSTFRSNKRLR
2662	16563	A	2679	159	382	RWLKKNHPTQARIQVRRLLDRDCQTQW LWESGVQPLATTPRHSEMOGWPGAVAH ACNPSTLGGRG*ITDPRPEKLEDCLT GTARHRLGCGSGQCSLWLPDGGIQRWG VGRAQNLTPVIALWAEGRSLEVR
2663	16564	A	2680	29	367	DCQSEQLRLRLEHHSQGV*GCSQP*S HHWTPAWVTEQDPVQNKQTNYNTHQRA GEVWRFINCLSTEQLTLYSEITQILAL SVRN*KLL*YVKS SVISARTQISGGKIF
2664	16565	A	2681	256	1	RNTPVRPMTCHRFPAITLVQ*ERRR DLIVILHMLTSTVILKQWTRPNVAH ACNPSTLGGQGRITRSARDYPOGHE T
2665	16566	A	2682	1	395	LLIKHILIAMALLILEREILGCLQCRK GNVVGPIGLRLRPPTDAIKLFARPLQ PVTITLVMYAPLAVIMAVLL*TPLEI PNLAVNHDLGLLCILATSSLDY*IL*S R*ASHSNYALIGALRACPH

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Yrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
2666	16567	A	2683	3	349	VRIDNAVCLLY*AWAEFTIALNT.IIR PDLDPGNLLGNDHIYNVIVTAHAFVII FFIGIPILYOGGPN*LVPLIIGAPDNAP ARITINIRF*LLPPSILLLLLSAIVEAGA AGT
2667	16568	A	2684	99	2	LTVAHACNPSTLGGQS*ITRSGVREQP GQHG
2668	16569	A	2685	325	4	SSFPMSFIINSFIIIFINTTIFLIPYDV VYSPEFKP*VCFCLTECDYRREPOCSF LPCKRN*VLAPFIKNPPFFFLARNFI FVAQGVQWRHGLSLQPPPPNTK
2669	16570	A	2686	382	269	WGFHVAQDLRLGLGNDPFLALNSQSAG ITGVSHEAQEPLTF*TPSY*ACVGGSSP QFILLVQHGLAGNSFCCP
2670	16571	A	2687	3	381	GRHYAIFTFPNSQICLFRITYKTKCKSF WLPFLNLVSLCAIRGYKTKKVPNSV*RG IFIHQGTGPIRLMOGWNI*TSINGIYH ISRIEDKNKMTFIDAEKWFHNI*HPFI IENIRPGVVAHICN
2671	16572	A	2688	289	91	IRYKELGVACSRTSRNVSYYCHHHHHH RCHYHHHS*RLAALCEBSGWRKALGT SMGRVAFERH
2672	16573	A	2689	3	211	LHHVGDGLDILLT*SAPIGLPKNDYR TEPPFPAPNEFLHLLSLKHVALGRPH TPRERKASGILR
2673	16574	A	2690	2	197	DILTTS*SAHPLPECDYRREPPRPASY AFIRYFCPALSCPWCIETGPIILFAYLR EESFVRSET
2674	16575	A	2691	253	356	AVFVKAIIVKTRNNRCW*GCGEIGTFL HCWBC
2675	16576	A	2692	211	339	PCHFLSILLQWIGEDTRGPMHEALH* PCCSHLRSCHCTPAMFTE*NSIP*KKKK KWLGLKQKQSNACNDP*PCHPLSII LQWIGEDTRGPMHEALHKGSDGVYA VRLITAY
2676	16577	A	2693	1	175	RHEGLNLQGRGCGPSSCHCTPAMVTE* DSVSKKKRKGKKKALILFSGNVLFC LG
2677	16578	A	2694	234	13	KTSREPWSFELSTKGEQCSFGLLYVFC PQMSHYAAQAGV*WNLG*LQPPPTGF KQFSCLSLPSPSSPASAS
2678	16579	A	2695	149	2	SGQEDPTKTRALQWRERSVVAHACNPS TLQGRGWNIT*GQEFKTSGLN
2679	16580	A	2696	2	194	CIGLGVVAGCSSRLRQENDMNLGGAC SETRSHCTPAMVTE*DSISKKKRKNR WGTTRFSN
2680	16581	A	2697	338	357	YLIRKKISNSKS*FSWNGVVAYACNPS TLGGGRGRTTRSAVRNQGQHDPKFFL VSS
2681	16582	A	2698	53	293	TTSIKSKWNNKGGEYKGCWENLALC RRLKCPVLAHSCIALKNTKILGNL*R KSV*LAHSSGCTGMAKSKHGRB
2682	16583	A	2699	2	335	LVAKVPLQACIRTFTSYIFTEFFFF FFQKQSSPGPPLKARAGTFLIGTFLIG VKRNFLPQFSKPGITGCPPLQPKFAFF KKKRGILIF*PGGVNSDDKIGIPPNDP
2683	16584	A	2700	166	3	DYERVPPIRIVK*GPTVV*AGV*WRNHG SLQTQITGLKXSSHLATCWDYRYE

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, = possible nucleotide insertion)
2684	16585	A	2701	209	340	YRMTVFPAKHGGSHTCNPSTLGGRGWM T*CHIEITLGNMVKP
2685	16586	A	2702	78	341	EVAQNCILLEPAIGCFASVTVV*SSVLL*F EL*VLNRNSSF*NFH*FF*NRVLCCP DMSVMA*S*PTEALTSQITRSSHVSLPS SWDY
2686	16587	A	2703	258	185	TM LAPVHSSLDGRARPLYLFKQKR*GLAL SPRLHWGAIIVHRNLEFLCSSNPPTSA SGVTGITMEVERHGMIGETFWK
2687	16588	A	2704	361	41	NFGPVYKTPGSPRPGWGLGKTPGFPQK FFPFPVPSPPFPKKNVSPSPGQKGP FKQVWGF*PRGKCTTQGPSFKVP NWDFFKGGPKKKKKKKRLLRN
2688	16589	A	2705	12	329	SCTLQLTTPRLK*SSRRSLPNN*DYRRV PPHPASFP*PSEMF*DSQTITLNSLKFS S*YYLVIFFFFKMEPCSTIQDQVQWCDLS SLQLPLPRFKRFSCLSLPSTR
2689	16590	A	2706	232	1	KRKRKSKFTYYKPFPLNSSFQCC*YAI GHIFRSITFFFLRQSGQLVA*AGVQWQ DLGSPQPPPPGFKPESHRLR
2690	16591	A	2707	135	1	CFFLIFFFSSSDTQGV*WQPPGPKRS SQLSSPRSDYRRISPR
2691	16592	A	2708	1	157	LDLILTS*SAKLHHPKWDYRRRPPRPAD YKYFLKEVASLIVKLVLCKLNF
2692	16593	A	2709	88	344	MQEHYTFIKRGNHILKRYIVQLHAKLID SLDKIDKPVQRNQN*L*KK*KSHWPAV AHACNPSTLGGRGGWITKS*DRDHPWLT C
2693	16594	A	2710	1	383	LRKVTVLGRFLSKRFLMLYFYTCVHV SVSDMNCWFL*LTETDYNVVFQ*LDFF KLSIKFLRCIC*CVY*IFPVPYCFPL YLICLFLSYPLFNYYVALLFYILCIYY YVIFSSSSIF
2694	16595	A	2711	227	1	IFPFSNSFLKSLGFPLNFAFF*PKPFF PFLSFKINQNTFFGFPFNFLKIFPKFP NKFFK*YLTFFFKKTKPK
2695	16596	A	2712	1	136	KNTRLSQGWPTPVLDTQEPBAGSLE RGRQRLQ*RNLSLQLPLPTFKRSSCLR LLSSWDYRRRPPPLNFCIF
2696	16597	A	2713	3	349	LTPRGQGSTVLEYNPATISIFGNDLNEI KMYGHAKTCNMWMTSSPIDTRKRQ* CSSVRNINKQ*CIQTGLVFGNFTFFF FFFFFFFFFFFPGGPPPKLQIFKRI NPQ
2697	16598	A	2714	181	342	TSQLNLPLPIKA*ALROKKEIGIQIL GKEKVKILFAHDTIVVP
2698	16599	A	2715	3	205	FRHVAQAGLELSASSLPITLASRSAGIT GVSHCVQP*TVSSLRLGFDTSFKIADI QSCPSWVLYLQSAEL
2699	16600	A	2716	388	23	ASNSKQSFKEGKRNQGVNVTSGOQL NKAATFDMLSVYQKTK*RNA**RQGS PSLKVENKKEYDSILLNIVLKLVAWT GHEKK*KAHRFDNLIQFANDMIVYVEN PKDSTKRLS
2700	16601	A	2717	4	194	FSCLSLSSWDYRSMPHPANFLYFF**R RGFTMLARLIVANSWPSIGITGVSHFAQ PFNYFFI
2701	16602	A	2718	1	212	LCCPGWETARLKRSSRLSPKCDYRHE

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						ESLHLARGFFLL*YGPYLIVVVSFNL YDFSLVLSYLGTSI
2702	16603	A	2719	53	299	KAVHVNIPFTRVHLMETQIVSLSLFF PSPFLHPSLSLSSFL*RDVLLCYPG*S AVVQS*FTWQIPGLR*ASCISSVSS
2703	16604	A	2720	139	320	QPTMRHSFSF*KQISITFLKVSLSLHRT LRFLFFFLDLRVSLCHPGNSTVALS*L TVAN
2704	16605	A	2721	1	99	ILLYSSITHIG*ILAVLYPYNFNTILN LTIN
2705	16606	A	2722	215	361	LTTFPTFPERESNPVQAE*GGGNLV*L KPRPPGLKHFFYLSLQSTNY
2706	16607	A	2723	335	24	AIFLRPEP*THPGQNGKTRFPLKQMLT GVGNARYSQPKRLRLKIPLNPEVQPS INPNFHPGIPFQAQKENFPFKKKKKKEI IMLNFLSLICYNLFFLYICY
2707	16608	A	2724	27	314	WKOLKYPFSDWINQWTHAMEVLAIK RNKVLQVLT*RNRLMDTKK
2708	16609	A	2726	1	112	GPHHVSQDGLNLLTL*STHLSLFKQWDY RHEPLOQAR
2709	16610	A	2727	271	3	RSPMLKNQAISKVIMVYIGTINRSAGPF AIFPIAYTNIIIIITLITTIPLGTTYD ALSHELYTTYFVTKAVLTSLFL*IRTA YPRFR
2710	16611	A	2728	121	1	ENKYPGAVAQAYIPNTLGG*GGNIT*G RSFETSLTNVEK
2711	16612	A	2729	2	290	NRHPTKBNITQMPTRHKKQDPQSSLVIRE MQTKTKVRYFILTMRKAVKKIDNTTC* *GYEKGSPKLQTTKCPIFEWNLKLNHS QIVEYPSIGORA
2712	16613	A	2730	98	264	LVSSE***TYQLFFPDMESCHSVSVV VRGSLNC*LHLPDPDKRSCPSVWEG
2713	16614	A	2731	2	286	FFYKATVIRTVYWN*KN*QTDQWNRKES PEIDLHK*SLLIPAKGAKAIQNRKSLF NKWC*NRMISTCKNESMLGVVARTCNPS TSGQGGRLA
2714	16615	A	2732	323	181	RDFVLLVETITLRLRVSSN*PCDLPASA AQSGAITGVSHRARPLDL
2715	16616	A	2733	272	131	GRVDRNLNPGGGGS*LGSCQCTPAMVKE TPSQKKKNKIIICFYAFLEI
2716	16617	A	2734	227	87	AASLTATLSLYPPIILTLVNPKNKNSYP HYVKSIVASTFIISLFFITTFIMCLDOVB IISN*H*ATMDPT
2717	16618	A	2736	25	415	PSKYLDDHLSAGLLVBOHRHSLCLPSL LHSDSLSLFAVSGKVSIAASIRNKLPLP ET*RALMM*NHGHPLRFQGM*PWT*EP GS*RC*KLGQPGQARLACNPSTLGGRG GWIMRGVRDOPGQDVET
2718	16619	A	2737	390	1	KGFPLETKRKFFPTNGFFPLLGKGVVF PKKLGPILQIVPPQRPFFPKPPFP PPPKRKQKPPGQGNP*RSPPGPPKKG GAPTGGKKKKKKRKKKKKTPRNISKP LSHPPFNFFPCATVRGFS
2719	16620	A	2738	96	331	QFTYHLEFPFNRLCYFFFS*KLQVG V*LCCDGLW*TPGLKQSSCLSLSTWDY KGVPPCLAEHFFFEKKSPLSL
2720	16621	A	2739	379	14	LRVFFPFSPPKIKCSKNSPOKYFFPPP VVFETPPFPFFPPFLFGKGFPPFSLEN



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						FCPPRGFF*RPPLF* FFFFFFFFF FFFFFFFFFVYLLLLYFLPLK*MLTF KTSISTQCY
2721	16622	A	2740	198	38	ANPLFFFFFIRDGVLYVRPGWSAVVQS *LTADSTPWAQVILQQRNP I E H D F
2722	16623	A	2741	290	39	MSKVGFLGVLGTSFRVLLKGFPEIKGDF LLANPLFFLFFFLRDGVLYVRPGWSAVV QS*LTADSTPWAQVILQQRNP I E H D F
2723	16624	A	2742	1	399	ILIRHISDIGTLYLLPDA* TGTIGTIDLS VLRNTELEPEQATILGNDPVHVIDTAR ALGILFFVIFPILIGQPN*LVPLIIGA PDMAPARINISF*LLFTSLLLLASAI EEAVPGTG*TVYPSIA*NYCR
2724	16625	A	2743	398	2	SPFPLIFFLMGFSYIFPPKKFPFLINP PKFSPPPPFFPKPPPPFFFP*EEKK NFCSPPPSPPPFFFLPPLFFFPF LKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKRSRSTSPTRP
2725	16626	A	2744	295	185	FFFFFFFFFFFFFFFFFFFFFFFFF FFLFXFFX
2726	16627	A	2745	374	4	LKKHKTTRVP*NVKSGK* NFSPPKIRP WAQKRAKKKKGAREKKAD* KKSFRPGKKV*G*PKGPORNPEKKPKVS QGFVNMGI PAPEKKPRIPPVAKIP*G AQKKGRPLAI
2727	16628	A	2746	2	382	QDATAPIIDELISFDHALI IICLCFL ILDALFLTLTAKLTNNISDAQEITV* TILPAIILDLALPSRLIYITDEVNDA SLTKSIGHWY*TYEYTDYGLVFN IILPLALEPRDLGLL
2728	16629	A	2747	2	374	DMPFVVRKRTNFRAGSTADRL PILLLTV ROLTIGIGLANSGLDVLHDTV VYVAFH YVLSLGAFAIIGGFIH* FPLPSGYTLD QTYAKIHETIIFIGVHLTF PQHPLGLS GMPPRYSDYDPA
2729	16630	A	2748	55	230	QIFAK*INKYLN* XXXXXXXXXXXX KKKGACLLKPHGAKKESWGRQ LFSFK GG
2730	16631	A	2749	161	3	NGNYTLVRKCFSTREKIKWVN* IFFFF MRWSFTLVAQAGVQWCKLGS LQPL
2731	16632	A	2750	362	1	PREKSPAIKGVKAGQCK PCDAPKGN PPKKINPTGTPKRVLKK* PREEKINS PQRKNTAKNKEAPQREI* KGPPRYI FFFIISFFFFFFFFF SIVNLGFT FIATTLA
2732	16633	A	2751	311	110	ITLPRHGGPHVOSOLF KRLRWKDHMSLG DRGKSLSSCHCTP VWRSKTFSKIKIG RNTDKAATCNIGR FSPWKAQA*QGS FTSLSNSRTL* INKINKSKDRQGGYL
2733	16634	A	2752	223	16	KKTPOKKNTKGGK PVKSPFOPLKST PP*IFFYVCFYFFFLY FYLLFRIPSP FFILFVYLLFILP
2734	16635	A	2753	367	10	PADRGVYRGRA SLSCSLHPLRASWP LCSPTQA*AMAGAP PASLPPCGILSIDC CASNERGSGV GVALS*SGAGDNL LVCRL SGKCRNHPSAS LTLAANDWCSY SAIL APPLKNS
2735	16636	A	2754	14	341	PGPNF*PGGQNS PGKNNLSLPT* KING

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2736	16637	A	2755	15	172	PGNPKNGGPTVEGTPPETRGSLLRTLQG PLRPSGTPTTRAPGTPVGNPGF*PRDF FAQKGPVNRGLKQGNPKGLNPPP HSWNECKLVQPL*RTVRFLPKLKLIDPP YYPAIPILGITYSEERKSVKQSRGG
2737	16638	A	2756	263	2	QRPLPFRNDPVFPFGDERTPRPTWGFIP GGVPLGKFTLLVSPFFFFFSPPNLPFF F*NRVSLCRPGWSAVV*SWLTAASTSOA QAI
2738	16639	A	2757	311	106	FVCFRLQRLLALLFECSCVILNHCNRL LCS SDS PG*QS ETVS KKKKKKKRKEKET GNL*PSLDMKGR
2739	16640	A	2758	23	328	NITVYTF*LVLYFYVGRATVVFPKPKFF FFFFF*FFFFF*FFFFF*FFFFF*FFFF FFFX*FFFFF*FFFFF*FFFX*FFFFF*FFFF FFFX*FFFFF*FFFFF*FFFFF
2740	16641	A	2759	1	338	DR*LFSTNHGYIGTLYLFGA*AGALGT ALSLNRAELGQPGNLLGLDHTYNGIDT AHAFALILFMSLAIILRSFGN*IVTLII GAPVLAAPRTIDISN*L*PMSVLLLLA
2741	16642	A	2760	120	2	INKYAWLGTVAHCNPFSTLGGRTA*GQ EFKISLANVVK
2742	16643	A	2761	251	3	CRQGIGTPTLHYSSSSSKWIKDLNVRV KTIKLSENTGVNLELELGDCLDDTKS KNSTRKIRK*SLKLETPFLGTR
2743	16644	A	2762	11	303	ALVLKRSCLDLLKWDYRHEPLHLAIS EILMYRPLC*IPDIFPYMYSRIDILFV Y*FFFFFLEIGFWFLPRGDLG*WEDPPP PGYKSSCLGLPR
2744	16645	A	2763	236	356	DWLFVFSVGRGCHVAQVGL*LLGSGD PDASAGQAGIT
2745	16646	A	2764	2	332	LTOTRGLK*SAICLCPENWYRCFEPHP AGF*F*RHEDKGV*LLIYPGTWS
2746	16647	A	2765	297	19	KKKSWFFFKKKCKGQATKPK*RGFFL KPVFPYFFPIG*GVPPFFFLISIIIPFP FFFF*FFFFF*FFVFPYFFFPFFPFLF FAMKINVFY
2747	16648	A	2766	1	147	QILRRLRWENKYNLGGGKCSERPLHCT PAWTV*NSVS KKKKNPILFF
2748	16649	A	2767	357	183	NWDYRPLSPRGKFLDF*VNRGFPPLTK LVSNF*PCNLPPSTSPKNGISGFNPRAQ P
2749	16650	A	2768	2	193	RWESCLNPGGGGYSEPRSCHCIPSWVTE *DSVSTTTTKEKERKQRTWSESNLQK YKDTNHF
2750	16651	A	2769	333	173	VSQDGLDLTS*STHLGLPKCWNYRREP PRPAQLKMLNIVLGFNSSPKSPLLE
2751	16652	A	2770	3	331	CMENCMVIPPKKVKHNYHMIGKPYFWK AVQQLSTELNII*PYDPAITLLGIYPKE LKTSFRTKTCI*MLTASLFIKATWKPQ RCPVSCE*LSNL*FVQWECYSVLK RPGRFQVLRVRFQHNPGGGGSEPK *GPCPAGQAQDEISKKKCTT
2752	16653	A	2771	209	55	RPGRFQVLRVRFQHNPGGGGSEPK *GPCPAGQAQDEISKKKCTT
2753	16654	A	2772	213	57	RPGRFQVLRVRFQHNPGGGGSEPK *GPCPAGQAQDEISKKKCTT
2754	16655	A	2773	148	1	KATGRKTWVSKRWGFWAHTCNPSLIG GRGR*TAQAQKFNLSRLTAK
2755	16656	A	2774	2	364	WSAVRRDWITALQPERQRETPSQKKKKK

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						KKKKKKKKKKGGVIRHGVKGRKP*TSGR PGRKNHWRQIQGQPKTPRERAENLONRV GLKKLKFCTPGHVGAGNPKFRNGKSGKP PEVHLNAGW
2736	16657	A	2775	121	2	HLRSGVSDQPRGRHGKAPSLIKTERLAGS GGTCL*SQLLG
2757	16658	A	2776	195	3	GRVDIN*LLALLLITITF*LPQIATGYIE KSTPYECGFDPIPARVPFSIKFPLAAI PFLFLDL
2758	16659	A	2777	3	285	PLNRNKVSLCCPS*A*TPGLKQSCCLG LPKC*DYR
2759	16660	A	2778	135	379	HWSATVKLYAILLGLLWESGTLCLCSKD VLFPG*SSAYSIESVINGQIKAT*VKG KARVLGAKKLANVQRKSPGPIAG
2760	16661	A	2779	364	1	GSFTGAVLITLTAHGLTSLFCIDANSRY ERTHSRIITLSQGLPTLLPLIAF**LLA SLANLPLPTTINLGLBGLVLTTF*SN ITLLLTGLNILLVLTALYSLYIFTTTQWGS LITHINNIK
2761	16662	A	2780	356	1	GCLRAHTWPKNEHGGVLEFIDKVCNQ PMTEDCINISITTQVAQIFLVHFLRLQSL TLSEKRRKKKKKKKKRRIEPEINTHI YQCLIENKGAKKIK*G*NSLNFNKTYLDP WISTCK
2762	16663	A	2781	1	204	AOVGLDASSPRIELITTFEDHALITIF LICFLVLVYALFLTIT*LTNTNISDAQD SETDCYSQSYIL
2763	16664	A	2782	1	522	YKNECGKVFVQQAHLAQHQRVHTGEKP YKNECGKTFPSQMSNLVYHRLHSGEKP *KNECGKTFPSQMSNLVYHRLHSGEKP *KNECGKTFHNSITLVSHKATHTUEKL YKNECGKVFVQKTTLAHRIHTAKKL YK*EECDKVFQCKSNLETHKMQFSKTD SAFSLQ
2764	16665	A	2783	1	327	ENRLNSGGGQCEPRSHCTPAWATERD SVSEKKBQKQNFHLNAQSNQKQLKSP* KYLKHPKTDILSKASQVNLQITADQSI LKFTKTFDQKKGRPKHGMYTYSNS
2765	16666	A	2784	335	128	FSLIFCRAGILPCCPGWS*TPVLQSSC SSLPKCSDYKQEPYLCATLKYQIPN FYCNPHIFKRMFY
2766	16667	A	2785	208	3	RPTCPLSLGWGVSFLFFFFFLRDVLICH TGYSAVAQYQNTAHCYSPRLK*SSCLSL PSSNNHRLIPPR
2767	16668	A	2786	49	332	VENGHSPINRCKVYPKSYNRLCKNTEE GVINDIGIAEPNTCSKSLILLIFPKGRI LLCCPGWIEVVOQLTAGSLGLK*TFH LSLPGSWDHR
2768	16669	A	2787	331	187	GCSPEKSPFNAAWATKDSVSEKKKN KKRKKK*HNSGEKINL
2769	16670	A	2788	325	34	ESQLRGLPSNIS*Y*NSRLR*LRPRL FLFCRDRVSLCCSGSQTPGFQKSTHRS LPKCDWYRRKSPSLAITYRLGLFPGSL SSAFYVAMVSGF
2770	16671	A	2789	3	150	AASTROLIFHTSKHFGFGEAAA*YHWF VDVV*LFLYSVIYNIG
2771	16672	A	2790	86	311	NHPIANDIFTRLENGFKKKISLVKNEP NKGT*SLISIKVLEHT*K*FIRPGVAAH

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						T*NPSTLGGGGWIT*SQE
2772	16673	A	2791	2	123	GGGACSEPRSHLCTPAWETE*DSISEKK EEKK*LQIYINI
2773	16674	A	2792	302	162	PLLRRLRPENCPCNLLGGGPN*PRSRNCP PAMATKRDSDLLKKLNKPF
2774	16675	A	2793	1	258	GGCSGLRLCHCTPAWETD*DPVSKKKKK KNFTRAKLLIPGTLVLGVKRGGPFKPR ILKLPWETQNLVFTKKKKIFLKNRGG GG
2775	16676	A	2794	199	3	VGFIFRHRDFFPHSKQLCTYSPAFTQLFS SGKLLKNTHLWPGTVAHACNPS TLGG* A RWITRSGDR
2776	16677	A	2795	1	302	GGCSEPRSHCHCTPAWETD*ST*KLK* INK*K*KIKRNNKGGKHFLLSSIT*PQ VASSPLTGQHRVYTKL*SSQKVLDSALT QSKSNAEVKVRNRTTD
2777	16678	A	2796	228	326	NONGSGVVAHACNPS TLGGGGWIT*G REFKIT
2778	16679	A	2797	270	1	KFGISAPFAFSPKV*KRGGF*NFLGNP FVKIPFF*TPL*NFSPKGNFPPFF*KT RFSXIFPNPFFFFFFFFFFGGVLLCPGWS ALTRSN
2779	16680	A	2798	307	36	FRNFCOG*BVSLCCPGWSQAPGVK*PSC LGFPKWDYRCEL*PLACSL*CDRNQT RISAVVLNIETHPLSLFLVLPFLKPKQ AGLLCF
2780	16681	A	2799	132	5	IFEVTV*CTR*HRRNQGVVGHACNPS TLGGGGWIMRSGV
2781	16682	A	2800	32	314	KQHPGNGFNPSSGKGPRASRFLKKKNFF F*KTPEKPHTPCKPSPGKGPRLPNH FFNQKQPLMPGNPDQAGFCLRDP*G GGHRRSPPTL
2782	16683	A	2801	139	3	AASFYIFFTETLPLTALITR*GNQPE RLNAGTYFLPYTLUGEG
2783	16684	A	2802	238	3	AASTSHVLSMMNYIIYIQKTFVPPFF RDKVSLCHTGNASVAQS*LTAASALTS CVQGLETPQPEYHTRPLRLFL
2784	16685	A	2803	110	291	KKLGVFSGFGKPKTKSNFIMAKGQLPN LG*LKPLPRGFPQPSGLSLSGTWIDYKHT PATR
2785	16686	A	2804	97	2	SYNNODSVLEKEKTNRSVKON*APIPE KKKKINKVGLTLPNCKTYKATIIKTIV WYWRKKRQIQQ*NRISPEIDPHKY
2786	16687	A	2805	268	1	ATFLFLYYTVRPPQIPYYL*ITFLSLP*Y RHSGBPYPVGPQYVQVPPGPGPFYDGP GPGDFPCKPLPIKKNWLVNMLPQLNPTVW PTIIT
2787	16688	A	2806	153	3	ITLPGILLVPLGVFLKVPFFFFFFF*D RVSPCRPDWSVAQSRITASS
2788	16689	A	2807	3	216	NAARHIVKPS*PLTGALSAVMITSGL NA*CHSHSISLILSLLSLTITQ*RR NYTR*TSVQGHITDCKKLVGLILF TSRAFFLS*FF*AYHISLSLPTKQLRSH WPTGLSPLNPLVPLNLTSELAS*VM PLSLHIASNTKPTNQKTHNIPMAQCN* INLIPRPPHIN
2789	16690	A	2808	168	354	FLERESGFVAQAGGQQKLS*WKPPFFPI LKHFSCLSLRSWNYGPTSVPVAVGVGF

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2790	16691	A	2809	61	360	WRNKIY YVSNSKCSNHRK*SLFFFFFFERESFV PQVELHGRDLG*LIQLMLPGFGKFPGLTP LRNGDDGPRPQPPANLGLVKTGFSPPVA HLGVNLGTLDGDCPALP
2791	16692	A	2810	236	3	KMPFOMRYTMLKK*QATRGFILALKNVIL KITFLAFIFFFFLRNNSALVAQAGVQWRDL GPLPFLPSGLKRPSCLSLPS
2792	16693	A	2811	140	210	NAKITK*KGKRGTLAHCQWQPMQ LWKTYGQFLKLLKLELLSNVPIPYL*I WKKKPYALLAI
2793	16694	A	2812	230	1	VKLCPVSKLTQVRLPSSSEVIFLANK FNIGV*LLPGSILLLLASAIIVEAGAGSG *TVYPLAGNYSHAEPYLV
2794	16695	A	2813	3	345	HSVRTDVHTRTCFTFGTITLAIPTGVKV FS*LATLHGNNMK*SAVAL*ALRPIFLP TVQGLTGLIVLSNSSLDTVLHDTYVVAH PHYVLSIGTVFAIIGGFIH*FPLFSGYT LD
2795	16696	A	2814	2	184	ARVGFPHIDQAGLKLTL*SAVYGFPK NDYRHPPLRLALKFNKIKKKKKKKTKP GEKI
2796	16697	A	2815	276	3	ARVHRIDHGLN*HOPGLK*SLCLSLPS SWD**SMQPCPDVDYGRSDQKPKTFKSP YVSTGLRHLGSSDLPASASQRAKITGM SHHALV
2797	16698	A	2816	3	94	HENQYSSGLIIMATAIKLGIAPHP*VP EV
2798	16699	A	2817	93	1	GGGCGSEPLRHCTPVMVTE*NPVSKKK TRA
2799	16700	A	2818	1	197	OTRAQSILLRLRQKQNLNLGCRGCSRP KSHLTRAWAT*PDLVSTKCTLIYLV QALHITLLP
2800	16701	A	2819	109	2	GVP*GVFLAQGLTLWAQAEVQHDLGSL QPCPPRLKRLV
2801	16702	A	2820	2	347	ARAPGAENVEVVFSSCFVMMVPGKRE NAELNQPSS*ESCHFFPAPPCSSCV* LCSIGPSLLGTLLFCQFTLSLPLFRKG *FSSSLKVKVFCFGRVLLCHPGWNAVVO TOL
2802	16703	A	2821	1	353	CTRDVTRSTYGGHHRFPVQKGLPVGI ILFITSQVFFPT*FF*TFYHSLTLPQ L*GHWPPTGTITPLNPLKVPPLNTSVLLP SRVSIT*AHGILI*KNRNQIISSLLITI LLGLY
2803	16704	A	2822	261	400	VEHSNSNKENFLGGGTGACNINLTLGG RGRIITWRSV*DLQDQ
2804	16705	A	2823	273	97	LNTFRMRQLTQLATVILRPHKQGFALL PQVNSN*AAQICHGLGPK*DYRRSP GOK
2805	16706	A	2824	159	355	KKFFSIFFF*FFFF*DRISLCHLWSAV VQSNLTAAST
2806	16707	A	2825	67	338	LSREL*LY*TP*KFFS*QLSLTSHSPSL PSALLLLISPTMLSQSDNHLNLSF LFRDSVLLCLLGYSAVI*SNFTVASNSN AQVVL
2807	16708	A	2826	3	359	HEQKYSFLHDSQTLFCF*DSIPTPSNM ETQOKSRLELVRIILLRLPWLPERLL

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						RSMVANNLVYDTSDDYHLKDLQECI OTLMGRLEYGSRRTGQMLKQIYSKFDTN SHNHDAI
2808	16709	A	2827	3	338	LERNLDITFLDPAGGSPILYQALF*FF GHPRAYILILPRFGIVSHIVSYFFGRLE PSGYLRMG*PIISVGILGFI*SHHIFS VGVDIHARAYSYPGSLVNAIFCTLEVET
2809	16710	A	2828	1	406	RHEGKLRRLRPTGPRHRRGATAMASAL VRATVRAYSKKLQPTRAALTILPSAVN KIKQLKDKPRVGVGVVTRRSCNGLS YTLRYTKTKSDSEVIQGVVFVTEKK AQLTLGTDMEDYD*LSSEVF
2810	16711	A	2829	332	3	GITVMQRTIATALIGYVFLGQISL*GA TVIAYILAAIPFQIGDLVQ*TVGCSVD SPVTVGFLAPFVFLAFPIAAVAALLLRF LQGTGSPNNPLGQASQSDKIAFQ*SC
2811	16712	A	2830	186	349	YSEREVAFPPFFGNGPCF*TOAENNGNL G*LNLLPFR*KEFSCKIFERTWNYKI
2812	16713	A	2831	303	590	NILITLLNKGSKSNGLNKIIITHVYTKI KIFFFFLQSLSVTQADVQWHLCLCSLQ PPPGFK*FSCLCILSSNDYKHAFLHAFN FCIFSRDGISPS
2813	16714	A	2832	1	370	EBLITFRDHAVTISFLICPLVLALPLT LTTKLNTNLTDAQDIQT*V*TLPAIIL VLGLPFLRLIYITDEVDPSLTIK*NG HQMD*TY*TYDYGGLIFNSYILRLPLLE FGELRLRDVDN
2814	16715	A	2833	207	1	QFFIFLRKSFPLFACAGMQRDGLSLQ SPPOFK*FSYLSILRLARKITLAQEFQ TSLGNMGQHPRA
2815	16716	A	2834	223	1	DNLAAHKGKTRVYLYKRNKLKGGGAGNL VSLDSIGSRDRHRRAPPCANFVFLV*M GFPHVGQDGPPELLTSCSC
2816	16717	A	2835	1	321	GTRKPSF*PVTGALSALINTSGLTM*IH FHSITLLILGLLNTNLTIIYQ*WRDWARE STYQGHHTPPVQGLRYGILFITSEGG LFAGFF*AFYHSSLDRTPQLGGO
2817	16718	A	2836	57	370	IWMGRVLKDRLYGVVCFRANRAVTSRV WAEQDPRVVKTLSDVPRKPLPPFS*ISVR GQIYFT*FFFFFETESHTVAAGVQWNG DLG*LOPSPPGFKRFLCLSLP
2818	16719	A	2837	2	345	AAHRRQIDEP*LR*RPGRHRHSW*SEET VERQRTK*SESSQTVGISITSSRNARRR ESEKSLHLETLNKEEDCHSPTFKPSTPD HPLKVPAPSPKENAMVKRSSNPARSQ SS
2819	16720	A	2838	15	376	AKIEPLYSGLGNKSETPSQCKKKKKKKK KKCKCKKKKKKTSBOTRLTQTEOFF CNPCKPKHLGARN*HPRAKQAKGNQPR EYR*TRKKKGKELNPQGGRSQKPKTQGO WNSAGGKK
2820	16721	A	2839	3	336	HELLASTLIIY*CRDVTRERITPLAHN TPPVQKILRYGILFITS*VCLAGLF* YLYHSSLPSLAQLRHNPPGTITPLNPL EVLPLITSVILLASLCSFT*AHESLIEH
2821	16722	A	2840	338	3	KIIFLYFLFLRSIAFLAQIEGHVAFSSF KLWPPGFKIFSASTFLVNRVFKGGPRAR VNPGGFIKSGFFPIF*VGF*LFFFFFFE

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						TESRSVAQAGVQWHDLSLQAPPPSC
2822	16723	A	2841	2	149	ARGCSEPTLHDCPTPAWVT*DSLSKKKK KKVRCGNGNVCRTMCLCCFW
2823	16724	A	2842	348	175	SACKVVSITGMHCHA*VIVSVLLV*TS LHVGVQGLELRTSDMHTLASVSGGITG MS
2824	16725	A	2843	338	118	DPGGACSEPRLRHCTFAWVTKRDFVSK KKKK*NTKC*HAKSGTVVVSFLVFS* YFLMRVSVHDPGSTR
2825	16726	A	2844	189	47	KCVALLLSLFLSCVM*RNACFRFAFCH DCKFLASPAFLPIQSVL
2826	16727	A	2845	335	139	EVSPSPG*STPDLKRKACLSLKKWD YRPGVSHRRLNGSFLTLQYEMLA*YFPI IMVTLQVER
2827	16728	A	2846	3	352	HEGRITFEWKKAATALGDVVKVGVADAD KHSLGQQVGVQGFVTIKIPSNKRR* DYQGGITGGAIVDAALSALRLVKRLG GRSGYRSGLGQOTSVRSSKKDVIETND SFDN
2828	16729	A	2847	2	269	ARGLSTNKKDITLTYQLTGA*HGVLT ALSLLTRASLGQGHLLGRDDISRIHV RIIPGCTLDGISVGRACACLTWPACSR KCARG
2829	16730	A	2848	317	28	SFLPN*KLAGHGRFL*FQVLRRLVLEG CFSLEG*GCSEPMSCPLTWATETDF SREKKRRRRREKAKRRRNRVPSLSV FLEBYVELTLL
2830	16731	A	2849	326	107	PHIVGQGLDLLPS*SAHLGFPKWD*R CKPPCPASRNFKTLKLHIFSNLLIE*N *KSITRGTLTQLGN
2831	16732	A	2850	224	3	SILQAMLRVSPFGNPLGLLQSQVDFFF *RQGLALSPCLDCSGLNACSLKLLGS TDPTLAS*VAGTPSSC
2832	16733	A	2851	27	329	VRTAINRPGGLPFCFIGQFF*RE TYRLGV*MLTPH*YLLSSISGLDCVIF FSFILFFVNFIVVCHVENVYLF*FLFVI LFVLGVVVCFFVLLFV
2833	16734	A	2852	351	60	NLLSSLGGRLPKPGSLPHFQITPHG GVPL*LPGPWKSRPEASINPRS*PPGQ PRGNFFPKNFFFFTVLLCRPGWSAV AQCFKKKNLLC
2834	16735	A	2853	186	363	LTQLNLIT*YQNIETYPQPYAQGPRSG NAQQIGHSPNG*QVPASGMHGLPWTQ GLKK
2835	16736	A	2854	17	239	HFTTLQISLTLTETLARHDSHLSQL L*RLRNRDLKSGAAGCSLGLHCTPT WTTQDPVSRPGAVASEH
2836	16737	A	2855	325	140	GPHYVSQDGLDLTS*SACLAFAKMDY RHKPPCLAAYIFIQSRVLAIVSISHS SPQLL
2837	16738	A	2856	1	157	GTRGFHHVQAGLEVLTSDNLPSASQS AGLTHSH*AHRSDDVANTSPG
2838	16739	A	2857	157	361	LLIRIVLSLWRKSSPLGVQASTPDLPL VTKPPPD*DKDSCLILITWDYRIAPP LPANLE*I*TG
2839	16740	A	2858	3	346	HEGNKFKTINVLLE*ANQL*SGLEGD KVIWRI*TSVTFLECMNGGQNDPLR QFTYKVGRIFFSLKDD*VNLCLGSSTV

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
						DLGSLQPPPLGFKQFSCLSLFSSMEPPCPA
2840	16741	A	2859	18	233	KNPTILCCKGGGAQA*KRLLGLRLRQERGLTPQGGCRDLKSLGIPPWATRPKLLLKKKKKKGGKKKTLF
2841	16742	A	2860	356	3	RVNFKIFGKRGPCPGPGGFVLTFGDLGPLFFQKGGSDSPKPLKPFPPFALKSTTLNYQFAFCVLRPTN*SVTQAGMQ*HDHSSLQPPPPSLK*SSQLGFFSSWYRHAPFSC
	16743	A	2861	115	374	IVCGKILNV*Y*Q*INKLQNKNDV*PTIKMLISQSLGLIFQKRREVNVMGMLKKRKNPPVAVVNCNKLGGQGGQIT
2843	16744	A	2862	163	360	LKRITWLLTSHSHHTSHDNGVTLSEAYGPRNY*TYEYTDYGGILNYSILPPLFLRPGDLRLDLA
2844	16745	A	2863	1	236	GTSFFFSFFPLPFPSTLPLSFPPNPTLLLSLHSHNLS*KKVLPSFEMESHVSNRLKCSGTISAHCSFAWATGDSIS
2845	16746	A	2864	67	364	VCVVCVVCVSVSVVCVVCVVIC*YIMYVCA*YRIRRYIMPLTVNVSCEPIHDSKSCALHTGATTRATR*PCLCHTIPVCLTVCLTVLHITCLSVCM
2846	16747	A	2865	2	155	ARGLTQENRLNLGGGCSBLRSHCHTIPAWATE*DALSKRKKKKOTYRGLI
2847	16748	A	2866	344	81	IQPNISFLIKIFISRGALLCCPGWSPNSWAQSSRLNLKPCWQYRHEPPLVAVQFL*KHNYKWKHKVHCVFSHYNKIFGTQTKTEN
2848	16749	A	2867	217	340	RVFSDFYNNLKNLKRKRRTMPGLVAHACNPSTLAG*RGQIT
2849	16750	A	2868	3	349	HEATSPITOELTTPHDAITLITLYCYLLYALVLTITKLTITMSDAHEHTA*TLIPAILDLIDLCLRLLYVTDDEVNDPLYLTITSIGHQWY*TYEDTDYGLIPNSYILT
2850	16751	A	2869	1	352	GTRIDVYTRAYPTSATIGAIPTGVKVFSLIATLHGSNMK*SAANL*ALGFIFLFTVSGLTGIVLNSLIDIVLHDTYYVAHFHYVLSIGAVFAIIRGFH*PPLFSGYTLDQTYA
2851	16752	A	2870	2	342	AAARFRTSLLAFALL*LPMLQERAGAAQTVPLTTLT*FDHMLQDHRHQLAIDTYQSEFTETYPKDKQKSLHDSQTSFCYSDSIPTPSNMEETQCKSNLELLRIFLLLSERL
2852	16753	A	2871	254	2	YPGQAYISQSDMQSYAYRHL*IQPPGVK*SSIVSLISS*DHFPVPPCLANENFFF*ROQLAMQLSRVLVNSLGLYSIAEPRA
2853	16754	A	2872	282	3	HTHLLAYITTHGHIST*HLSPPNITYSLCNKILLYTPVDH*ILRLAQSHNHLRRLLTHIHHTISVCVCVCVSVCAVCVCVCVWVLY
2854	16755	A	2873	278	3	LMLPNSGPGPWPQMLGKPOVKTPVVYKKGK*KKFPRKF*KNPGFPPFFFLRQSHSIAAGVQWRDLGSLQLPPLPGFRFRSCLNQISSC
2855	16756	A	2874	2	348	ARA*SLILVSLITPNATSNLGLLPYSF



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						TTPTQLSINLANDIPL*AGINVIQYSSK IRHALAHFLPRGTIPLHILAMIESMS LLIQPIAMAVRVTDNITAGHLIMPLTGS PTV
2856	16757	A	2875	1	260	GTRRNHIDPAGRGCSKSRSPHCIPAVVT D*DSLAKKKKKKPKQIILGNQGTGNQK* RGNPFRGPWGPBRQKIKELGPGGKHGKS KF
2857	16758	A	2876	176	1	EHLFCKKLLGEBRGSLSKRFGKCRVNP *KWSRPGVVAHTCNPSLGGRGGQITR SG
2858	16759	A	2877	168	1	GVRVFGSSVVRFSPTACAGVWRNLGS LQPLPPOPK*FCSLLSSWDYKRTDPA
2859	16760	A	2878	67	333	WGLGRAVAVRVSRYETTWAGNLKGA* FQQLFFFFFHLLFFFFFFFFFFF FFFFFFFFFFFLLSFFLFFFFFFFFF FFFFL
2860	16761	A	2879	335	1	GRKEGRREKERKKKIKERKCRKKTIF KKHIPSPLAFPRKAWLKSIQIKLVAH* KINRQAIRGCPNKRPHFPQNMIIKPRE EGEGGLETSDGERNLWIFGPGSVGPLR
2861	16762	A	2880	3	345	HEHEHETASTILALIFNNILSGQ*YIT NTNQYSSILLIMAILKGLIAPHF*V PEVAQGTPLTSGLLILT*QKLAPTSIIY QISPLNVSILATLSILSTIAGS*GGLN QT
2862	16763	A	2881	347	156	WLIFVLIVEMGFFHSGQAVLKLLASDP ASMTSSQSGITGLRHCAQPR*APLIALC LPPSAKI
2863	16764	A	2882	338	2	IKKAL*HE*LRKKKSPRTSSSKAP* NLPRS KKKKSSNNYQL*AHKLQKVKE MGKLLSTPNLPLSOKVAEPINQPTSS KIETLIKKPVHPEKSYGEIDEVTAKFSRA
2864	16765	A	2883	206	1	IRTRPPTTWIFVYFVYLAETSCPTFLA GVQWNNHNSQL*PPGLKESSCLSLSS WDYYACLHAEIV
2865	16766	A	2884	341	140	DGCREPRSRHCSPAWVTE*DSKQNKTK QKQKRYTNISSPQTSPLCYSFSAITPLH NMPGNIMFSSL
2866	16767	A	2885	360	247	PHRVQDGLDMLTS*SAHLSLPKWDYR REPPRPKAL
2867	16768	A	2886	229	351	KLNNRPGVVAVNPSTL*KLNNRPGVV AHA*NPSTLGG*GGWIMRSQVRDPNQH GETP
2868	16769	A	2887	359	2	FYSSSSSSSELVPCRODVQVPHYLEGLF LRSCFMEIKYDT*KKIKYTHVHTHTHT HTHTHTQREKERDFFRFTAKWKANL SGYATASSIRAVLWTTITLV
2869	16770	A	2888	4	305	ADSHSKYTRAGITKLLKRSKI*GYHO DWISRYQDLPFHEHIFKHSYWKRRQ VHDHDIRSPSTSSQMYEHLITNKNONIA EN*EKDSFLSKWKNON
2870	16771	A	2889	1	436	IALT*YDITL*RVGPRGREGTRATV ITNLISAIPYIGADVVK*G*GGYSLS PLTRFTFTFHFILPFIASLATLHLLFLH *TSLNIPILRITSHSHQITFHPYTTDOYS LRLLPFLSFTTLLLLNLFYFP*TT LTFFP

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						IRESAVKSHLTLPARRGLQDGTLLFTTS EUVFFAGFF*AFYHSSLCPTPOL*GHWP PTGITPLNPPESPLNLTSSVLLASGVVIT *MTEKLSHYLREBAFKTG
2903	16804	A	2922	410	1	RAGYRQWGLSLATVIGQLGLPVERGHWG PSGEGGTQQRHCSSELVLDLHIVITQNR NHRPRCGSLLSELKFAFLAQLPGRQSK TLSQKKNKQTTTKRNTKQPGSVAHACN PSTLGG*GRQITLPSGVDRDQPGQH
2904	16805	A	2923	2	145	ARAARGDVI*SPHVFQRDLNLLSRDL PALASQSTGITGMSHQCPG
2905	16806	A	2924	29	340	EMNEVERGRK*LPHDSIQSR*BYRCAP QCPANSCVLM*RWGPAMLPKLVSSDPLA LASQSGITVSHCAHLVFLPLSTSPFI SQRHLLPRA
2906	16807	A	2925	2	337	ARVILTLPGFGITSHIVTVYSGKKRPGFY IGMD*AMISIGPLIGTV*AHHIFTVIGID VOTRAYFTCATIYIATPTGVKVFN*LAR LHGCNMI*SAAVL*SLGFIPTVUSGQA
2907	16808	A	2926	76	388	RYCTPAWATPTPSQKREKKKKCQTFPE SSFPVCLENGOGGNFISLFFLLIILSL FFYFY*FFFIIFVYSYVYFYFLFSYFF FYFFINLILFLILNYFFFFI
2908	16809	A	2927	48	374	KDEPTDMGSAHPQVFGNROVGANED RINSHGGPVMPGQGYQLVRLVY*II IFFMILLFSLFYSYFLFISIFVLVYFC LPIFLFYSFFFIFVFFYYFTVIF
2909	16810	A	2928	3	294	HGPHYISQDGLDLLTS*SAHLGLPKCW DYREPPRPARFPFLRIWLYILKALYTV LQCYREYBAYRPWCWTHRMGGQGVGR RRTQKHLIGF
2910	16811	A	2929	7	420	IRREDVLLITLTSLSPTAARTCYNGRR GNRLINSLAYSKBLAASKLRKPSHGLL TPIRCVLVIRGHIF*LLPPSHLLLASA DMAGAGTG*TV*PTLARNYSQPGVCVN LAMVSLHLSGVSSILGAITPTAIDNME APAITQYQTPLEFV*YGLITADLLVLSL DLTAGITILLTRKLLSTTFDPAGGDDP ILY
2911	16812	A	2930	11	253	GLAHKADSP*KFFFSKPFNFPPKFSPI FSPPKKFLSINPHIVFKPPPKGKIFT FPDPLKGPDPVFPKADPPFFFFFFFFFF FFFFF
2912	16813	A	2931	70	341	DSSFFS*LAILHGSNMK*SAVL*MLGF IFLFTVCGLLDIALPNSSLDIALDLYY VVAHFHYVLSIGAVFAITRGLIH*PDLF SGYTLQDS*AKTHCAIIFIGVYITFPFH HSIGL
2913	16814	A	2932	3	340	NYGHPAGVNLIIPTVHLAGVSCILRAI NFTITLILNKPAITGYCTPLFV*SVLI TGVLLVLSIVLSAGTITILLTRNLNT FFDPAGGGHLLYQLL*LPQHPAYIL
2914	16815	A	2933	2	364	EVQKGLRYWHLISITSEVLFAQYF*AL YHSSLAFTPQLQGHWPSSGTPPLNPLRV PLLYTYVLLASRVST*AHRIQNNRN HIIQALLITILLGLYCTLIQAS*NFPP FTISDGIYG
2915	16816	A	2934	2	367	PRVRPRVRYLLFGA*AGVIGTALSLEYR

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						ARLQGPONLLGNDHIYVIGTAAHAFVIT FFIVIPITIIIGGFGN*LGPLI IGAPDMAF PRINNISF*LLPPSLLLLASAIIVEAGA RTG*TVYPPPL
2916	16817	A	2935	3	365	YHIV*PNP*PLIWAISALIMTSGLMT*F HFHSITLVILGLTNLTITTYQ*WRDVSR *STYQGHHTPPVQKGLRYGIMLFTT*DR FFAGVF*ALYHSSSLAPTHLQGHMPPPT GITPLNPLE
2917	16818	A	2936	3	144	DSHGRHVING*TCVITTCFIRQLIGHFIS KSHFGPELAA*YWHKKKKK
2918	16819	A	2937	3	422	QRLAETHHETISGLYHKGAA*PSALGTD LSLLIRSELQGPDLGLNDHIYNT*TG HAGILF*FGLPITIIKGFN*LAHALITG APDMAIPRINNISF*LLPPVILLLLASA IVEAGAGTG*TVYPPPLAGNYSPHAGSVE RTRGLFSNTHIDITLYLLFGA*AGVLG AALSLLIRSELQGPCNLGNDHIYNTV TAHAFVITFFIVIPITII*CFGN*LLPLI IGAPDMAFPRINNISL*LLPTSLLLLLA SAILEA*SGTG*TV
2920	16821	A	2939	225	3	NISNRMKQTVPRGEPYN*VPVPSLMPH KMFIFETGSHSVYQAGVQ*RHLSGLPH PPGIKQFYLSLPSSWDY
2921	16822	A	2940	1	247	PTRPPVISTYPTAGTLTALSSH*PPT* VGLSINMLAFIPVITKKINFRSTAAIK YFLTQATASIIILLIALLPNIKKKKK
2922	16823	A	2941	3	369	TRDSTYLGHHTPPFHVGLRYWRILFTIS DAFFAGFF*AFYHSSSLAPTHLQGHMPP PTGITPLNPLEVPLLLTSLVLSAGSVST *AHHSIVSDDRYQITQALLITLLGLYF TLLQASDFE
2923	16824	A	2942	3	401	LTVCCVIVLRLKTLFFFNKPPFLQKGY FNTPEKGF*FKKPNRRVGPSPMTDPTML TNLIEKGV/KAPPRILMGGGINMT*GF VTPRAPFPLRLINPMLQQIDLLTLKA SGGSPASGNFLKELGLRSINF
2924	16825	A	2943	189	348	RNARGWYDKEKRLRLGVAIDCNSSTL GQDGR*IA*QGEFETSLANNVXKPL
2925	16826	A	2944	2	349	ANSNYERTHERITTLISGLQTLPLPLAF **LVASIANLALPPTINLGLSGLVLT FS*SNITLLTGLIILVATYLSLYIPT SQWGLSTHHNNIKPSFTRNTLMFTLL SPIL
2926	16827	A	2945	621	929	GCSSGTGCCPILCLDLPFWSCRGVGGSP SSTAHLCPGRWSGRCLPPLSAS*VDS AMSLQAARLNMAVQIVKASYASTK YQSQCMASLAPVEMW
2927	16828	A	2946	379	395	SNHFGRLREDEHVS*PRDFPBLTSQ SAGTVQASHCARPLVATSIHKDINKYD DRS*NNINGITFIDLLIYFSLYSIYL SIYLSIMYSPIVACAGVQWRDYGSLQPS SPGPK*SSCISLSSSRNHSHTPPHGWVD PKIP
2928	16829	A	2947	2	357	HTYDIRKPRR*TLACALALLTSSGLAN TDCFHYITLLCLLNTILITTYQ*WRDE TRSTYQGHHTPPVQKGLRYGIIIFTIS ENYFFAGFF*AFYHSSSLAPTHLQGHMPP

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						PTGTTT
2929	16830	A	2948	2	357	PRVRYSTIDHSDIGTLLYLLFGA*AGVLGT AISLLIRAKLGHGPNLLGNHIIYXVIGT AHAFVILFFIVIPILIGGG*IGELII GAPDMAFPRINNISF*LLFASVILLILAS AIVEAG
2930	16831	A	2949	2	217	KNLKIYQYGDWCLWSQLLELRNRDRLS SGG*GCSELCSCHCTPAWTTQQDLKKK KNFVFPVGEVKGRRML
2931	16832	A	2950	2	354	ALPMYIARLTTHSNVLLILERTTTTTAD VRNPRIRAJARTASCLGGGLGDAISCCY GIATKDRPTLGT*PEVLLGALPGAGGTQ RLPRMNVVPAALDMRI,TGRSIRAHRAIK M*LVLD
2932	16833	A	2951	3	150	LFSCSPITSSDPITTLTLLIT*TLRLPT IMASORHLSSEPLSRKKKKKK
2933	16834	A	2952	283	344	EKKKKKKKKKKKKKKKKKKKK*KLRRKKK KKKKKKKKKKKKKKKKKK
2934	16835	A	2953	3	378	DAMADANNQTFLEN*SVLITAVLLLLSL RVLAAGITITLITDRNLNTILFDPAGGGH PILYQHLF*CFGHPEVILILPLGLIY RIVTDYGTGK*PGYIGNV*AMRSIGFL RFIVRAHHIVTVG
2935	16836	A	2954	3	387	ILYQHL*FFGHLEGYILLPLPGFGIISH MVTYYSKKEEPPGYIGW*AMISIGFLG FIGRAHHIFTVGIDVDTRAYTYATIIII AIP*GVKVF*LATLHGSNNK*SAAVL* ALGFELFTVCGITCI
2936	16837	A	2955	2	432	PRVPRVKKLIAYFELVLSL*GLITTS ICLRQTLKSLIAYSIISHALVVTAIL IQTP*STFGAVILI LAHGLTSLLFCIA NSNVERTHSRIITLSQGLQTLPLPKKKK KKKKKKKKKKKKGGGLLKESLGGPNLTG EGK
2937	16838	A	2956	12	391	SYFISSSKPHLSPPNLSPPDEATSKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKK KGGGFK*KRIIGSFKKGGGKKIFFFKG GKKKKTGFFFKKFFLGGKY*DNLPKX NKTVGKKNFLLGGG
2938	16839	A	2957	1	352	PTRPYPFVDAGEAQHRTCTCRRLRALM SSHHRWVLTCTHCSLVFFLYCCTTY IFVLFI*SSOGLTLIFITCIIPLGSTS FFLFTTIVFSIIIVTTRFRLLYSIIFL SYLLC
2939	16840	A	2958	1	243	NLRINPKREIELNRSIIICNKIKAIKS LLSKSSSHNDVIAFY*TFEELITIL LAFILPKKKKKKKKKKKKKGGP
2940	16841	A	2959	373	3	FSSLKKKVFPPFFPKTQSLGLLHLKK NFPQKPPPPKKKFSQKNPPPPKKKKPP* KKKPPPPPI*HPPKILQPPPPPPFFFF FFFFPPPPPPPPPPPPPPPPPPPPPP GFIVKFRTRG
2941	16842	A	2960	2	136	PRVSTLPISTYKNNRALKKAHLIMX*F TEYFKTTDELVLHNDT
2942	16843	A	2962	1	358	HTPPVRKGL*YGLILITITSKVFVVRPI *AVYHSSLCPTQLGGLWATGMTWNLN L*VPLCTTFVILA**VSIT*AEHLIDL NRCHVYALVITILLRLVFTLLPASEYF

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2943	16844	A	2963	2	373	EAPLTTS RAYDIVRPRP*PILGAIALLMTYGLAM *VHWDICI TLLILGLLINTLAIYQ*NRDV SRESTYQGHHTPPVOKGLRYGILFITS EDVFFAGIV*AFYHISLAPITQIGHWP PTGITPLNPLEV
2944	16845	A	2964	403	61	LFFPLEKNPLPGFSAPFSPSP*KFFP SPKALIPWGNFSPFFPPPKIRFLPKIPP WFFSPFPFWEKLFSSPPPLMFQPPRVLF KGPPLFFFFFFFFFFFPPFREGECW RL
2945	16846	A	2965	2	360	LIPNLAWTR*GHHFORINAGTYLLPPT LDGSLALLGLTYTNTLGLSLNVLTLT TAQELSNS*ANNLV*LAYTLAETIEKIP VGLHL*LPKAREAPLAGSIVLAVALSK LGGSGKN
2946	16847	A	2966	321	2	STGMHFPINMALNPPPPPRPPPI.FPP NPKTKPNPTQ*KGGFPPLGPF*KKLSPP LTLFPPPPPPPPFGHHGPGWQKKKKKVF FFCVCSFORVHNLYKNTHQQ
2947	16848	A	2967	200	1	RRTYTHLLACLRGLAFSPRLCEGGKI RAHCSLQLYGSSDPPT*APQTAGTKQHN ORIAQCNDN
2948	16849	A	2968	2	354	LITASSSETAPLQSSGLDRALKLIK*K EGVLNSI*SGNGKSYANVYRLLYLDP PKIYAEATP*NVNSTLETKSPKTIQK FPEDREFKNDFFKTKNGDRETAGFHP LLELV
2949	16850	A	2969	99	400	ALGHIPTFTSGLTGLGLANSLSHVLN DTYVVAHFPHYVLSLGAFAIGGFTH* IPLYSCTLDOTYAKIHPTIIFIGVNL TFPQHFLGLSGMPRY
2950	16851	A	2970	2	377	NILLTLTAQELSNS*ANNLT*LAYTIA FIVKIPLYGLHL*LPKGVAPAGSIV LAVALKGLGGYGIIRLTILNPLTHIA YPLVLSL*GIITTSICLKKKKKKKKK KKKKKKKKGGGP
2951	16852	A	2971	1	407	GTRSYTHLYRVPLEIKSYVLDNHTVI MVISGHVRLAFYGVHLLILNLLDTHI LYPFLVLSLGVIISSIFLRRTDLESL IAYSSISHIALVVTAILIQT*SFQAD ILIIVHGLTSSLCLCLANSYER
2952	16853	A	2972	10	259	SREVALYFEGWASA*RMFSSKKKKKK KKKKKKKKKKKKTKTKTKTKAKWN *RTEKIRHTRPLPLSSRAKCYDELIT
2953	16854	A	2973	12	400	LACRTPSLYLQAGELLSEVNDHNOCK CVRKNMFTLFFFFFTKTLCYCHICIAL SITCFLAISISGLFAFLLNSFNHPII VP*NPSLSIYLCLHSI.FYVGFPPSPDMX IFSILT*TLFPCLLFHL
2954	16855	A	2974	125	3	RPRRPAQVGVQ*KNLSLQVPPPGKFL FFPLSLSSWAS
2955	16856	A	2975	2	332	RECTNYPAOPPPPLPEAEGFOPPLPTD TG*LECLPPLGGQHRALGLGATWHLEN ACALVADLTGTGPKSGPFGQACGSG RLPLSLGPIPLPGQGHITSAWGHHA
2956	16857	A	2976	7	329	SRDILVMTEDGEFF*GHV*P*DRSGAD TPRLGCHNPPTGITPLNPL*VPLNTSV

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						LLASGGGSI*THHRLIEYIRHQITHALL ITILLGLYFTLLQASRYFESSFT
2957	16858	A	2977	2	339	AHHIFTARIDVD*RAYFTSATII LAIPT GDKAPS*LATLHGSNMK*SAAVL*ALGF IFLFTVRGLTGIVLADSLDIVLHDITY VGAHFVYGLSIGAVPALIGGFH*CPPLF
2958	16859	A	2978	394	0	QGCSEL*SCHCTPAWVTE*FPFVSKKKQ RK
2959	16860	A	2979	149	383	PLCFPSQHWGKSSNCLSLKYFPSSCLP LRCKAELDDVHQADKELDVVHACNPS TLWQGGGRITLARSV*DPQGH
2960	16861	A	2980	2	378	ARVSTGFLGLVGAHDFVIGRMDLYTRT YCTPATILLALHTGVVPPI*LATLHGCN MK*SAAVL*ALRFIFSTVGLTGIVLVP N*SLDIVLHYMYAVALEHYVLSIGAVP AILGRPIHRLVPE
2961	16862	A	2982	2	409	PAVALAYLKEFVDDSKGFLWQKPLDLDG IRECCQRNFGWNRTRDESIFPVLKQLD AQQTQLRIDSFFTLAQQEKDDAKRIKSQ RLNRAVTCMLRIEIASSEIAVSVDP* QKELEGLDKAVACHLYMYETDP
2962	16863	A	2983	3	453	HASAHASAHASQQRKGAPREKKCGREA QHEGLELRVENLQAVQTDPSDDPLQKVV CFNHNDNTLLATGGTDGYVRVKNVPLEK VLESIAKHGEIEDLIVLVEQML*IVCPD HYS PVGLNDPMNLL*LNWGNRLYFPFHS VYLMHFRTF
2963	16864	A	2984	3	417	LILPGRGLSHIVTYSQKKEGFGYFLCN V*AMISIGPLGLVRAHEILFTVGINVYS RAYFTSATII LAIPTGVKVES*LSLTHG SNMK*SAAVL*ALRFIFLFTVSGLTGLIV LANSLLDIALHDTYYV*THFHYVLSI
2964	16865	A	2985	273	408	NKIFIF*VSPPLFFFTTTTTTTTTTTTT TTTTTTTTTTTTTTTTTFLAVFTFI
2965	16866	A	2986	176	335	TFQPSIELNRATLLPELESGGIIAHCSL ELLGSSPLASAS*IGATTGSLRY
2966	16867	A	2987	65	398	KKEFKIGRKAAEIKNTNNAFGPGFAN ECTVQWVFKFKCKGNKLEDEECGRPL EDDNDQWRAIEADPLTTTREVAEELSV NHSMAVQHLK*VGRVKKNKRWPHELS
2967	16868	A	2988	2	158	PGWSLTPDLR*STCLSLKDCWYRIHKRP SPTSRTQTDHAPNKNSSHSPPIYM
2968	16869	A	2989	435	23	GVVPPNPQKSFYFQRLKRWGGGGRKP PPKKKGFSQKTDPGF*KPDPKRRKKIF DPKKKGFPKGLFARGPPLFFFFYFFFFF FFFFFPIITICLHSRPPRRHHHKKFP PNPDSRFTWQHLATSLNWKED
2969	16870	A	2990	410	3	QGRGHFFSGAFITKPAKKGISQLCLF PFGGGSPPGLVVRGGGPGWGPLCHKG PVKKTGAPRGKNGISDFCFPLPGLSFR SGFVWALLSPPLFFFFFF*DRVSLSHHP GWNVAQS*LTKTSTSWQVILL
2970	16871	A	2991	371	132	QKSLPFRVKGFPPFQVFNALYPSHTA FYSW*KRSTPSKKKKKKKGRERKKEE RKEGRKGRKERKKEGKEIENA
2971	16872	A	2992	336	1	CFWNSRTAGLK*STCFGLPKNDNRHES PCDASSVLND*QLSTVQRAT*WQKSLV LKAPPARGALPVSRAVSPSSSHFAYF



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						PPGFFFFDP*GKKFIFPPFF*FCDPPGF FLSPPPPPPPPPPPPPPPPPPP
2588	16889	A	3009	3	302	SLASCLSYLVGVIFLGGPKPTI*LNST PHKK*NPTRYVKTCTQIFLALLPKKKK QPRCPSAGEWINKMIVACTRYNLAIKR YRILIVATV*MYLEKI
2589	16890	A	3010	1	409	RHSDATFPPIERLITFDHVALVITFLW LLVLCAFLTLTKLNTNISHAQEIST V*TLAAITLALMVLPSSLRLIYTDEN DPSLTIKSIGHQWY*TYETDYGLMFMN SVTLAPFLFEPQDLRLLDVNRVV
2990	16891	A	3011	157	2	GRVDLKIQLAKGQACQSGHQNNH NPGKSGCS*LPCCPD*VWQ
2991	16892	A	3012	2	423	AKAKAHVITYYSGKKEPPYIGMG*AM ISIGFLCP/IGRAHHITP**IDGHTRAYF TSATIIILATPIGVKVF*LATLHGSNMK *SAAVL*ALGFIFLFTCGLTGIVLANS SLYIVLHDTYVVVAHHVVLISGAVFAI
2992	16893	A	3013	2	140	ARANTLLTLTAQELMDERANNLT*LAY TLAFIVKKPLYGLHL*LPKARVETPMDG PILLAAKLLKLGSGIIRLTLINPMTK HIAYPLGLSL*GIILITRSICLRQTEK WLIAYS*ISHIALVVDILIQTP*SKHF TTNSHCPRMGQSQQLNNTSLHYSFYS KETSRLTPLMT
2993	16894	A	3014	2	420	PVLAAGISITLTDRLDLTLFLDPGGGD PILYQHLE*FFGHPPDYLLILPGFGIIS HIVDYVGRKEPSYIGMY*AMTPVGF GFIS*ARRHITVVDIAHTRAYLTSVSL IVIPTWRQVS*LATLHGSNM*YALF
2994	16895	A	3015	6	292	AHHIFTV*IDVITRAYTTSATIVLAPT GVKVS*LATLHGSNM*SAAVL*ALGF I*LFTVGLGIV*SY*LDLIELHDTY* FVMGCPKRVF
2995	16896	A	3016	3	422	TPYIIGGFG*LFPLIASDMEFFPRIS NISL*LLPPSILLASAVEAGT*TD* TVYPLAGNYSHPGASVDLITFSLH.TG VSSILGAINFITPIINIRPPAITQYQTP LCA*CDLMTAVILLLLSPDLAAGITILL
2996	16897	A	3017	21	490	TPFGRRHLMFSLHLGGCSILGAINYI TTLINIRPPAITQYQTPFV*SVLITAV LHLLSLPGLTAGVTILLADQNLTTFD PAGGGDPILYQHLE*FFGHPEVYLLIL GFGIISHIVITYYGEKEPPFYIGMC*AM ISIGFLGIIIV*ARRIF
2997	16898	A	3018	98	402	LSQSXSFPQSGKPSQDEMPQISPOST DVIINT*HFNAGMKLNT*HQPHGLIDF FPKKKKKKKKKKKKKKKKKKKKKKK KKASSSSKKDPPGGGT
2998	16899	A	3019	399	229	PPPPGGGGGQPPPPPPGGFLPKSPGVF YPPPPGKKLSPPPGGFFPPGGFF*GAP P
2999	16900	A	3020	2	401	SDAVI*ALGFIVLVGGGTGIVLADSF LDLELHDTYVGAHFHYVLISGAVFAI GGVD*FPLFSGYTLQDYAEHHFTIIL IGANVTFLPQHFLGLSGMPRRYSDDPA YTT*NLSSVGSFITLAAALL
3000	16901	A	3021	413	67	PPPPGKIFFKKIPKKKIFPPPCF*IFPP

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						PLPFFKFFFSFSPN*FFLGQFSPFFFTQK KIFFFKLPNFFFSPLKKKLPFFPPP* IFFPPRFFFLKPPPPFFFTFFFTFFFTFF FFF
3001	16902	A	3022	2	332	LTLSILSTLAGS*GGINQQTQLRKILAYS SITHIG*ILAVLPYNPNITLNLTIYII LTTTAFLLLNLNSSTLTLLSRT*NKLT *LTPLIPSTLLSLGGLPPLTGFLPKM
3002	16903	A	3023	1	412	RGPFFFFFCVFFFTFFFTFFFTNKGCR HSKRFFFTFFFKKKSSRPTLRDV*FYFK GWSRLPFFSPQGRGFFPLSHQVGFEN EVLNVFKKNLRLFRGSPARKKKKKKKHL E
3003	16904	A	3024	279	1	LGRNTRLMKSKGKNDILKTINCGKLANEP FRQPRVLGIGGEAPRAGSOPPSRAPPA* TPQPSAGSM*PPTGRAPRGPAFAPAP GARSPGRPG
3004	16905	A	3025	151	401	EKPLQGPNLTGEKKKFFSLKGGKKKPP GKFLKKTFFLGGGKGKTPPKKLP*GK KKLFGKRGKKNPKTLAVKFSKKKK
3005	16906	A	3026	416	140	YLSPLKKFFTPPPLRMLPPLNPLKNIFF PPQLKIFWGGWAQNSPPPKGFFSKNPK RVFLPPPVRKRYNFFPHGKILAPPKNL* SAPPPPIFF
3006	16907	A	3027	379	31	PPPRRAGVFFFKNPKPKPPPPRGRF* PFPPLKF*FFPKQNLGGGAIPTPPP KRGLQQLPTERFNLSPPTQKRINFPFPG KGQPPPLKPPPPPPPPPPPPPPPSL NSFI
3007	16908	A	3028	28	420	WQQTMAHILPLCNKFAKCKIVPRT*SET KPMSTPLQFD*TYKGRSKCYAHERHTW KQ*CVFSLYQIIP*EKTWKQCGTNE* NQFFKQTHL*NHTRNDQICFSKIGLEY YYRITTRQHLKLRITUCIL
3008	16909	A	3029	1	401	LGNNGEAVSRKRYKSKQKSHNVVVF FFFWGKPPFVPQARGGGRNFC*PKWP PGWGFPGAPRGGGNGRQKQGRGNFG V*REKGGSMGGPRGA*NDGPKNHPWPP QGPEITGGTTRPHPSGIFKKT
3009	16910	A	3030	285	397	MFIKGGLNLRKLRGAAYACNPSTLGG* AGRITRSGD
3010	16911	A	3031	265	2	KRESSCIKATNSNSLFFLF*SVFFFFVF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFF*HFKSALLMVTDLGLNSD PRV
3011	16912	A	3032	410	49	GFSPPPP*KFFFSFKPLNFWGGGGPNFP PKKKFFFKNPPVFFVSKKKKKTFSF PB*NLADPKLILKSPPPFFFFFTFF FFLSNVSNGLNINNYILPKDPCSPCTTFP ILGLSLISL
3012	16913	A	3033	177	2	VTPFFFFFTTTRSHSVARTGV**SDRCS LQPHPSIK*SSHPSLPSMDVRSMPH AS
3013	16914	A	3034	75	395	MSYKHXKKKKKKKKKKKKGGAP*KKPPGG PKLTRDGKKKFFSLKGAKKKPKWKKKK TLILGGRKMGTTTPKKLKLKKKKIFKQ *RGKHKPKSLPVEKFASSGRIRKK
3014	16915	A	3035	400	83	KKEGPAPVVSPTPTPLLEGVGRSGQTR

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						NP*PTTPTHRKSLPS*KKSIDNRGIPLY PPPPRVKPKKSPNPNRRC*TKIFPCP SPWAPKTHPPFQKKKKKRVYK
3015	16916	A	3036	3	196	DSMPQT*NGSFAKARKKKKKKKKKKK KKKKKKRGGPLKKTGGP/KLPGGKKK NFFFFRGG
3016	16917	A	3037	1	411	PCYDVCVESGCADYSIVIIKKKKKK*K KKKKKKGGPLKKNPQGAQNPVGVKKI PSLKKGLKKTFRGNPEKPPFPGGONGA PPQONKPLGKKKKRKKKKLQFPW GKKISLGGFYLLKIIYPPGRGFENPS
3017	16918	A	3038	3	429	NFFPKKPRGGNFFPPPKKGFPPSPPLK FPPFPFPPFPFGGGPHFPFPPKRFPPQ KPPRGFFPPL*EKNFFFPFVPFAPPP VFFLTPEPP
3018	16919	A	3040	1	111	IGLSOMPREPSDYDAYT*NISSVGS FMYLQQDNK
3019	16920	A	3041	76	967	QLLKGVSQVCPLNFRVRSFLLVGS WSSLASGVKQPTPAVSIVLKAARLELP IIPRGLVVSLSAGVKLQTPAVSVTAHKS SVDPNISGAQLASPSGSRTAAGGAACQ SRCLRVPALLSPWVDGTGRRGAGGGARR GSGSGRTGAHGVGRRLRHGGLHVPSPAPN KGS*GLARNRAQRWAGTAGGSPSTPSAA AGPSAKSLTALCEQWPAAPSAGPTKPT PTRASWASVASPSGSGCLSLHTSLQ ABGVSSLGQPSKGLPQCSGGABLLKC RQSGSPGRGQTESERGL*GLPQCSGGAE GLLCKRQSGSPGRGQTESERGL
3020	16921	A	3042	39	141	LSIRGLNIIIKRQL*DWIKQDS*TLCC P*EIH
3021	16922	A	3043	2	405	LPSNNHIYGTLYLLFSFRAGVLTALS LLIPASLGQGNLGNNDHIYNAIVTAHA FVIIFFIERFIIIGYGN*LGPLIIGAP DMAVPRINNITF*LLPPSLLL*LASAIE EAGAGTG*TVYPPLAGNYSHPG
3022	16923	A	3044	3	134	HLNPGGRGCEPRRLHICFWSWATE*DSV SKKKSRKGNLTGLFI
3023	16924	A	3045	44	187	DPRVROYQTLFV*SGLIIFAGLLLLSLP TLGAGITILLDRNLHATAVDPDGGGDP ILYQHLF*FFGHPEVYIILPFGFGITCH IVTYYSKKKEFPFYIGW*AMISIGFLG FAGAHILTPGSHDVITRAVPTSATII ALPFGVWPS*LRILNPLCRITSPISP NPRGRHITYNRQPPHRY
3024	16925	A	3046	434	40	GAPFPFPRGFFFLNREDTFFPPPKQK GFSPPPKKFFSPPALETFGGGNPNSP PPQKNFF*KKPFFFPFPLPKKLIFFP PFLFFPPQIFF*TPPILFFFPFFFPFF FFFPFFFGCKINFIVRGF
3025	16926	A	3047	1	399	LFTGGGLTGIVLTNSLDIVLHDITY*VV PHPHYGLSIGAGFAIGSIN*FPLPSG YILDQTYAKIHFTIIFIGVKLTFPQGH LGLSGMPRRYSYDAYIT*NISSVGS LISLTAAILITFMS*EAFASK
3026	16927	A	3048	116	367	GASMLSSMTFLKELVGGFPVPSVYLFK LQILRQSS*TMCFVLCFFEIRSCSVTQA GV*RRGHSL*POPPGLSHPSRDHGHV



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						HWPTGTITPLNPLEVPLLT
3043	16944	A	3065	1	137	HTFNFSIYQATVIRTVVYVYNNRHTVBSPEINPIYYS*LIPLF
3044	16945	A	3066	4	426	KLEN*KNVLKEIKEMAKQTDILFS*LQRLITVRMSILPKLIYKFSALPIQIPA*FL*IKILIKCMRKGK*TRIAETIFFFFFLSQSFILSPKLDHRGGITANTCPDWAIRGKLLKKKKKKPKTKPEKFFIQKATGAEGGVH
3045	16946	A	3067	411	187	RNLNVPFRPTHTIVLLVKTGVSVQVGGQGGKLLLSKNPSPADPFSWDYRGEPFRPAKRFFF*LAKKFKIYGGPN
3046	16947	A	3068	193	471	CCCKKWSGGKTSPTFVIGELQIKRITLGCYTFPTLNAQIKKSTRTCK*GYGAILMLLLCWRECKIVQSL*KRVAQPII*LN IYLAIKLNI
3047	16948	A	3069	323	478	FFXPKFLFFPFLIKYPIYF*KLFLVLYLFX IYKFIYIYFNFIYIYIILYIIF
3048	16949	A	3070	1	378	GTRRFFPHSITLILGLISNTLIYI*WRDVTRESTYQGHHTPPCQKGLLNGIILFITSVEFFVAGFF*AFYHSSLAPTPQLGGHWPTGTITPLNLEIPLANTCVLLASGV SIT*AHHSILERNR
3049	16950	A	3071	201	2	TPIQLPLKHYHT*NNFNFFPSIGSCSIAQAKVOMCDLCLLQPTLLGLKHSLSLQSSWDYRHA
3050	16951	A	3072	261	1	EKAMGGPFRVKIGPBGPTTKGWPLKGPLEGGQRLGTGPFKSNGRLFFFFGSNEVSLCCPG*SRTPDFK*SACLSPLPKMDYRHG
3051	16952	A	3073	333	52	EIFKKKKKGGGRFFNCKVFPKPRVSNGRPRAQPFLETFYFFPERGFFTFYFFETESYVYQARN*WNYLGSQCPFRFKRFSHLSLPSGWNRYCK
3052	16953	A	3074	7	214	SOLQENRLNPGGGCGEPSPSCHCTPWNA TE*DSVSKKKKKKKRGGWVPSLGGGP KKKNPFNQGGL
3053	16954	A	3075	180	419	QKHSILYLYLFRDVTFFFLKGSFVWSQVGGQGHNLG*LKADPPRLTHFSCLTLRE TWKNRPRIYFCFFIKTGFHVTRE
3054	16955	A	3076	371	208	QKLSGHGGSRL*S*PF*BAKAG*QLVSGGRCSQL*SHQCTPAWVTE*RLVCKR
3055	16956	A	3077	349	3	TFCKQRYIMCRSLCHHPPTTWSTKKRPPFQKGGDAPPYKKVQRGNPPPLKGRPSRGPPKCKVKFAPVFLFPRPSDPPFPPLPLFFFFFF*DRVLFCPCGWSAVAQLTATS
3056	16957	A	3078	124	1	ISSETPAVKSSFWGVVHACNPSTLGR*GKEITRSKRDH
3057	16958	A	3079	205	1	CLVQNTWACVSHWRYIMSKCGC*RLGLM CVCVCVCVCVCVCVYCCCCCCCCYC*DELSLCHSDSAVA
3058	16959	A	3080	3	413	GHTTPVQKGLLYGILLFT*EGFFFSQFF*AFYHSSLAPTPQLGHWPTGTITPLNPL*VPLINTSVLLASGV SIT*AHRLI*NNRNIQIALLITLILGLYFTLLQASEYFRTPITISDGIYGSTFFVATGFHR
3059	16960	A	3081	1	321	NSLNPGLGGCS*PRIHYCTPANGTELDLS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth end	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
						ISKEKKYPYHVYHPSMISTYINRQQNV NHITYMLVEHSQTQBCFMISGNFFFN LPVLVGEGBKQHSISFKLFFNF
3060	16961	A	3082	117	484	VLKYPIDSEVNVLFSICSEFVDPVPL FFFPGKVSFPCPAGIKGGFGFLEPLA SGFKRIFFPNPLEKNE*RARPPPRGKFW NFFFFFFFLKRELFAPRMEGRGKILVYL KGPPWGYPHF
3061	16962	A	3083	381	227	CISRDGPHILGQAGLELLTSSDPFALDS *SVGITGVSHRTRPLLLRLNVCF
3062	16963	A	3084	2	391	SHAYHIG*PSR*PVTGLSOLINTSGLA M-IDHSITLLLCLLTNTLSIQ*WRD VTRSTYMGHTDPVFKLGLGILIEIT SEVFFPARFF*AFYHSSLAPTQLRGHW PPTCITPNTLLOPLINT
3063	16964	A	3085	2	248	IMRSGDRDHG*HGEPISLKKYKRLAGH GGMRLMSQLLGKGTGDSHHVLLILET FYSLRERHILTSVPTLGMNMYAQDIR
3064	16965	A	3086	276	243	EKWPD*SRACPVLCRGNGYSKGRCLC FSGWKGTECDVPTTQCIDPQCGGRGICI MGSACNMSGYKGRSCREAPRYIPEKE
3065	16966	A	3087	3	130	GFYHVGGQGLELLTL*SACLSLPCMDY RREPPRPAHTPHS
3066	16967	A	3088	277	2	SSSSVFCLLVNTSSSSSSAARLPLTG FLPKAIIEFTQNNLSIITIIATITL LNLVYPYLRILYSTITLPLISNNVKIK* QFEHTKP
3067	16968	A	3089	404	60	FSHGIMRFFSPSPSPKIFFSPQSFYFLG GGGARMPPPKKRFFFKKTPRGFIFFP*K KKHFFPPPVKFGPPGFLKSPPPFFFF FFFFFFFFFFFFSPPTTFVFLMLKSD ND
3068	16969	A	3090	405	186	INAKPSPATNVDGMWLNHRTFFYPTA TACLSGAMRTFSRMHV*DHKTSLNKF KTEITLSTLSNHKLEP
3069	16970	A	3091	371	1	SPPLVQKGLRYGILFITSVFFAGFF *AFYHSSLAPTQLGHNPTGITPILNP LEVPLINTSVILASGVSI*AHSLIEN
3070	16971	A	3092	263	3	NKRSPVNLNWKNGSFFFKAKRVKISWK GGGGFFFFSWRSPTFVAQAGQWRNLS SLQPLRPDLR*SACLPDPD*DYRREPQ YP
3071	16972	A	3093	1	392	FFFDKPKMFLINPKMELTYFELKR NEATAGENC*DAVKAVLGKFPVLSTYI RKERPRINLSFQIKHNTKIN*I*GKQ KKKKKKKRVGPETPKFLIVKSGKPPKV ILTGAWGPIKFLSFITRL
3072	16973	A	3094	3	367	EM*IEITMRHYHNTARRLEK*KTNDIKC *AGHTSGTGLIHMQE*RMVQPLAKIV* QLL
3073	16974	A	3095	3	257	IEVSQDCLNLLTS*SARGLPKCNDYR EPPCLAWLILPDDCVTPQKLLKHNLN NLSCIDVLWGLYLSNFSQSNFPFFFFF
3074	16975	A	3096	189	414	KGLNVNVS*CKMFPCLSTFFFFFERGFC FFAQAGVQGHNLSSSLRPLPDLKQFCL TLERS*KYRPAPPCPANY
3075	16976	A	3097	1	299	RNVRYPSFMNTDAKTIKILANQTCQS KRITHRDQVGLPGLMGQGYFI*KSIXSI

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						NAIHHSRLKKRNHMPISBAKQAPNTH S*PMKKKKLAFOET
3076	16977	A	3098	362	126	FIFTHTHTHTHTHTHYTYTYI LASQW NAIRGRMKCINKP*KDMEELKCLPSER SQSAKATVLYDSNYITLKKAKL
3077	16978	A	3099	3	423	RHEHAYHIVKPT*PLTGALSALLMTSG LAM*FPHFSITLILGLLINTNTITYQ*W RDVTRSTYQGRHTPPVQGLRYGILF ITSKVFFAGFF*DPYHSSLAFTQLRG HWAPTGITPLNPLVPLLYTCVLLASGV
3078	16979	A	3100	392	83	LRNTNCGHAPFNSPPFPFLVNS PA YQNKEDVQGP*PEFFRQAPFFKKK KK*GLALSSRLKYGWISLELLGSDDT ASASRVARTTQCHAGPT
3079	16980	A	3101	81	247	GGWGGPPLKPPFL*KATGRNFPWPPKG KKKPPNPRGGKKGGPKPPVIFPFF
3080	16981	A	3102	3	388	HEKKEPFF*YTGNG*AMISYGFGLPTV*A HHIFTVGIYVDTRAYPTASII LAIPG GKVFS*LATLHGNK*SAAVL*ALGPI FIFTESGLTGIIVLSSSIDIVLHETCYL VAHLHYVLSIGAVFAI
3081	16982	A	3103	3	387	HERHEELSNS*AMML*LAVTAFIVKI PLYGLHL*LPKARVAPVAGSIVLAAVL LKLGGYGLIRLLTILNPLTKHAYPFLV LSL*GIIITSSICLRQTLKSLIAYSSI SHIALVVTALIQTP
3082	16983	A	3104	3	381	HEQSHAYHIVKPS*PLTGALLALIMTS GLAMGPTFPHFTHLILGLITYTLITYQ* WRDVSRESTYQGHTPPVQGLRYGILL FTT*RAFFPARY*APYCPHIGPTPQLR GHWPPTGITPLNSL
3083	16984	A	3105	412	111	FLGHPLFRKRWGKKRGLKNGV*HPPA PKGKPPPLKKKKKPGGGAPLYSPSG GEGKINPLTPEGGPKNNISPPPPPPGG KKKNPPPLSPKKKKK
3084	16985	A	3106	298	98	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF F*L*IIY*ACALNNIRGAGELYRSD FVCY
3085	16986	A	3107	2	417	ATVIGLDVTSNTEQLTFPHDALMNT LII CFLDLGALFLATLTKTNM*YAO EI*TD*TLPAIILMALPSLRMLYIT DEGDDPSLTIKSIGHQWY*TYEYTDGGR LIPNSYIRPPLFLPGEIRLLVDNR
3086	16987	A	3108	8	430	VGINVLTSELPLNGGLITFPHQGIYSPF PGGRWALMWGSGWGLVMS*TDLLGLPLCH APT*NTOLLMLAVASPL*PAIRIGCH SKTNALHIFLPROTTPPRPLATLHET NSLLTPPIADQRLANG*TAHLLHLS V
3087	16988	A	3109	3	453	PRALKFYRDWPGHERKRLMKGDPCRW LIKDEKGLMQCKKKCKTFFWAPKIPLV FPDAQKNGS*PNPPGGGNPLRPGP* RKKKPALMGPPSPGGNPKSFFYLNP GPAH*PRGEN*LGDPFENLFLPLKKIF LNGELRCSQT
3088	16989	A	3110	398	2	SLFQKNPNPLVG*KKGRALPGGPPPLP PPLGGAGPGSGQGRNGDPRPWPNNPFF



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
3102	17003	A	3124	453	3	FTTPIWVPIKGGHKKKPTVLN*PPTKK PPDDKILKKKKDDCTSLARN SSARRGGGVPPPPKCIFFPPPPFISWG GGGTSPPPPPEREVFPKNHGGCFSP* K RGKYSPPPPRMGPPPGVFFKGGPPNFFF FFFFFFFFFFLFFF*FFFFFFFFKKKNMF FFKAIRMSTKPPVPPFFFCNYRVVERPR VRPRVRPRV
3103	17004	A	3125	443	2	YFTFPORYIMGDSLAGVYNPPPKRGT PFFPKKIFSIAPGWGGGDELPPQRQW GGPPDPLGLRRCQCKIPPPKKKKIP GGVCVGGVGVCV*KKKKPPPPFLHAGLK PGCFVFFFF*FMEFCSCCPGWSAMARSQ LNCNLHL
3104	17005	A	3126	3	186	PVIYSTTFAGTLITLSSH*FTF*VGLE INMLKKKKKKKKKKKKKKKKKKKKR GGGL
3105	17006	A	3127	171	38	KKKLLFFPPPREKNGPKNFKLRAP*FFF FFFFFFFFFFFFFFFFWSESS*VA
3106	17007	A	3128	16	189	ILGSEIWMV*FF*F*KKKKKKKKKKKK KKKKKRGADPKTTPGGQITPGKKKILF SL
3107	17008	A	3129	401	85	LNVFSSDQEKRGFFPPPPPNFFSFRG FFFLGGGGPIPPPPKKSFFSINPPGVF SDP*KKKIFFFDPLKADPRFFFKGPP FFFFFFFFFFFFFFFFFSQF
3108	17009	A	3130	2	312	ANNLI*LAYTTAFIVKILPLGLGL*LEK AEVAPLAGSIVLANVLKLGAGYILRL TLILAPLITKNTAYPPVFLH*GGGV
3109	17010	A	3131	449	3	FFFFFFFFLGGDEIFFFFCDEKREKPP LGGGKKKPPFF*NFQKDLGLVLAADPP LCFPIKKKKGGGKFFSPDLP*KGQPFK KFFFFPPPPKGGPPPLNLRGVFFKPP PKKALSFFKKKKKKKKKKKKRAAR DLELADAW
3110	17011	A	3132	95	448	VINRE*KVCV*MKKKKKKKKKKKKKKK KKKERAGKGG
3111	17012	A	3133	60	442	LGGFFFFGKRGFCMLCPRMGAAGIPV NGTTPRGV*RNFLAQP*EGGIITGPPEL PQ*FQFLRNGVPLRGPGGFPTPLIGEP PPLPPQKGGKNGRNPPLKQFLVLPFK EFSSLA/PSWEARGDP
3112	17013	A	3134	236	45	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFGAD*VILFRYFQ FEATIMGV
3113	17014	A	3135	441	88	KQTPKGLFF*KARRRLELPPPIVNF FSPSPPKFFFLSPFLPGCVLFFFP PKKGFFKNDPRVFFCPDLKKKNFFFLD PFFPGDPRVFFYPDPPIFFFFFFFFFF FFFFFFF
3114	17015	A	3136	2	328	TMLSPKPPQQLNQNCSPRHYEPQLTQR TWR*KKKKKKKKKKKKKKKKKKKKKK KKKKRGGGGQKKKVGGEKKKPG*KIFF FFIKVKKKKTALGKKCTQFWGS
3115	17016	A	3137	281	2	KATKSGTPIPSQCGQLAWSWAGTGSQA PPALLHS*PIGKIPKNCMPVGRKSPQLP RNTSWQLGAVAHPSNSSTIGRGRITR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
3116	17017	A	3138	448	3	SGVDRTRG FFFLPSPFFPY*KRGSFLGRVVFNPFP PVPFPFPWDSQIFGPQALIFLPPPPPLF FSFVVGFEQTALFPFNGFFFGFFHGLFP LLRFPCPRK*VFMGGFFFFFPLRDKVYS LCHPGWNAVAQGEFTALTSTKAQAPTRP PTRPPTRP
3117	17018	A	3139	2	436	DR*LFSTNHKEIGTLYLLFGA*AGVLST ALSLLILAEIGQPGNLLGNHDIYNVTVT AHALGKIFFIAIPITIIIGGFON*LAPLEII GAPFMALPRINNIS*GILFPSILLLLAS ATEAGAGTG*TDYPLAGNYCHPGAGG DLITF
3118	17019	A	3140	362	2	KPRGKFFPPPRRGGGFFPPPPKKNFFFP KGKFLGGGGKNGSPQKKGFPQENPGG VFPPPKKKKQIFPFGKMGAPPGFF*R GPPPPPPPPPPPPPPPPPPPPPPPPPPPP LKSPCKKL
3119	17020	A	3141	440	102	PTPPPCCKFSFRFPFKTLFFPTTNLWF FSPIPP*NIFFSPQALIFVGLAFIFFP QKIFFSKFFPPLFFITPDLIKKFFVPPP PFILSPKLIFFKPPPIFFPPPPPPPPPP
3120	17021	A	3142	1	79	FKLDYFSIIFPVALVWISLIEFSL*Y INSDPNINQF*KLDYFSIIFPVALVFT WSIIEFSL
3121	17022	A	3143	3	441	FFFFPFLKKKFFPPPPNIGPPPKSL*K PPPPPPPPPP
3122	17023	A	3144	223	3	LPYKLPFLKH***IQDINQESRG*HFL EPDPFKMKSGSTVAHACNFTLGGRG RTTSGV*DHQDQGHBI
3123	17024	A	3145	65	414	KKKKKKKKKKKKKKKKKKKKKKKRGGP PKKTRGGPQNPPPKKKKFPQKGGKKK PPLGF*KKTPPLGGKLPDPKPKNTTP KKKKK*GGGQTPPPPPGKKFSPPRN KKKK
3124	17025	A	3146	410	31	RANQAFPRGKPLCDLAVGNLSRTQLA LTI*KWINWTILKRLTSGH*KTPIKTK RYPIEGEKISDEELYLY*KYLIGKKK PDNPVEKHANDLKRSFMGNILTVFKGM QR*LGSMHICSL
3125	17026	A	3147	182	241	SHPSHISTININIKGLL*PLPIPNPDV NLNLGLLFIATSSLAIVSYIL*SGGASN SNYALIGALRAVAQTISYEVTALIIILLS TLIRGSFNL
3126	17027	A	3148	254	1	KTRGKIKIKDPLTRF*ISVC*ITKSI*F FKLLPFFPLKIKSHIPLKILFFFFFLPET EPRSCCPWSTHW*GILLATSTGQIQAI NTPANAGGCTFFFFFGSGNFPDRHTP RFFPPGLKNTFFFSVTFPWSGAGQIA PPPKKVF*KLIRGFFPPDPKKKIKFF SPGFAGADPGVLSGDPGFFFFFFFF FFFFFFFFFFFPLINFLSLQGFF LVSKELFPLGLATVKPTRGRCQCG
3127	17028	A	3149	499	2	KNKAVTQVCEPKNKGDFHHHTHTSHT HTHTHTLQ
3128	17029	A	3150	256	146	TISCLCTRGEHPLSPRRAGPYTQSP/LHC CVDVVDKVFSSWKDLTDWPLGLDIEYF TGGSFILRQVCRGAAVTLDSAVEVL
3129	17030	A	3151	333	1	

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, _ =possible nucleotide insertion)
3130	17031	A	3152	43	379	SVSARETSA*KAEILALTRALWLGKQK NRTSLFGADYIWRGAPEPETPPKRAAG ALHSLAQPFSSVALPPCFEDPCAPSLSPG *HALRPLPLPGLASEIQTAPSWIVPPKS LSPAPQPCPIPTLVVPVGKTPP
3131	17032	A	3153	398	12	NITPGGGRFFLEK*TRERKFFPPKKRGF FPPPPPKNFFPPGGNFFGGGGQISPP QKGGFPQKNPRGVFFTPPKKKLIFSP GRMGAPPGE*RGPPPPFFFFFFFF FFFFFLKKKSWRLAI
3132	17033	A	3154	371	105	SPSPQVNFIRGPKPPPPK*IL*RAHP LPKKKSNPFTWGPQPPPSKFSKFA FFPLPPFFPKKPPPKKIFFTKSTV I*KNPFFSGQSPDSIK
3133	17034	A	3155	3	371	DVGADPLHSTGL*LAQY*PEA*TA SSIAHT*DVVYG*VIRYLHANGA*TF ICLLHIGRGLYRPFYLSKT*XLGLL LLATITTAFIGYVLP*GPI*F*GATVMT NLSAIPYIGT
3134	17035	A	3156	1	398	IATPTGVKVF*LATLHSSNMK*SAVL *ALRYIFLFTGGTGLVLPNSSNLVL HDPYVVAVHFVLSIGAGFALIGFIH *FPLFSGYTLDTYALIHFTIFGVNLT FFQHFGLGSGMPRRYSDDP
3135	17036	A	3157	401	46	PPGGRNFFKPTPKKKIFSTKKKKGFPP LPPKNEFFSPGGFFGGGGPPPPPK GFSINPRGVFFSP*KKKIFFPPPG*I WAPPRVFLKGPPIPPPPPPPPPP KKSVRA
3136	17037	A	3158	404	18	FSSPPPPPPGGGVFPNNRKNFFPPPP PEFLGGGPPPPPPPP*FPPPTPKNV FSSPKKKNEFFPPPGPPPPPKPPPP PPPPPPPPPPPPPPPPPPFFLFFFP MEKGRPGDIGSNPPS
3137	17038	A	3159	3	192	SLVIAGCPRLNLSSTNLPTSPKSPCK FNC*KKKKKKKKKKKKKRGALKKN PWGGKK
3138	17039	A	3160	205	80	VQRDNFGFLQSPSGVLFCLSLPNKW DFRCGPPNPG*FFS
3139	17040	A	3161	3	384	LIVPTIILPLT*LSKKHIT*ITNTTTS LIISIPLLFNFQNNNLFSCTPFS HLSPILKKKKKKKKKKKKKKGGGA FKRTPGGAALMGGRFTFFPGGEKIN RPGVFWKQIFFWGK
3140	17041	A	3162	348	70	GPPPKRVFSKTPKVLNKPQKKKKFI FPPVNLGPPNPLKGGPPPPPPPP FFFFFPPWGGCDR*CSNRHSSPRLSG TKKSPSVT
3141	17042	A	3163	2	353	LKTPILSTCLTIGSLALGLPTTGPY SESHI*FANVLYTNA*ALSIILLATSL TSAYSTRILLATAGQPPFTLTNIETK KKKGGPNNRYPLAQVYGGQNEKPLI GREII
3142	17043	A	3164	1	221	PTRPDKSELESCHCTPAATRGDSISR KKKKLSTRFA*YTEAINSIIYSINIGT FKTYFPKITYDRHDFD
3143	17044	A	3165	26	383	IPFYO*SLI*YTRKKKKKKKKKKKK KKKKGGG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
3144	17045	A	3166	251	381	GNLGAGWRLITPVVPAWWEAEND*SRG QKIGAILANIVKPHL
3145	17046	A	3167	391	115	LFKKISPHAGLWFFSPLTP*NFFFSLK PFIIGRGLAPIFPPPK*RFSLKNPPVVF IPPLPMKPKFPPPPPVRIKPPYISFKGA PPFFFFF
3146	17047	A	3168	94	389	SPGILGQKQIGIPIGNHVPGLAAPVTP *FRFKPRLP*GPGPKASPLALKPERAQ VGGTTPPPGPRGNQPPFKRNQGLGF RFRGKLAERKGFHL
3147	17048	A	3169	3	363	WATLQPPQQSSTQSQRKKKKKKKKRQ KPPFFPFKKKIFSPGAKGKGFF* KPPKKKKKIEFPFPPPLKKKKKKKKK KKKKKKMGAGFLKPKRGAPPPGKRKLI FFFLKGV
3148	17049	A	3170	2	171	KEPLGIVIRW*AMISIGPLGIV*NMHI FTVGIDVDTRAYFTSATIIIVITGVK FS*LATLHGSNMK*SAANL*NLGFIPLF TVGGLTGIIVLTNSSLDIVLHDTYVVAH FHYVLLIGG*FYLYHNHCYPHRRQS I
3149	17050	A	3171	390	27	QSLTVKSPYPVVLITKTRGH*VWAGL TRYQSLCENPHIRSEVCTITNPPPLPL VSESPVKHSCVQVLDVSYSSGNL*DHP *TSDVWELYVDGISFANPCRVSLKKNIS PAPVTPRS
3150	17051	A	3172	127	310	KNPGGAKILRGGERKNFFLKRGGKKH LIGPKKTFFFGGKKWAKPK*WRFFSPF SP*KFEP SLKALIFGGCFPSPPKKS FTSKNQVFETSPPFKEKIEFPFPP*NF GPPRVFLKGPFPFFFLGVFFFFFFF
3151	17052	A	3173	376	3	FFFFFLRQSLAVTLAGV*RCNLSSLQS PPPGIK
3152	17053	A	3174	365	14	RNFPSFGGAPYNKPPPPPPGKKKK IFFQKKKKKKIIFYPNNGFPPPPKKKKN P*KPGPLKSGFFFFKKNQNLWGPQPI SFPKKKKKKRAKTVQRKYNNTQLVSA ETQLL
3153	17054	A	3175	1	377	VPLHSSLGGRARIHLRKKKKKNPGFLKN FGPLALLGMGVGNIKGLKGQKGNPAFG AHTGGGCFSLRGRNTPFKRARGIICYN SPH*KET*KALEPRGYKGL*QALALPNL KSGKNEHLRGAP
3154	17055	A	3176	352	125	GHEVLDSSDLFASASQAGITGVSHHAL *EILLSMFETTWACDILLQNTISFIKSI PCFGLDIFIMPHYCRFFP
3155	17056	A	3177	139	366	TAHTS*GY*VKNYINLSFCFFFFFLERN HSA*QKQKQHNRSSLQPFGLKQFSC LSDPSWNLGLVQHLVNF
3156	17057	A	3178	206	1	KTILFKKDFEKNTPKKVFLGVPRNLSLF *KILTLPPVLIINPYFFFFFFFTVSLCH PGWNAVVPRIEP
3157	17058	A	3179	330	1	IVSTLETICYIAYNEERKUTPITLRIYVI GGNGKFLGL*IKQHIKKIILHDKVGFIP GMQGVFNICRSINVIHHSIRIKGKRAQ WLTPVIPALNEGDAGCSPEVRSSRPA
3158	17059	A	3180	3	399	HASAPLOSSLGYRARPCKKKKKKKRGG GGGFFFPKGGFGPLPKGFFSGKGLG KWGLGAGKTPGIKKPLKGGPKKRGK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						KGQKGPHF*KKKKKGGKKLKKGPF*KP FKKPIILGRGVQ*NMILLGG
3159	17060	A	3181	2	204	CPTACPFW*NRKLLMPKKKKKKKKKKKK KKKKKKKKKKRGGAPFNLSLGGPHPTGAG KRNPPFFWGGY
3160	17061	A	3182	71	377	PKRGGQPRQKKIWWGPPPPGAPPQKMGF FNPRGFKKQITFFPPPPPPPEKKPPFF* KKKKKKKSNCS
3161	17062	A	3183	151	2	FFFLLESLVPLLLKLPQRIEEEGCSTNS MEAVLLLPKPF*TKKEMF
3162	17063	A	3184	152	387	YKQSLYVVAICSTSLFFPTFLKRSFC FVTOVWQGNPT*LANPLGLKPKFFCL TLQIGNNRLPDPQVIFCFK
3163	17064	A	3185	22	336	YEKCTALLQWSSFTWREBTHQSY RKDPSLASKNVIVSYLSPIVE*FFFL RGSPPAPQAGGQPNLGSNKLPLPGMLP FSLCTLPGGNCRPFPFGPN
3164	17065	A	3186	344	1	WVLKRIFFYPRGGPPFPFPPLGGQGP IPWARGF*PDRGPPFNGF*KKKKRGG GGPDPGFPFPGGPRGVFFLGGGGPRK PKKIKKKNPGEKKKTSFNQKRRKTK TT
3165	17066	A	3187	296	1	NEPKILTLPRKTKVYKSGENQVPLIFQ GIKNIPWGI*PKKERVCV*SNRNV VPVFKKRGSKRSNKSCKYDCTCTMPIV ALFTIGKIWEQPKY
3166	17067	A	3188	2134	1	GVAHACNASILGGQGRIT*GNEFETS LANVPC
3167	17068	A	3189	1	159	LQDRS*HGRPPSIVKIKLARRHSLRL *S*LLGRLEGRMRQETCLNPGAR
3168	17069	A	3190	119	340	QIKKRLVLSARGNNRR*TYK*VDIF FKEDICMAGRMKRDLSLIREIQIKT TITCYLIHARMGTITRD
3169	17070	A	3191	75	1	LSVNNFNFTGVAHACNSTLGG*GG
3170	17071	A	3192	343	1	IFILGGQPCSPVFPFGGGGGGFLP QNFFPRGKIFRPFF*KKLKKRPAWGF F*NFNPNPLGFNLFVFFFKKQIQIFF LGGVFFVFFVFFVFFLAGGDSLALSPRL EC
3171	17072	A	3193	105	368	KFKDPFPPPPFVPPPKQLPFPPEKIGA PHF*TPKGPPPPKKKK*KKKILKGGRG KKKKKTPPKRQKINGPSKKNPWGGGK TPPL
3172	17073	A	3194	1	365	FCRDEVLLFCPLWSPPTGLQPSHLCLP KCSYRC*PPYPAQGVFLK*HLTKSLSC LKLPMASLCTQDKVPAPQPCVKGISKF LCHLLSLTLPFTHSLPFLGPNFLRQHR SVTQGVQHR
3173	17074	A	3195	1	362	GNQPIELAGVYLLFYVLEESVPLLLAL MYTHKTLWNLILLTLTGQELSN*AN NLI*LAYTRALIVMLPLXGLHL*LPKX VEA*LAGSI*LAANVLLGGYGIIRLTL ILNPLNT
3174	17075	A	3196	137	3	KGQPRFPPLSLKKGGKGGFFFF*Y RPLCHPGWCPVQSN
3175	17076	A	3197	1	266	BGRGCSL*SCHCTPA*VIVRYPVSKK KKKKKGGGKGGKGGKNTLFGPKRGK LRGPQKGGKIGPEKCVNNLKKGIFFR



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3194	17095	A	3216	393	260	SRTRTRGRTRG VSQDGLDLTTS*STRGLPKWDYRREP PRPACTLCISSTYNDP
3195	17096	A	3217	3	387	HASASSSSRAPPPPPFFFNKKTGSKLELT TRGTIVLKTCLFFKKKKKVLGGPKPLP PKGVGKPLKGGPPGNPNWPP*KGPGCHP *KNGF*DPGPKKSHIPSMVGKGSLLP GPLGGPSEVYFSPILRA
3196	17097	A	3218	77	406	RMARPELGLPGLNLSNDHIYNGIVTIAH FVILFLVILPIINGGPGN*LIPLIIGAP DMAFFRINNLSF*LLPPLSLLLLASATV ERAGAGG*TVYPLLAGNYSGPGASVK
3197	17098	A	3219	394	2	KRYYPDLNLFNFWGSLKLPVKKVSS LKKKKKNPPPPVFLQWGGKNNYKGGGL KPKSPNLI*PFFPKQEAR*VYFPPFP PQKDFLRFFFPFLRQVSLCHPDWSAVA RSOLTSASISRAQAGRV
3198	17099	A	3220	376	157	KFFPSP*KFFPSPKPLKGGGVGPIIP PKKRRFFFNQGVFPKPKQKKKIPPOP PVNFGPPFRDLKGGPPPPPPPPPP
3199	17100	A	3221	394	1	VPPFPKFKTGPVPPPPPREFFFP*KKGF PPLGGFLNPAIPNPPPPGPKVFGFGP PPPPGGGFFSPPLSP*NGERVVFGPKI PKKKFLKWKGGGKFPFKKPIPPPPPK KKKKKRAAARDLELDAN
3200	17101	A	3222	207	402	SILM*LCCLFPLPGVTPIDGAPHSYRE CYPVLDGVVMGVWDKDLAPGIADSLRH FKVMREKRI
3201	17102	A	3223	309	3	YFFPHLGLAIRPVCVCFTRFYKATVQT ANSWYOLRYIDQ*NGTEISELPPKIYK VICDHDHKKQNGKDSLAKNKCWEN*LA ICRKLKLDPPFTYAKI
3202	17103	A	3224	3	382	LDRERPPFFWGAHMDIPOLVNLSTNK GHMANFNFLGYKKGGWKKKKKKKKKK RGGPP*KKPPGGPK*PQGRK*IFPMQ GKKKPPGGFLEKPPPLGGAHLGNPPPK YTPGKKKNLKRET
3203	17104	A	3225	133	2	PPFTESHSTVTRLCSGTISAYCNLCPL GSSDSPASAS*AAGI
3204	17105	A	3226	349	2	AGVPFGNFFPLWGGGGSPRGGGLKPGF PQRCNPPFFPKSQPTPPGGGPLPPPP GGGAGSPLPQGRFO*TKIGFFSPRG KKKKPPFPKKKKKKKKKKKSEMPGMV LNA
3205	17106	A	3227	3	239	LNKVGRCSEPSRHCTPMAT*DSIS EKKKKKPSRGILKVGITQAFLALAN LYLIHPTAKQIQWFFITYSKP
3206	17107	A	3228	205	1	IGLKIQNSCLDKSLKKRQATDWRKY LQNSDASVFLIYKHLQLSNYKADP IE*WAKGNKLIH
3207	17108	A	3229	174	1	VQHLSDKSEFT*PSEETLVLRIPVQ PGVAHVTNPSILGGKGRTRTSGDRDE PG
3208	17109	A	3230	2	340	KNSVTVLLCVSIFPPTFCFF*FVENV F*FKLN*IN*FTYIDRVLLCHPGWSAVA *S*LTALNSWAQVPCLSILLAHHAN LIIFKTIAYIIHINYWYDTPYFKFYIN S



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
3209	17110	A	3231	1	313	KKSTPYGQFDPISPARVFSIKFPLEA ITFLLDLEADALLPLE*ALRFIFLPTV GGITGVVLANSLLDVLHDTYVVAPEFH YVLSIGAVLALITGGETH*EP
3210	17111	A	3232	207	355	ELSPFRLKKTLY*LGWVAHACNPSTLGA RGQQLA*AOEFKTSLGNNAKP
3211	17112	A	3233	3	353	TTQQ*LLKLTCKQTATAHNTKGR*ALI LTSLLTFIATNLIGLLPYSLPTPTQLC INLMAIPL*ADAEVIGFRSKIKNALAH LLPQGTPTPLIPILVIMETINLLIEPIA LARRL
3212	17113	A	3234	2	355	KYLINRLITNQ*LIKLTSKQMITTHN TKGR*SLTLLSLIFATNLGLLLEPY SPPTTQLSINLAMDPL*SGAWVIGFR SKIKNALAHPLPQGTPTPLIPILATIE TSLLL
3213	17114	A	3235	43	370	QGCVKGVLEBQVRKWLTDSEGRKDL KORGSPGSWEHVGWGSVGMG*SAWGT QARWLTPITIALWEABVSGVLRPGVQWH NLGSLQPLPRFRKFSYSLFSSWD
3214	17115	A	3236	15	356	LITPSLEKMTSHNTKGR*SVLLSLI IFATINLLGLRPVLPPTTQLSINLSN VIHL*AGAMVIGFRSNIKNALAHLLPQ GTPTPLMPILVIEITIRPLIPALAVRL TA
3215	17116	A	3237	1	376	GTRINTLTLYQ*WGDGTRESTYQGHTE PVOKGLRYGILLFITSEVFFPAGFF*AF YHSSLAPTPQL*GHWPPGTPLPLPLEV PLATVCVLASQVSI*AHESLIENNND QLICALLITIVL
3216	17117	A	3238	1	358	GTRNG*YTHA*ALSTVTGASITSAQGS RIILLTLTGQRPPTPLTNKINNPILLN PIKRLANGSRFAGPLITNNISPGCPQT TIPLYLKITDLGVTFGLGLGLDLNYLT NKLIIKA
3217	17118	A	3239	258	390	RQGLNLAGLVNLSRPLSSHLGFFPKW DYGREPPCLGN*LIL
3218	17119	A	3240	2	372	ARARFHVRSDGLDLT*NTHLRLPKC WDYRREPLRPGKTFLEKKKNSIFLFF RBGFKEKSILGKFPPTGGVLLITGNH GWGCKGTTELLVPSRPFGLAFKICGLWA HDTPHVRNML
3219	17120	A	3241	3	283	HEELWGGKGTGAAGLRISRRPTASLTQ T*TIMTH*SRITGCTSGRGTWRSRHS CAWGNAGLYRVAVASRGGRGMM*PTPPH WLCWANKVP
3220	17121	A	3242	170	3	IKSQGLVGFILGPFSSQDSLELVFVPGF FCF*DRVSPCSRGWSAVVQSEFTALV
3221	17122	A	3243	2	385	ARADVTGSLSTTHDPTGGQGVFS *ISTLGSNMK*TAELTLAGTFLTA GLGLGLELTSNLDIVLHDTYTVQDFH YVLSIGAVFALIGGLH*YLPFSGYTLY RTYAQIHFAIIFGEN
3222	17123	A	3244	1	106	GTRYVGOAHLECLTSSDSBPASTSOSAGI TGVSHSA*PASTSOSAGITGVSHSA
3223	17124	A	3245	2	360	ARANTLTAY*WSDVSLINTYQGHHTPP VOKGLRYRIILFITSDEYFSGFL*AF* HSSLSPPTQL*GHWPPGTITPLNPKMP

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						LLNTSVLLASGVSYT*AHHSILTBNNRNQIIQALLI
3224	17125	A	3246	17	160	GG*GCSSEL*SCHSPANVTEQDFDSK KKPAILASCLAKHLNPLSSH
3225	17126	A	3247	236	2	WARIYMTPLSPSPFLKPVQ*KNFYIYST YSLDN*NPSSPKAKGAPKKSYTLPYLHL CVCVCVCV*VCVCVCVCVCVVV
3226	17127	A	3248	2	2220	FFGGGRSPSPQGYFLNNHSSPSPVPL NPGPA*FPYPTTKGNFPDQK*PSPPKN IKTPPSPFTSS
3227	17128	A	3249	2	372	AYTISFIGKISFYGLH*LPIKAHVRAPI VGSIVLVAEILLKIGGFGIIHLTLIPNPL TKHIAVYFGLGLSL*GISITSSMNLRLQD LKSLIAYSSI SHIALNVYALILITQP*SF TGAFTLIDHG
3228	17129	A	3250	293	56	BGS PKVITENKSPPHHLLFLEFFFPFF *FFFFFFFFFFFFFFFFFFFFFFFFF LAMFYLSFPFKQDNQRYQYSIK
3229	17130	A	3251	169	370	LKMTFLRGAPASKPRQEPPEPHYCSHH HHHHHHFL*VTKGQPHWSPSTDRDGW L*SPS*EDQR
3230	17131	A	3252	22	156	GERIGLGLGGGQSEP*LCHCTLAWGD TVRPLAKKKKKKKGPPF
3231	17132	A	3253	3	400	QNTPLILD*GGLTAVILLILYLAVALTG IITILLADRSIDSTLFYPAGGDDPIIYQH LF*FFGHPEVYILILPGRGIVSHIETNY WGGKEPPGPGVMV*AMIAWGLFETGIG*A HHIPTVGVVDVETRA*PTSAT
3232	17133	A	3254	373	31	REVGPPTF*KIFFPFGKLNFWGGGPKF PPPKKKGFFKSPVGVFPFPPG*KSQPG PGKKPPQKGINISFPAGGKIGPPRGTL KRAPPPPPPPPPPPPPPPPPPPPPPPPP TIL
3233	17134	A	3255	1	379	LNLTQRQ*E*V*KPL*LPPT*KKKKKK KKKKKCGAPKKNLGGAKFTNGRKKKIF FLEGGVKKKAGGCFKKRGKKCYLGI FEKKPFFGGGKWNENPPKKIKGLREKKK F*GKKGKKKPERAG
3234	17135	A	3256	42	376	FCYISLVHHCYINDLSFERKKNI*FVGQ INSSISIA*BAHCNKSLLHAKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KGRSSLLKKK
3235	17136	A	3257	353	67	CYPLSPKFFPSRSLKFWRGVGTISP PKKKVPSONSQRAGFPSPNVLKRPQGN FKTP*KEKNFPFPPVKFGPPKESLKR PPLFFFFGGLQ
3236	17137	A	3258	2	129	PHRISQDGLDLS*SAKGLPKWDYR CRPPRPARNKILLS
3237	17138	A	3259	205	415	QQRNRRLIHLKPSARTNSYNRQGPTTIPS IADNPRIRQSSTIYIVRVHHPVPSPA IEGPVSV*ALLHSITIVAGNLLYRPH PLAKESPLIQ*VTICAGNITLVAGSWA LTQDMSKRIAPSTSRLGLIIVTIGVN QPHALLHITHAFVKAILPMSCSSIIH NLSKQDIDKIGGLITIP
3238	17139	A	3260	3	393	SENLSTLITQ*HLL*LLPS*PLAIT*F ISTLAKTNRTPFDIAWKEARLYSGFNIE YAAGPFALFLIARYTIIIIINTLTTTIL

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						LGTTTDLSPELYTTYFVTKTLLTSLLL L*IRTATPRFRYDQLIHL
3239	17140	A	3261	2	400	ISDLSEK*FKRLVVKLIMEAPEKGAQC KEIQKMTQEVKGEIFKE*IA*RKKKSKP QETLDTLIEMQSALESFSPNRIRKQVEREN SEIAKDRI*FELTQSNKDKGRIRKRYEQSL *VAMDYIQ*PNLIGLIGPERE
3240	17141	A	3262	450	129	NNLAFN*V*EFCVIAKLKLVKRRYPFIR ERMFANHISDKGLSVGIYKELPRLSNKQ AIDLTF*KWANGHGGSP
3241	17142	A	3263	238	3	REKRIGLKKCLAQSHPSINTAKSIITYM FSPILTILSRKNGQPGIVAKTINPST*G G*GRWITRSYGVRDCTQGRKVP
3242	17143	A	3264	350	3	SPILLASQDINILGPRFPLNKKKIKTIRA PLSLGLN*RFSEVVLIP*KPKPKWPGG TFILVVCFLKRGPFPLSQKKKKKNPGVA HACNPSTLGRGGRSQQELETSILANTV KTR
3243	17144	A	3265	69	200	RLECSGVISAHCNINLPQSGDSPASAS* LAGITVNVKPLVIAK
3244	17145	A	3266	223	408	GGFFFFPPGGSGSGNFGLEPLPGLLRK FFCLGPPRRGD*GPRSSPGSGFWFKKN GVSP
3245	17146	A	3267	185	420	DQGLWGFIIYTYRQSLA*VEVMNPSSL* PRTPGKHTPVPSLLISMDYGRTPPHLT NFCIFFDGRGFFF*DRVSATHA
3246	17147	A	3268	3	392	TGCHSIPQAGVQWHRHGLQFPFGLR* SSCLS LPSSWIIY
3247	17148	A	3269	1	398	IFS CISSRIHQKRLTKRPFKPPPKKSP VLPIGKKIRETFWGAFAKSPPPNQPKGAQ TLPKIMWDMQGGALAV*KA PPNVF KPPGSKPNQSP*LGPGPLKWKGGELPH QKGGFSKAGEKKKGGRLL
3248	17149	A	3270	422	183	ETEVVSLPKVITTEKPSMLKKTINIQVQ ESYRTPSRFLMKTTSRHLIILPKV/N TERIL*MOODRGNINQSSGCSA
3249	17150	A	3271	3	35	KNNSLIPTITIAITTLALVYFLAPLLY **SSSPPS
3250	17151	A	3272	155	1	KDFFFFFLQSGFTLVAQAAEWCLLSL QPKPPGFK*FSYNSLSSWDYIG
3251	17152	A	3273	413	71	PPSTGLFLTRYEVSPFPFPL*KFFFPF SGLFQGGVPPFPFPKKGFFPKYPRLV FKGPLLGGGLPPPPP*TLPLGSLPLA PPLFFFFLFL
3252	17153	A	3274	336	45	DRVLSCFAMRAVARSHDFG*QLQPPPR VKVFSCLSNPSSWDPRHVPFRKGNFVL VKTGNPWNIGGGQGRRLCPICPANGT DKDSVKKKKKS
3253	17154	A	3275	206	366	SVFFVFLGFFYGALLCFNPNWLECSGT LIVHONLHPPSGKSSASPS*VAGT
3254	17155	A	3276	334	75	EMTKRVRERRRTHITITTFE*EPRNRP FTLFDGRPSCVFFFFLKYFFFFFF FFFFFTFFFTFFFSARSFYILFPRH VT
3255	17156	A	3277	144	17	KAPLFFFTFFFTFFFTFFFTFF*PRG* HWNQDACMCNLTKS
3256	17157	A	3278	2	109	YHIVKPS*PLTGALSALLMTSGIAK*F HFHSITL

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3257	17158	A	3279	404	65	NLVSSPKRSVFIFSPISOKIFPPFNWKG SKISLPKGGGPLLILLIRQRTPIPPPPF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFL*TACLF*TPKPTIK R
3258	17159	A	3280	226	383	GI*KNSMDGGCTGPFVVFETGSHSHPGW SIVMRNLGSLQLLPPKPKRFSCLSL
3259	17160	A	3281	91	26	LLLLLLLLLLLLLLLLLLLLLLLLLLLL
3260	17161	A	3282	3	321	HTVIYYFGKNEPFGYIGVA*AMISVGSLL GFM*AHHIFETGGIDVSPAYLTCAIT I VAIPGVKVF I *LATLLSGOMKRSAAVL *TLOPIVGF TARGITGIVLSNS
3261	17162	A	3283	393	112	PFLVFPFPPFLKPFSSRRFPFWGGV APVFPKKKGSFKIPGVFPFPPPLKKK IFSSPP*WAPPGVFKGPPFPPPPF FFFFFFFF
3262	17163	A	3284	360	47	PFLHRMVPPPPP*KFPFSQITKFGKVF SQNPFPFKKSFDPKNPGVPYSPPKKKK KFLLPPIFFPPPPFPFTTTPPPPPPPF FFFFFFFFFLPLPFMSVSF
3263	17164	A	3285	386	157	FFSNPLIPWGGGPKFPFKKRFSSKN PPGVFSPPPLKKKKKFPFP*NLAPPRD FLKGGPPPPPPPPPPPPPPPPPP
3264	17165	A	3286	3	385	DANVCKLVGVFPCFVKISAILTKI LIPINENKSI*YLLKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKPTPKKKK KDSR
3265	17166	A	3288	81	270	IIKLEKKKKKKKKKKKKKKK*KONE KTRGPKKKVHRDVTKKILCYKICFPNKG ISLIGT
3266	17167	A	3289	3	145	LRLRQSDHNLGG*GCRFPKSHRLLA NATQSDISKKKKIKGGV
3267	17168	A	3290	404	47	GGGKIFPKKGFPEKFTSKKKKKGFPF FPKKNFFPPGGGFFWGGGGFPFPKKK GPVPKIPRGVFPPTPKKKKIYFPFPR I NAPPGIF*KGPPFFFFFFFFFFFPLV LNDILLA
3268	17169	A	3291	106	362	KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKGGGGKKKKPRGAQII RGKKKI I FPFKKVPK*KGGGDL*KKSPGCGNNLS NTHKE
3269	17170	A	3292	3	226	NPLVNLNLGLLFLATSSSLAVSYSL*SG GASNSNYALIGALRAVAQKKKKKKKKK KKKKKKKKKKKKGGGV
3270	17171	A	3293	337	2	FFNELLESKNKTEKNHDYKERIMHF DRYKFYMLFCPGVLIFFLYLPFFYYF FFFFFFFFFFFFFFFFFFFFPLNSINT*F FSINTHKGMRGGGGGAGPRLSNGRV
3271	17172	A	3294	327	21	KFFSPNKKYFFFPFKFPPTPTKML* KIPPPPLISPPKKNQCPPPPHIFAPP SDPFGPPHHFFVFFLFFFLMRTGSRY IAQAGLLGLSSYPGAS
3272	17173	A	3295	367	101	PFFSYF*KKKNFFPPPLWPPPPNPL*N PPPPFFFFFFFFFFFFFFFFFFFF FFFFFFFFFLVNSLCRRYRG*SLLY YAWL
3273	17174	A	3296	178	2	KGPPFFFFFFFFFPDSITLFTIKNEK KTRCTSIGE*ITWYTHGETYSVMKRN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
3287	17188	A	3310	1	364	LYITGPTALIALTALL*TPLEIPNPLVN LNLGLLFTIATS SLAGYSIL*SGGASNS NYALIGALRAVPQTISYEVTALILLST LLIRGSFNLSTLITQTGHL*LLIPS*PL AII*FISTL
3288	17189	A	3311	215	2	GMARLAKARFLERKGGKRSLSPLMGSGP PTSGTGTFTTTT*DRVLLCQPGMSAVA QS*LTTASTFWAQAI
3289	17190	A	3312	153	3	MNKICMCMVCVCVCFRSHKHIVCAWCV Y*V*TYTVCVCVCVCVCVCVC
3290	17191	A	3313	149	1	KTPPGFFPGAGPF*FKGPIPLFFFFF ETEDGVLLCRPGWSAVSRDA
3291	17192	A	3314	282	69	KGGTAAPFSSWPRVPLKKKKKK*GL TLSSRLVQGHLSLGLGSSDTLASASR VARIIQQCPHAWLT
3292	17193	A	3315	479	60	MMQHSIGQALVEITGMVNLRPVPIPALW EAEVGEFNSISKTNKRNSNIVQMSILE NLIVRINAPFFKFLIALLNKNSKSKSIW NLKS**STQ*SSRNNVGGITISDF*THQ QATELRQEFLLITGLWHRSTVSRFFHA
3293	17194	A	3316	129	3	SPHQKVMADAVAILCSPTSLG*GSRIT GSGDQDHGQHQE
3294	17195	A	3317	3	156	EPHRVSQDGLRLTS*STLGLPKNDY RCEPPRPASFSFLIVRISPEL
3295	17196	A	3318	36	340	TGLVIAEHLHFFFFFKGFWFCPPGGRAG PQNLNMRFPVSGGGKIFCPGPPKSGE*R APPPSRGKFWFFKKKGGLFPNPGGV*TS DPRGT*PPLPGKGGYR
3296	17197	A	3319	326	2	KAFFLNFKEPEGFA*GLKFKPNSLLPI* SFIKRT*AFILCL*IQLNADGKILPKP GVLPFKKCFNFTPLPFFKNCSTNGL FFFPFFFFGGLSLCRPGMSAVA
3297	17198	A	3320	175	312	QAGVQCDLSSKPPPSGLT*FY*CSLP RTWEYRCPPSRPCNPSIF
3298	17199	A	3321	363	51	EWGPKLIVANLPSVSRREBECSPQRGAH GQGGGGGQAR*REGPDWTGAPVMG SPSLNRGAGRPPQPGSSSKRRRVRVC TPHSLIGGGLSFFICKOM
3299	17200	A	3322	344	187	LROETCFNPGGIFGKLPDP*PAANAT RGWVSKKKKKKKKIRICVLT
3300	17201	A	3323	3	313	TRRRERERERERERERERERERERE RERERERERERERERERERERERERE FHSPFPWGEKDFLPRPPKGGRGGRPP PPVFFFFFKKGAPPGGV
3301	17202	A	3324	365	1	SLGNWRVTPPPPLGPRGSSPPRDKRG SPGRVKPGVKFPFKVK*PPPKRLDPS GA*FFFSKKIKQGGPPRKKKKKAEELS TICTKFPQLQSEVMQVPPPPCTCSSSG INICKRHC
3302	17203	A	3325	1	269	ARATSSLSLSLSLSLEFFFFPLAPI QLLAGGLFYPPKGAHNLGGGVFF GPKKKTAPLAGRVIKKKDPCTP*L SPPPGGFFPGGGKGLSPPPAGLTGD PPWGGKAPPPKSGGPKKKKTILERER ERERERERERELV
3303	17204	A	3326	1	316	ARGERERERERERERERERERERERFV SPPGPDTLDQRGVSLFASDPTHEIYLP CPLAGPLSRNDPEELGVCFFSESHRN

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3304	17205	A	3327	2	369	FPFEGVGDIQC*HRGEGSP ARGDVTRESTYQGHHTPPVQKGLRYGII LFITSEVFFAGIF*AFYHSSLSPTPQL RGHWPPITGITPLNTLEVPPLNTSVLLS GV*IT*AHHSLENNRNQIIRALLITII LGLYFTLLQA
3305	17206	A	3328	1	259	GTRKKHSTILIRRIDIKFMPFRHISPI ELVKI*ALANIRC*QQCGKGNMJC*F SKLVQSTGRATIHVALVLSLARSRLSLS LH
3306	17207	A	3329	2	352	ARGTLLLLLLFFALTTPRWCDVTRKS TQGHHTFPVQKEPLVGLGKLFITS*VI FPAFF*AFYHSSLTPTPLLGHWPPITS ISLWPLKKPLNTSGLLAGSVST*AH HSINQ
3307	17208	A	3330	3	361	HREPLGYIRMA*AMISCTFGLIVRAHH IPTGIDVDSTRTYLTSATIIAMPTGGK VTR*LATLHGSNMK*SQGL*ALGF*FL FTVGLTGLIVLNS*LDIGLHDTYVVA HFHYVLS
3308	17209	A	3331	1	340	GTSGDTRAYFTSATIIIAIPTGVQVFS* LATLHGSNMK*SAAL*ALRFIFLFTVS GLTGIVLANSLLDIEHDTYVVAHFHY VLSIGAEFAIRGSIH*FPLL*GTTLDQ T
3309	17210	A	3332	2	352	ARGDVTTRAYFTSGTIIIAIPTGVQKFS *LATLHGSNMK*SAVL*ALGFIFLFTV RGLTGIALANSLLDVLHDTYVGAHFH YVLSIGAVFAIIGGFH*FPLFSGYTLD QTYAK
3310	17211	A	3333	85	370	OVSHRVRCFERERERDRYRTORECR AKEIYSGFFLSASMECSLAQAGCKE LRMCHCTPANTVQGDVCS*KKK*HWEKK GLWFLGVNIST
3311	17212	A	3334	362	3	QEVKSMNRDHTHLSQRQEQMNSVEKK KKKSQEKLRVHTQHT*IFIAVLPIV AKNGKFEPSTCEWINNM*YIHTMEYY SATKNQLHVHT*MLNNIYTFKLKARO KMITYSC
3312	17213	A	3335	3	351	HGGTTLHHLFLLTGSNNPLGITHPSDK KTFPIYYTIIKDALGLLLPILLSLMTALL *PDLGDDPNYTLAHPINTPAHIKPE*Y FLFAYTILRSQGNKLOGGPALLSILIL ATIP
3313	17214	A	3336	17	350	FIPTLTETNRNTPFDLAGESESLFGLKI KYAAGPIALLPITEYTNIIIDTLSTTI VLGTTVDAGSPRYATYVTKLLVTS FL*IRAPVPLVYGLILL*KNPLPL
3314	17215	A	3337	2	349	ADSLISFTLHLPPLVLAQNAFVTH RKSNFLPTLSRPIRAPVPLGLPACI HMKHPHICRLH*PPLSGYTLQTYA KMHFTIIFGVNLTFFPQHFPLGSGMP RYSYDPDAYTT*NILSYVGSFISLTA LIIFWM*EAFASKKVLIVEEPSINLE* LYGCCPPYHTFE
3315	17216	A	3338	2	386	ARAILNAPFLILTERKILGYIOLHRGP NVVGPYLLQPFADAIKLFTKPLKPAT STITLYISGPTALNIGLL*PLPIPN

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						PLRNLNLGLLFTLATSSSLADYSIL*SG* ASNSNYALIGALEAVV
3316	17217	A	3339	175	16	ILQDLFPFAWHPPLFLLPLFSRFSLAV TEAAVQWRNLGLLQPLPGY*SSWC
3317	17218	A	3340	1	359	GTSNLSLGFIVATCGLAN*ML*GGKI N*YITLRLVALAAIHTILYEITLSIILL *TLISGSPNLSTLITIQEHL*LLPS* PLAII*FISTLAETNRTFFDLAGESEL F*GLNIEYSAR
3318	17219	A	3341	1	363	GTRGGTILPAMVIMLIDVPSLRILYITN KVNPSLTIKSNQHGY*TYQTDYGG ILASYILPPLPLQGLRLIDVNRVVL FETPPELINT*QDGLS*AGPTILGLKT DAIGRVNO
3319	17220	A	3342	181	315	FKSPFTFFPFTTXXXXKXGNPFGPTL*G PFYWGGERGPP*TGPG
3320	17221	A	3343	3	183	HEVSQSCRELLTSGDPASASQAGISG MHRAWPV*TFHIFNICYGPGTVLXPY LNL
3321	17222	A	3344	83	354	VLGARCPCAGVSRVSMFWFLMQCLL PWRCCSLTLYANRADRPV*TSRTGPV MVAHACSPSTLGGQGVVTRSGV*DPG QDGETP
3322	17223	A	3345	124	379	GGICFMVVISGLSHRLAHCRYTVGVN LLCSSLPLFLLPLPLPPPGGMDIN IIIFIIFRDKVLCCLGNSAVT*SLT TA
3323	17224	A	3346	3	368	YEFIP*PLTGALSALLMTGLAM*ILHL SITLLILGLLSNLTLYQ*NRDVTREST YKHHTPPVQKGLRNLILLITSEAPFP AGVF*ALYHSSSLATPQLGGHNPPTGMT PLNPVQGPLL
3324	17225	A	3347	1	352	GTSAGDVNG*ITRYHADGAKYFLACR FLHSGRGLYGYVYVSKT*NIALNLIA TIATAPIGYVLA*GQILF*GATVSTNLL SDIPYIGTDLRSQI*GGYSVDRPTLIRF FTTFH
3325	17226	A	3348	2	360	ARAEISPLHNLGNESETPSQKKKKKKP PGGGGKNNVYPSTGTPPENPKGGE*RE EPPLTKRVF*KKKVPFEGPRVKNLGG KGKKRGPPAR*KNPVFKAGKGNPFGP QAPFFKK
3326	17227	A	3349	226	366	POSFCSVASWFGDLMEI*AWQFPEYKF GKVPMDPFGCLPLAKKKEEEEEEE EEEEEEEEEEEEEEEEEEEEEE
3327	17228	A	3350	2	374	ARGGGYSPHATLRTVTVFHSILPFTTA GLAAIHLFLHETGATPL*ITSISEKT TRHPYFTWKDALGVLLFPLSLTTLTCS PNLGLSPHDYTLNPLNTRPHIKPE*DC LFATYMRSGPN
3328	17229	A	3351	1	266	LGLVHPTLTLTKLSSHSIDAQRIQSV *NLTAILNLNMLPSLMMLYITNRFVD PSLTIKSIGHONY*AYETIDFGSLYPC YILP
3329	17230	A	3352	207	362	ILFLKQRTYVLFPSN*GSSIFELHLS DAYQTKICSSGKVYKLCWEKN
3330	17231	A	3353	178	365	NHGTDKGLRYRYTYVQEDNSVIR*LKI FNQLSKNTRNSADKIMKRCPPSLVNI



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						MP TKPP
3331	17232	A	3354	359	3	LQVRLMLPLGQFLIPP*NFCCSFFPKPI PFFFLFFLKGIVFFFGWARGQFWVFG PPPPKFKKFFFTLLRWGRTRDFPDSRG KFFFFFFFWYF**RLRFTMLRLVFN* EQVISC
3332	17233	A	3355	2	354	AREPSF*PLTGALSALMTGCLSM*IHL HSITLLILGLLTNTLTITQ*NRDVTPE TFQGHHTP*VQKGLGYGILLFTTSVEVF FMGL*AFYHSSSLAPTHLGGDAFPPTGV TPLNAL
3333	17234	A	3356	1	364	QTRKIKCCSALS*PRILHSFHRK*PMWIC ISKLTWHTKTRHVLNSSLPLCPNHS WICHRRRLHSLIS*PLRLKPPNLRQNP FHYTHGRK*SAAVL*ALGFTLFTVGG LTGIVLANSLLDIGLHDTYVVGAFHYV LSIGAAGFAIIGGFH*PPLFSGYTLNQ YAKIHFTIIFMGVNLTFPPQHFLGLSGM PRYSDDYDAYTT
3334	17235	A	3357	2	376	ARGGQPRDYLTLLPSGQI*FHVITYYS KKKPFYQIMV*AMISIGFIFIA*ARP IFSUGIDVNTRAYFTSATIILALPTGVK VFSWLATLHGSNMK*SAJAL*ALRFIFL FTVSGLTGIVLCN
3335	17236	A	3358	357	139	AQPWFFFLFTVCHAAQAGLKSIGSSDL PTASQSVGTGMSHAMPERS*QNTF TVYVQS IYSDIRKMF
3336	17237	A	3359	277	1	SCQKDISIGFLFVGFVVRGVAGCEHLG VMTVLVTVGSDGKERER*RGIRHTPP PSERVQRERERGRDRDKERASQRKP EMDRETS C
3337	17238	A	3360	261	2	TICSKCAMLCSKTLTINTCASRDLAH GP*CPNLCSGITSSAWTDISRLLFTCL FVLRSQSLTVAGAGVQWNLCSFQPLPFG SC
3338	17239	A	3361	199	354	HLPPYMPMATAFNFFFFFTETHTFFPQA GGQWDFG*LKP*PARLKQFSCLN
3339	17240	A	3362	3	364	HEDRDTPAYFTCANIILALPTGVKVPN* LATLHGSNMK*SAJAV*ALRYIFLFTVS GLTGIVLSYSSLDIVLHDTYVVAHFHY VLSIRAVFAIIGGFH*PPLFSGCTINQ TYAEIHFT
3340	17241	A	3363	3	360	HEETIYIPKQDKYSFLHDSQTSFCFNSI PTPSHMBETQKSVSGRLP*AGMBETC QGSRRAQPLSLPLQLKLLRISLLLI EMKLFSEVRVLKSMFANNLYDTSDDY HLKDL*
3341	17242	A	3364	352	27	VYLSQKNSAASVNMVTVDRSLSPYT LCWHRPDLRHFFVLSLVYVTVVERGSQ IAQAGVQKCHSSL*P*TPOLK*TCSC LP*VAGTGTTHYTGPIILLNLN
3342	17243	A	3365	347	99	GGPPLPRGFSPPPGAPLAPPNGPPES PPPPPPKTAPOKKKAPSI*PAGQMLVEQ NRPQPFKKPPGVGF*NPFPPLNMGF
3343	17244	A	3366	3	319	HEECIAHTLCCFNLS*RTVTLHMF IVTAI*YLLSSQYVIGYIYVCIIHTHI MYIHTHRHTFICVCVCYIYTSIC
3344	17245	A	3367	3	474	YELLLNGPILNAPFLILTERKILGYI

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						QLHRGPNVAVSYGLLQFPADATKLPTKE PLKPAATSTITLYITAPITLALITDLLL* RLPFPNPLDNLINIGLLITLNTSSLPVYS IL*SG*A*NSNYALIGALRAVAQTI**E VTPTILLSHRYKMLRN
3345	17246	A	3368	2	348	ARGLQDATFPPIEBELITFDHALLITVL ICPLGLVALFLTLTTRLTNTNTNISHAQEI ETV*ITLPAITLLVLLALPSLRLNLYITDE VNDPSLTKSIGHQWY*TYQYTDVGLLI FNS
3346	17247	A	3369	64	363	KKNGFVPPQKKKGGRISVNG*PLPKRGK NFPF*PPGEGGTGKGGPKK*TWI PKKR GGLI*FWKQFPPTGPKGTHPPGPKRGK *RGGPPSPGGFNFKKG
3347	17248	A	3370	34	355	ARGKBYETVAEKKKKKKKAPPPI* NPGKKPLALKFPFPPSQKAPPALFCP *KGPFPKRVFKKKKKFPFPGKGFFTG GKPP
3348	17249	A	3371	1	374	FLHSLHLSRLLYLP*KFSMFTILLKAY YTLGVGVGVGVGVGVGV*PLNKHINHF TCSTVGRSNPIFPFPLIN*RPFTT
3349	17250	A	3372	429	3	FFFLAKKKKISRVRFPGRPFPGGRKPF AKGPPRAPQKGGKGNPSPPPLIFPK KGGKPKQGGPLPKKGLGFPSPKVFVKKG VFKSGRGGP*NFGFRGFPSPSPPKKGGK KRKPOS PGFFFFFFFFFFEILGCSGRSR T
3350	17251	A	3373	2	404	LQTDLSLIIRADLQGTDLGNDHNYNA IVTAHAFELIIFTEIPITIRGFG*LLP LIIGADPMAFPRINNISE*LLPSILL LASAIVSAGAGTS GTDVPPLSNYSHPG ACVDLTILSLHLAGVSLGAI
3351	17252	A	3374	2	417	AFV*IAHITRDVTVG*ITRYLHAKGARI FFMCLFLHIGRGLNYGTFLYSET*NGI ILLATATATAFIGVILL*QGISF*GATE ITNLSAIPYIGTDLIQ*I*GYVSVDSP TLTRFTFTFHPILPFIAGPNPLHIT
3352	17253	A	3375	85	1	FWPGAVAYACYPSPTLGG*GGMTRSGVR
3353	17254	A	3376	396	1	KEGYIKGPNENF*KNPERKIFSRQRK GGVFSPLPKKFFFPKGLIFLGGGCP FPPPKKRVFSKNPPGVFINPP*KKKKIF SPPPENWGPFRVFLKGGPPPPPPPPPP PPPPFOTLFLGGCGYNTKLR
3354	17255	A	3377	3	118	LLPFSLLLLLAYAILVAGAGTG*TDYPP LNGV*KTGA
3355	17256	A	3378	301	82	ERKGPQGGKKGPKAQKPEKKPKKRP PPKN*FSPNPKKKGKDPSPSKKGG GKGVPPPKKKKKKKK
3356	17257	A	3379	2	195	DR*LFSTNHKIDGTLTYLFGA*NGVLS GLSLLTRAKLGQGNLLNDHINYVIVT AHAFVIIIF
3357	17258	A	3380	21	411	VFCNTH*DTGTYLFLGA*AGVLRSLALS LLTRAKIGQGLLLNDHINYVIVTGA FVMNLFIIVITVGGSGN*LGPIELGAP DMAYPRINNIGF*LLPSSLILLAYIAIV ENGAGTG*TVYPPLAGNY
3358	17259	A	3381	2	421	GRVGGRVGSNHRIDGTYLFLGA*IGV LGTALSLLTRAKLGQGNLLNDHINYV



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						TRGFWV
3372	17273	A	3395	417	3	FFFFFQQHHPGFANNA*YHFPVDV*L FLYVSIY**GSYSFSINS
3373	17274	A	3396	229	1	RSPWIKTMGFSCYKDFP*TNKXDTTYQ NLMDIAKAVLRGKFIALNVPINKLERSQ ISNLISQVKRQQAAMWMPVI
3374	17275	A	3397	344	163	ELKSPQPRKRNGCFPLAVDPDEGF*NLN FCNGQQLNAPGGYPCFIPNGFPVNAVG KTF
3375	17276	A	3398	1	409	HRDITGLYLLFCARTGLIGTALLLTRA ELGQPGNLLGNHDIYNGITTAQALVRIL FTVIPILTGPGN*LIPLILIGARNMAVP RINNISP*L*PPLLILLAKVIVAGAR TG*TYGPLAGNYSHPGACVDLTV
3376	17277	A	3399	3	396	KDYGILYLSPLS*AGVILGAKRLLRK LGQPRNLRLNDHINYNIVIAHAPVITPF IVIPILIGPGN*LLTILIGADNVALPR INNISP*LLPPLSLLLLAYGIVAGART G*TAYPPLSGNYSHPGASV
3377	17278	A	3400	49	350	KNSHTSEVQAGQEQKSFPRSKHKGKAG SDAPAYVLGCLCRSISSEFL*FFSLFF FFFFKRDGV*QGYSSGSNTPGVKQSSCL GLEPKYWDYRREPLHRA
3378	17279	A	3401	1	398	KPPAIIQYQTLPLFV*SVLITAVLLVLSL PGLGAGITLITDRSLNATTFDPDAGGDD PILYQHLF*FFGHPEAYLILPLPGPIIIS HIETYSKGKPEPGYIGMG*AMISIGLL GLIA*AHHIFIG*LDVITRS
3379	17280	A	3402	388	42	TLFNLPEGAKCVHPFPKKKKKKNPSEA MGDPPLPPLLRGKKKQKPP*MKSGAPV THFAPAPPFGKREDEPPPKKKKKKKK REKESNRVQIKRKNKGRPLVLDPAE ESQ
3380	17281	A	3403	413	2	SDPLKNNFLPLPKPPISSGGLAPFPVPO K*GSLPKIPRGRYKSPPKKKTNALPPR GKPGPFRASSKRPDLFFFPRGRVPLCH PG*STVQCVQAQCTLELLGSSNFLTSS PVTWHRQGPPIRPNFFIFRGRVP
3381	17282	A	3404	433	274	LGVVAHACNPSLELG*GGRTAKSPGVOD QPGQHSETPISINFPWYFRISYFHI
3382	17283	A	3405	131	427	GPPPPQPFPPFGKRGNNPPPPFFSEKRD VF*QFLRRRGPKKFPKPPFFCLQKISL FSEKKKKKGGPPLFPQKKKGGGGPHY KKBGFTLNSFLPQGDGVSSVAQARVQNR NISSLQALPPGFT
3383	17284	A	3406	413	137	SPDPDPQGGIIFFFKPR*ETFSPPENTG FSPSPPLKFFPPFKGFIPLGGGPKFP PEKTRFFQNSGCFPPFP*KNFPPL DPVILGPRVVF*GPPPKK
3384	17285	A	3407	319	540	TVFKDQCEESTITLNVDIRNHNLLDLSL EQHGKGDIL*GANAYICEKNKVRVAV LCLILITFNGREKNFFW
3385	17286	A	3408	2	403	SLHGGGSCIVGATYPTTITINIKBAGY TOYQTLPLFV*SGLITGILLLLLPVLA GITILLTDRNL*TTFINPGGGGDPILYQ HLL*LLSRPEVYILPLPGPIISHTGY YSGKKEAFVYIGVV*ALISIGC
3386	17287	A	3409	2	142	KKENYRPVSNLRDAKSLNQICLHI*KII

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3387	17288	A	3410	407	48	HCNQVGFIFGMQGWENIL PEGGKIFFTYKPEKKIFPTQOKKGVFPF FPLKNFFFPGRKIFGGGGGNAPPPKK GFFPKI PQGVF*SPKKGKGNFFPGKI WAPQGVFLKGPPIPPPPPPPPPPPPPP FFFLGVR
3388	17289	A	3411	3	402	SYRL*QLEDKAAPPQDFTQQLMPEKQ HRMVDPKEDMHKQLVEASETLKSAKE L*DAHQQOKLALQRFLEFNEFLMAELYSH NHKVMKDEEMEVAMHKADEHMQET*RS KKLTKRMFLTQWRRTITVIPS
3389	17290	A	3412	1	224	HLFQLRLRLKLENLLEGRSCSELSNH HWPPWGT*DL*LKQKQSAVLPNNNTI KKLTGSRITDICTEYNK
3390	17291	A	3413	202	1	IVMSWIRGVVTH*IPSTAGGGGMITRS GVDRDLASAFOSAGITSVSHCSQLIFVT VFYLSPLSELY
3391	17292	A	3414	407	309	PSFKASKDRITLLGNANAGDLKPTPMF IVHSENPRLKINYTKSTLVPVLCIRNI KAMMIAHLFTAWLNHFKPQIVETHCSGK KISFKILLINKAPGHRRAQMERHKNV VFMLANTPTILKMDQGV*TFILCLSI
3392	17293	A	3415	404	46	LKKPPFQFKRLKIKKKKGGGGGPP* PPFGGGRGVPPRAGVSKNPVQGETLF FFINPKFPVGGGP*FLLRGVNGKNF FNLQGGGFKKRFPSPPPPPGKGFPPFK KKKKKK
3393	17294	A	3416	23	404	SVLITGALLLLSPVLGAGITILLTDRN LKTTFDPAGGDDPLYQHLL*TFCHPE DNILLPGFGIGSHIVTYSGKKKPPGY IGMA*AMKPIGFLGDLAGAHVFTG*ID VNIRSYFTSDTINMG
3394	17295	A	3417	38	469	SQTTHASALFDPAGG*DFPLYQHLE*TF GDPEVYILILPGFRISHIVTDYSGKKE PPGYIGMA*AMRSIGFLGFIG*AHIFT V*IDVDTRAYFTSATIIIAITGVKVF *LATLHGSNMK*SAAVL*ALRFILFTV GGLT
3395	17296	A	3418	1	419	FSTNRHDIGTLVLLFGA*AGVLTGSL LIRAELOQPENLLGNHLYNGIGTAHAF VIIFFIVIPIIIGGFGN*LDPLIIGAPD MAFPRINNISF*LLPPSLLLLASAIGE AGAGTG*TVYPLGGNYSHGASVDLT
3396	17297	A	3419	397	107	KNSAPPSPPIFLP*GPKFAFFPPGKRGV KKIF*KFPAQGQGVYLRGGGSPSPQ TFNNPKAAFLVPPPPPPVFGNPKKKK KGAFFSSNR
3397	17298	A	3420	3	253	RCREKRLCHSSANALAGVSEKKKKK KNWQ*CLAGICSYLDLWPLGLFKNLQSI GRIVELQLELKQYLHGITYQTLKILH
3398	17299	A	3421	1	393	RTRTIKTPAITQVQPLVGCALITNAL LLLSLPLVIAAGTITILNRYANTTFDP VOGGDPILYQHLE*LRGYPGDYIVILPG FGIISHMWAYYSGKKKPPGYIRND*AMI SIDFLRIIV*AHIFTVEN
3399	17300	A	3422	142	377	LSKNCKYKPSYGVQVQCKFFNQLSKFLS VKLLYCMVKLC**EG*NAQPL*QGFVLV ALKINIVLPYNPAISLPGIYSTD*KYT

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						DTQNLHTTVYSSSLTIKRN*KQQRCPSEVGE*INKCFIYTTYYSLTKRNKLSHMK A
3400	17301	A	3423	2	435	LILPGRGIIISHIVTYYSQKREPFYIGMG*AMISIGFLGPIV*AHHIFTVGIDVYTRAYFTSATIIIAIPTGVKVR*LATLHGSNMK*SAAVL*ALRFIFLFTVGGLTGIVLANS*VDIVLHDTYYVGAHLHYVLSIRAVAI
3401	17302	A	3424	2	436	LNIPTDPAGKQDPLLYGHLF*PFGHPEVYILLPGPIISHTVITYSGKKPEFYIGMG*AMISIGFLGPIV*AHHIFTVGIDVTRAYFTSATIIIAIPTGVKVR*LATLHGSNMK*SAAVL*ALRFIFLFTVGGLTGIVLS
3402	17303	A	3425	1	193	PIRPPTRPACSELRSRHTCPANVT*DSVSKKKKKKPSARGAHVCTPTFLGGQRKKKFCFAP
3403	17304	A	3426	3	446	HKKFLFPKSFNRFVPTPKKKNRPGPGF FFFFLKKIFFPPPGGI*SGFGSLQLFP PRVKKFFSPPPPEKGGPRAPPGPGNFF FFLKKGPSFPGGGLK*NGFPFPPPPF KKGVPKGGAPPPPPF
3404	17305	A	3427	202	1	FSFGRLMGTIKLPYTHSFILMNSQNNLEKYKVGGIPLSNFKYKATAIKIMWYHBNRYMD*WNR
3405	17306	A	3428	159	1	NPFHEKNFCSPFQMSHSACQAGVQWCDLSGLQPSLRGPKPS*VSLVSWH
3406	17307	A	3429	22	298	ESVASTKATERDMSDRMLEASOMPARYSOYPDAYTT*NIILSGVFTSLAAGILII PMI*EAPASKRKVLIVEEPSINLE*LYGCPRLRGR
3407	17308	A	3430	267	26	GITFFFFWLEI*LYWLFANKLYPHEQIWGLVFFPGLLLDFSFYSYDIPFLLLCLGFSNPF*CLIHCFPSVIVLLF
3408	17309	A	3431	274	376	NKG*ISCSISPPQTVRRLT/LSRLEC SGVISAHCRLCLPGSSDPASAS
3409	17310	A	3432	177	47	FYFFFFFFFFFFFPPFSLLPFFFFFFF FFFFFFFFPPQINRSFIASFYHK*VLIFKKN
3410	17311	A	3433	379	83	FKRHFTKREDLRMTVEHKSUSSAATRA MQIETIMAHCYTFMRLAKIKKYQTKCC *R*RVTGILTYCWRECKTOPFWKTVR RFLQYIYHIVIGYV
3411	17312	A	3434	214	3	AASFSTFTSTYVCIPLKSRKMIN*NYIKLASFCYTTTKINMKRQPTDSEMFANHTIHHHGLLIK
3412	17313	A	3435	1	353	GGGGGG*SELSQ*KUSNAM*QLQHR RMRQDLLSFGDQG*SEPC*CYTPANARVRLCQNRSVNEESLHDCNDKK*QNI* IISVPEKQKMKOLENLNELLIDNTPS LARDL
3413	17314	A	3436	29	394	VFMEDVDFPPPPPPPPFGKRNPPPPDP GGGGGPF*IFGPPPGRGKNPPPPPGK GGGKGGPPPPPPPPPP*KGGSPPGGGG FLTPPLNDPPNPQRGGGV*TPWPGP GSDFLNPPFF
3414	17315	A	3437	108	2	PVAHNSCNPTSGORGWIS*GHEPQT

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						SLANTVK
3415	17316	A	3438	215	3	LLLLREFFLPNHRVVFVFVFMKQGLT LTEAGVQWRSHSGSLNPQTPLGLK*SSCLLS LPSIWEYSAYHHIR
3416	17317	A	3439	1	186	QTSSFSFPRKSVITNPFPLKDDV*TH*KE AKNLEKRLDEWLIRIKSVKTLNDLML KTSTRP
3417	17318	A	3440	290	3	PGLGGGPRYSRSPGGIGPKIPINPEGEG SIKLNTPPPAPPFGGPN*DSFLPPPPPKK KKKTHVLPAGSGNLLQPLQGPAPPTTEVN GSLAQGS PKVL
3418	17319	A	3441	163	2	PKGLVKPRKPDQKLNPFPGPFFFFFFF *I*DKVLCHPGSAIVSSLSGDA
3419	17320	A	3442	131	1	RPRRLTKTSIGHWY*TYETDYGGLI FNSYILDPIDPIEPGS
3420	17321	A	3443	162	2	PGNAHSTGHLPLRPHRLGAVTHAGNDR TLGGQGRNIT*QGEFKTSLAKVRP
3421	17322	A	3444	2	130	WEKIFANHVSDGLIYRIYNELQQLYK* KTNGP LKKRPKSTRP
3422	17323	A	3445	2	117	LALLGLCKPOLK*ATGGLDPRYVDYRHP PHFACFSKI
3423	17324	A	3446	350	101	KAFSSSLGSSRRKKGSDAGFCILFKVTP FGFVWTLLEKKGIDPPLNPFPPPLRLVL KGSKNPF*KRGPFFFFFFFDFNFYWN
3424	17325	A	3447	106	1	LLOPNGLGPGTVAHGCNPSITLGG*GER ITTSVGR
3425	17326	A	3448	28	333	GQQEONSISKKKKKKKKKKTTPPKRGKRK IPGGKKKPLGKSRAPPLGGGEINPPPG KRAPEKIPEKKPRGNWETFKRMEKGLK GQ*PGNP*KVKPLWGGK
3426	17327	A	3449	81	339	PVSSCPGVAGALQAMTLEFVKYQHEV VANCRAISALTELGKFGKGRDVTYVQ QALLVWGLAS*PIVSSCPGVAGALQ AMTLEFVKYQHEVAVANCRAISALTELG YKIGTGRDITDGVQALLVWGLASQFV QPGCGPSAAAAAM
3427	17328	A	3450	166	322	RDFSTTVLITDRTSRQKITPDSVQLNLI DIYKTL*PTIGKYTFPSSTYRSLR
3428	17329	A	3451	257	354	KFLSPFRDEVLLCCPGSAUV*SA*TAAL LSSW
3429	17330	A	3452	286	3	TDPPPIKRAKEREMLIQTKIRSIRENFI TDQOKTEL*EQQLYAHRVNDLDEMKF LEGYK*PSMTHGKIENLCRPITSKDIES VIRNLLTDDP
3430	17331	A	3453	358	353	R*KLLMMPD*IEYNKT*NICTVKEEK CQPGTVAHACNPSITLOG*GGRT
3431	17332	A	3454	108	353	THLGGNPVRLYAWLLHVLVASYRIFSVS HCKDQTYLPILL*NFIMELGTVAHTYNP SILGGQRRIT*VQEFETSLANWKC
3432	17333	A	3455	342	50	GPVTNPNTPPVPLGGKRELPPPKKKK* KFWGSDPPLFFKKPKINPRETPPESCPK KKTIPVVK*GKKTP*TPSKKKKTPTPT ELPLKKKKKLN
3433	17334	A	3456	343	2	KAPFFFFFKKNSQKGGLEFFFFFYNPF IPGPGPTFFFGFFFFFKGDPVE*LCK FPGGGLDPLKDPGVPFSPF*FNDTTP PPPPFFFFFETVSLCRGHSVAVRD C

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3434	17335	A	3457	2	259	LTKPTESGTEBDKKGRDSKESGKTERTE SLRSQNGGNSV*SCPSTSTAAINTAA AANPLALNPQVLSLSLSCCPI SIKGSFV P
3435	17336	A	3458	186	334	AGGNKKMKERNM*NGEIP*WFKQNPQA GAHACNPITTLGGRGRRINRSG
3436	17337	A	3459	207	1	YFKPTLLKNDGKYLNRITDKFDPDRDNR TSNLT/L*EHALFPSTCGIPMRDRI RGH EVNLNQFQIRITQ
3437	17338	A	3460	268	3	PLNPGPKQSSPPGLPKPWPFREGLPLG PWFFPVGNRGR*APFGTNPLAFFLFFL *DRVLFCHPGWSVVQSQLTVQPPPLRL KQFS
3438	17339	A	3461	350	2	AKTAHNNNA*GPGSANKCTVRWKK*L CKGVKRLDKALGNGWSKVAINQLRAII KGAPLPTKTRVKAKRINIEPSAVIQH.KR IGKVKKLKGVVPHLHKKRNRFEVWSS LIIP
3439	17340	A	3462	312	1	HIVTYYSGKKKPPFYIGMV*AMISIGFL GFIV*AHHITVGIIDVDTRAYFTSVPII IAIPPGVKVFS*LATLHGSNMK*SAVAL *ALGFIPTLLPVGGLTRIVLA
3440	17341	A	3463	181	3	FLPLLAAPSGLLPLSGFLGVFLFCFPET ELPRLCCGTISAHCSL*LLGSSSDCAS GTH
3441	17342	A	3464	176	263	VGHDAHNPSILGGPFGWIT*GQRKPVDA A
3442	17343	A	3465	239	336	EPGEVAYSCNPFSTLGRSGWII*QGRFE TSLT
3443	17344	A	3466	88	326	QTSLLATI**PLH*KNPLPPPPPLPPTL TPPSPPPPPPPPKKKKKK
3444	17345	A	3467	4	345	KKRREERKKKKRKKKKKKRERERKK ERKKKKKKKKKKRGRGQKKRKTG*IE RKO
3445	17346	A	3468	265	335	QMRPDRHQF*DKVLICHPGWTVAAS* LATATRSGLSPSGWDCRRVPPCLASF
3446	17347	A	3469	115	342	INKQINKIKPTSYNLLISQSL*FKAL TLINSVKAQRGKATEKK*EGSIS*FMR FKQINHLNLIKVGQKPESTD
3447	17348	A	3470	56	328	RTYPTKQPMRDPEDPTSRPRYIERHLY ITDEVNDPSLTIKGIGHQMD*TYRYTDY GGLTFNSYILPPLPLEPSDLRLLDVNR VEPATRA
3448	17349	A	3471	3	329	RIGARDESSLAV*HKPRKTRKRLLVWF VNDSLVMRPDRKNHQAFNRKCF*LVDV GIDPYLVYHLRPHQAQGLI FLYECVMGN RMNGRGGAITAD*NLGKTLQCLSL
3449	17350	A	3472	154	2	PNLYPKSYWKEDINTWPFIVALVITV KIQKQPRCPMDKSLR*L*YIH
3450	17351	A	3473	132	340	AKTRNITTLCLDF*LIETVR**MCVFK KKKKKKKKKKKKKKKKKKDPPKKKKK IK
3451	17352	A	3474	3	345	VYSSIFAGTLITALSH*FTF*VGLRI NMLAFIPVLTKINRSTADIKYFLTQ ATASIFLLIATLNNILASGL*TIITWTN QYSSLIITAMAILKGLIAPFRRGREFQ IY
3452	17353	A	3475	1	254	PHHVQAGPTPDLR*STRGLPKCWDR



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3453	17354	A	3476	351	186	REALCLVHITLLYLPMTGPFRITQKLLKAA VFVFLQIQHQAFTQSLITLFTYFISFPQNS SVLSADNTMGPHVVGAGLELLSSSDP LAPAS *SAGIRGVRIDNTPVLTITLN
3454	17355	A	3477	330	3	GEKVFEIPLTRDNVSEILRCFLMAYGVE PALCDRLRTQPPQAQPHQQAANLAFIV HELNGSTLITNEMDKTLESMSRYRKYEW NVKRLRLRIKTARA *RLGRSQVK
3455	17356	A	3478	373	248	NRLNPGGGGSEPRSQHSTPTVTFEYDS VSKK *INNGNWK
3456	17357	A	3479	3	92	EGQGCEP *SRYSKANVTE *DCVSKNF F
3457	17358	A	3480	380	2	VEVPLNTSVFFASQGSVIT *AKHSILN NRNQTIQALLITNGLGYFTLLQASEYL ESPFTISASTYOSTFVACGFHGLRLVLI GSTPLMTCTRQILFHPISKHHFOLEAA A *CKHFDVDDVCTFL
3458	17359	A	3481	225	1	ERAERVVEQVIALFSPNYLRLSPFTTSP TPVVRHKFRPHLGYINPQTVAHICNP TLGSGGQITRSGD *DHPG
3459	17360	A	3482	332	1	IKYFLTOATASITLLAILFNNTLSQ * TITNTINQYSSLITIMAIIN *GIAPFH F *VPEVTQQTPLTS
3460	17361	A	3483	277	1	LSMSSFTSSTSPASINS *ALLFSSAES NSLECTFSSSPSPNSSEFSSSPSCSC AS *FSNSQSLIKASSSTEAPLNSSASC FLPLPLVG
3461	17362	A	3484	404	209	ALSVOPLNRPRQENGVPFGKASR *PRF PPCGPAMATKGELVPKKKKKISFLGHD QSLLELLQR
3462	17363	A	3485	31	347	FCILERKAPLYVV *CKKFFFFFFFFFFLE KGFFPLPLLVFWCTYHLKASLQ *VFL FFYLLCYSSLPLFFTLQSLTPHFLV *TFETYDPLMFFFTLFLFLV
3463	17364	A	3486	327	161	QKKVRDPYEQ *ANKFK *EEMPRFLEK HKLPLKTQETINQ
3464	17365	A	3487	311	3	PRRRFQLTNQNALPPLNGLNKTIPPKK KKKKEPLCPTCCVCAAFVCLFHLC * PCDCAHDCDNICVCVNI CVYCVVTHLH TGLCSVDCHICVGTCC
3465	17366	A	3488	245	1	RPRRLAALLITIT *LAPQNGYIEKST PYECGDFPISPARVPLSKFFLVAITFL LFDLEIALLLPLP *ALQATNLPLIV
3466	17367	A	3489	2	400	AAPTGLGLGRQKGYKQRQLLCLWSA TLLFLYFLNKL *LTKKKKKKKKKKKK KKKKKKKKKKKKGGPRGCPNQLKKGIG KPPGGFFKGGGGPKKIFFFTRGALFFK KKPQKINLGPDPGLKNFLKKKKA
3467	17368	A	3490	57	366	INVFAKQDQPLCACSSPTISVRSR PDWYQGLNHPIYLIYLRWSFALVAQA GV *WHILASLPLPPEPKCFSC
3468	17369	A	3491	25	384	IKQTF *FWKZGLSKNPL *KNRFS PKLGVLPPLPFGGPPFFGQAPGCF KKKKPPPKKIFF *KKGAPFFFFFFF FF
3469	17370	A	3492	170	41	AQPDQHGHTFTLLKIQKTRHGTCL *S QLIGLISFITQKITC
3470	17371	A	3493	1	240	VLSPADKTNVKAANGVGAHAEYGAEA

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						LERMFLSPFTTFS*FLDFFFFLEKIGFPH HVQQSLSGLPITSRDPSPAYNSILGS
3471	17372	A	3494	359	204	TQWLMPVILAFWEAEVGR*PEVRSLRPA LNSPFFKRLVIMYIMNIIILS
3472	17373	A	3495	1	178	DRLSFGV*GSSEL*LCHCTPGWATEPDR VSRKKKKRKKVGLGKNAKQKQIPRGYYR AEL
3473	17374	A	3496	361	1	LGPRLKKRPPWISIGYKVAGLPGFFFT PPQ*G*NFGCLKRGGFFYYFEAKGWFT PGGKQRGPPRSLEPFPFRVKLFFPPNLP NNWGHKGAPPKPPFFFFFLRNSFALVAQ AGVQWCDL
3474	17375	A	3497	276	79	AEVYKIKCELGAVAHACNPSTLGGQGR LIRS*VSASFTHKYQJQALMKLLNE
3475	17376	A	3498	3	476	FGTSHSLTLTLTRCLNAGNNLTSCTPT FTTDHLATPLLIIT*TLPLTSMASORH LFRFELSRKKLIISILNSIQSLIITFT GTLELIFVYFFFTTLPITLAIITR*GNQ PERLNAGTYLLPPTLVGLPLPLIALIYT HNTLGLSLNILLTTSAGE
3476	17377	A	3499	581	2	AHACNLNLTGGGRNIT*QGEFDTSLAN K
3477	17378	A	3500	380	135	RHQSGQIGKIPSLVKIPKLTFFPKGVL* SHLTKRARQEKGLNPKSGFN*PKLRPC PPTIVAKKONPVSKKKQTRQEPSA
3478	17379	A	3501	1	386	GSR*GNHPRTNAGAYFFVYI*GSLPL LIRLIYTDNTLCSLNILLTLGQELSN S*AHNLI*LAYTIAFTVKIPLYRLHL*L PKAHAQAPLAGSIVLAVALKLCGYGII RLTLILNPLKKHIDYF
3479	17380	A	3502	2	389	EKL*KKQNYRATHRLVLGAGESGKS TLAKHMRLLAVGFWKSGKEOPHARS YDGRKATKVD*LANLKRGITRTIGAVM SNLVPPVELANPENQPIVDYILSAMVNP DFDPFSEFYEHAKALKE
3480	17381	A	3503	2	379	PPGYGMV*AMISIGPLGFTG*AHHIFT GVDIVYTRAYFTCATIIILAIPTGVKVS *LATLHGSNMK*SAASL*ALGFILFTV SGITGIGLTNSLDIRLHDTYVVAHFH YVLSIGAVFALIGG
3481	17382	A	3504	281	68	FRMRFGWHGSOTVSENYPKLLKETRENP NK*KNIPCSWIGRISIVRMETLPRVYR FNAPFKLSPFFFTL
3482	17383	A	3505	139	263	ETGSHYVFOAGL*LLASDDPPATASONT GITVHSYVVOQL*PIFWASAVAGSLSEAR S
3483	17384	A	3506	2	427	LKTSMTINISITLTL*LRPAWH*AGYQTP FFV*SAITAGLLFLFPLVLAAGITVIL TDRNLATYTFDFPAGGGDEILYQHLS*FF GEPEGYLILPGFGLISHICTYYSKGKG PEGYIGMV*AMISIGELGVIG*AHHVFT GG
3484	17385	A	3507	343	3	GNHRSRSGGASSPSSFSHRSLRLVSSGS LGRJ*NSKSSKTSVSCGVARDTEKPL SKI KASSSDSCSVMAKANAVFTSTTG EKPASASLSLSVWASGSSPPGARNSSS S
3485	17386	A	3508	3	363	GGDKAARRIALENLDIT*KWMRTHEK

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						AKQLLSKQPP*SRRTGDLKLEQLTSLVR ETKRKC*RVL*IDRALTSHLYSLLTQCD ALGDASADLIQKTS*LOREFGYTAKTQK LLCRNGET
3486	17387	A	3509	3	434	GGPDHVARGISGRKYDIGQRKMGWTKYC TKELLQSOPGLGSPPTVDLEL*LQIELLR ETKRKYESVVLHLGRALTAHLYSLLTQCH ALGDAFADLRKSPLOQREFPGCYAQTK LLCRNGETLLGAANLFVSSIIYTLGATKTM EDTL
3487	17388	A	3510	1	401	GRKRNFP LHSQTSFCPSDSIPTFNNHE FTQHSNLELLRLISLLLEPMLFPVRL KSMFANLIVYDTSDDYHLLKUL*RG PTLMGRLLDGNRR*GGQLKQTYSKFDTN SHNHDALLKNVGLLYCFKDMN
3488	17389	A	3511	117	2	FKPTFSEMSHSA*AGVQWRNLGLQP LPLNFKQFSC
3489	17390	A	3512	491	90	EKVKIVLAGFFPKPPFPIN*KKGLK*R KGVGPRGYTVNHP CGYKPGGPGVQNP PGQKGETPFPQKKNKPGGGGALIPFP KGGGRGVPLSPEKPLKFPFGPP*GKK KNRFRKKKKKRON*PKSQSC
3490	17391	A	3513	2	31	GRGAPTTSLINVAGTKIARVVRNKLIP GAICSLTCGGAHGTMPARDERNLLSF TGSTGGKQVGLMVHBRGRRLVBLGDN NAI IAFEDAHNLVYFSTLFAAVTAGAP KCTTARRQLIHESIHDBA*VHFFH
3491	17392	A	3514	2	390	KSFHRTFLFENITLAPDPBPGPDGFPVA YPMMDIQRQEDQTLNRFPYGFPLPVD F*RKIOSYFASGA*LDQDGRLLSALD DLQLANSTI IAFSTDHGNALGSHGWA* YNNFDDTDHDLI FYDT
3492	17393	A	3515	3	410	RTGNWAGQGHYTKGAEVDSVLDVVRK ES*SCDCLQGQFOLTHSGGDTGFGMGT LITIKIRREYPNRMNTFRVMPLEKV*DT EGEPYNATLLVHQLVGNITDSTYSIDNEA LYDICFRTLKLTPTYGRDHLVS
3493	17394	A	3516	1	396	GEDAANIYARGHYTTGMENIDLGDLRIR KLADPCTGLQGLVPHSPGGGTGSGPTS LLMERISCDYKKNKLEVS IYPAQVCT AVFEPYNYI LSTHTTLEHSD*APMVUNE AIYDICRINLHIERSTYTNL
3494	17395	A	3517	2	399	EKIGYNPDTPVAFPIGNGDNMLPENA NMWFKGWKVTNRDGNASGTTLLSALC ILPPTSTDKPLRLPLQDVYKNGGIGTV PAGVSTGVLKPGHEVTFAPVNGTEV* SMRHEHPFRLALGDN
3495	17396	A	3518	1	402	GEDAANIYARGHYTTGMENIDLGDLRIR KLADPCTGLQGLVPHSPGGGTGSGPTS LLMERISIDYKKNKLEVS IYPAQVST ACSEPYNSILTHTTLEHSDCAPMVUNE AIYDI*RIINLIERSTYTNLNR
3496	17397	A	3519	1	408	GSCTAQKLYNS*TKTA*WSSNHTKNP FSKFPKLQNVWTHPESHEDNTAPTRLYN IOGRHPYVGLPNQWAGSCIIGTTPKSPF LLPIKTKLGLFPVYASHAKRSIAIGNW KDNEWPPERIIQYYPATWAGDL
3497	17398	A	3520	3	162	ETVLLCCPGWL*TLGLRQSSCLSPKCS

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3515	17416	A	3538	107	349	SVTFPPFFFLFKQAGSHFVV*AGGGGQGN FD*LRPKPPWLRSSLLTLTPSSLDYGGPP PIGPSNFGIFFRKRGFCPLVQASPF
3516	17417	A	3539	274	3	PRRMSLPLTQMGPLPSXMGPKTKLCPKK KKGKIPPRKILEPDVFTGQFYLMFKKIT SIFLKLFGQCRERGTFNSNPF*EARIALAK TK*DKN
3517	17418	A	3540	1	374	ACALVRNDHIIYVGPYALGSEIFFTET PIII*G*DN*LGPLVIGAHVVALTINY ISL*L*PPSVLLLLACATPEARAGTGCT AYPPLAGDYSHRAAYVNTILSLHLARV SSLWWDGSIPT
3518	17419	A	3541	427	76	RSSLSFQV*TK*PGQNGTFFKAPKLRRG APRC*PAGKGSIKTPQSPGGRGTPC SKKKKNRFTPPSFAGGPPFLKNKGGF MFWASKTKNGLNKTLGNPQPPGLGRLS PEWUG
3519	17420	A	3542	234	88	FFFFFFFFFFFPPPSLFFTTTTFFF FFFFFFFFFFFPP*ILYFV
3520	17421	A	3543	30	419	TFSFFPFLFFFGPLVLGGRKQGRNDKPK PGAACKPTTSPPKI*KKGAPPPRVNFK KF*KGGLPFPSPGQNLKSPWGIWISGN PLWVTPKPNQKKCPFFFKGPKCNFFFG PKPGGKCTOIFFFLWEKK
3521	17422	A	3544	159	411	VSRDISPVRLSPSSCFH*PFLHISSSVE GRFSSFAQPLFLSLNCTFFPLFLLLRF *DRVSLCHPGWSAVA*SLTATSTFVVK
3522	17423	A	3545	2	351	CLARTSGVRS*ASLPGQUNSYIHYLKL CMRELSFPPYLLIYSISLY*HTIMVIY FLVL*STLNLILYLFVQIFPALASGS SEWMLCLNNTLAVHVCVCVCVCVCR VCAC
3523	17424	A	3546	397	1	KPFPFCSYGKKGKIFLLVFFRLTPKPF GAGRKIFPRGPGFLKNPKAL*TFPAPP PFIQKKGFLQQA*IPFPVFLFKKKPK FLCSP*GGIGVSLFFFFSKTSCSVTQ AGVQSCDLGSLQLEPGLKR
3524	17425	A	3547	76	354	FLFNFMGKIPIKFRGCVFFFPFGGNYI FLVFLKIFFFFFGGFFLPPFFFLKKFPF FLGFFFGKISQKIFPPFN*IFLLXGA PPLFFFFFL
3525	17426	A	3548	197	1	INNKQQRMD*EKIFAKHVSXKGLISQI CK*LILHNSKCTNSPVKQARDLNRHFS KRDTKMNM
3526	17427	A	3549	175	309	KSTLKVHLYSISIPNFYFF*DRVLLCHP GWSAVA*SLTAASTRP
3527	17428	A	3550	3	196	GFHRVSDGGLDLTS*SAQVSPFKCWDY SHPPPPAHRTSLKKNKMRVLIIMMTI TYPAWVC
3528	17429	A	3551	3	360	RAVEIFCHDVCVSSGQADICLLLLCPTS IKVCPSSLSDIVIVIPDIYICIIYII FFFFFQARS*QCCLNDKR*YCSLWPTP PGFKKLSVSLPSIWLRCAPSHPPNFC VEGKNGV
3529	17430	A	3552	326	1	KDNHRILKMLAKSGKVRHYVDFDGIQI SKMSEKMGVKKPIGKERTKPKKKPSR TEDPKICTYVL*PDKKQKRFNLT*GIQ LG*KEIKLSLPAADMMVYLENPIV

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3530	17431	A	3553	186	1	RERRRLIKLEMTFTPELEKTIITFKPT*NO KRVRIAKSILSQNEVOGITPPDFKL*Y KDTVIN
3531	17432	A	3554	3	366	KISLGNMVKPFPNFV*FTYI**KKBIKK NSIGVL*PGTBQSKHEFKILPSKRNKI ASKRIKYL*INLT*EGQMYTENYKTLI KEIIRDINKYKIPCS*IIRLDLWMAV LTKLIYRFN
3532	17433	A	3555	239	1	GRGRMLPVSLLNITRVTAPCSGSITLV LIALPSLRILYITDEVNDPSLTITSIGH QWY*TYEYTDGGLFNYSYLLPP
3533	17434	A	3556	3	123	QWGLEWVSDELPTSSVSAGITOGSHR ARPANILNSVP
3534	17435	A	3557	237	2	KGFSFPIQKFGPLGVFPQKKTKKINR PPKOLTPVS*KOMLTPLELPFFFFLRQ SRVQAQGVQWNGLSLCAALPP
3535	17436	A	3558	87	379	KKKKKKKTLQKPLGVPLNPNGEAKSQT INELLLLKIATKKKGNLKLKKKKGDLF RGNYNPLFKKIKDDPTNGKNFPCS*MGK ISPEKMTLLPKAI
3536	17437	A	3559	390	181	KKKKKNFGGGGCPFFPTFRGG*GGGPPQ PGGGGAPKV*ISPPPPPGGKKSPPQKK KKKKKKGPPHPL
3537	17438	A	3560	2	101	VIVTAHAFVITTFIVITPIITGGFNG*LV PVDA
3538	17439	A	3561	2	126	INTLLALLLLIITF*LPQLNGYITKSTP YECGFDPISRERG
3539	17440	A	3562	16	349	PAFQKITLAMEKATEQTGGAKACQGT NNIMKFLKKKCIPTIIPWISFFSFLFFF FETKPHFPNMPBGKGNL*LKPLPLGL KQPCILAPRKGNRYRHLPPVNGFFFF
3540	17441	A	3563	6	130	TLEKILRDNESLRS*GQSECLRHCHPA WLTE*DPVSKNY
3541	17442	A	3564	3	152	GFHCVRQDLDLTS*SAKLSLPKCHDYR RKPHPAGKGTIFYIDYSTIE
3542	17443	A	3565	241	3	NLVSHVISMRKVINLVSNVTSSNSNH TWLSFIKLYPIIISIVFGQIVVGVVA KFFSDDF*DRGVPITQIVYTAPN
3543	17444	A	3566	71	256	SVFLLATVFLYPLATSFPPFLNRVSLCPQ WL*TPGLKQFSCSLPKRMNYRHEPLTP GSNFF
3544	17445	A	3567	1	392	AGAGTSGTFDYPPLSGNYSHPGACVDLTI FSLHLAGVASMIGAIWMTVMNTEPPA ITQYQTPLFV*SGRNTAGILLLCVPVLA AGITILLTDRTNTTFFDPAGGGDPILY QHLKGKGIICSHDRDI
3545	17446	A	3568	334	409	LQTVHACNFTSLGV*GGHITRSGV
3546	17447	A	3569	3	467	PKNPFGGFFSL*EKRYILPPPP*INPP PGFF*KAPPPPPPPPPPPPPPPPIQI YFITF
3547	17448	A	3570	3	420	FFDPAGGGDPIYLQHL*PFGHPPEYML ILPSGILLSHATYSKKKPPGTTGMV *AMISIGPLIV*AHILPFG*IDVIR ATPTSATIIIALPGVGVPS*LAWLHGS NKK*SAVLGALGFIL*TRGLTSIV
3548	17449	A	3571	1	418	NLNIHSPIDLPFSNIPA*NFCSLGA CLILQIT*GLFLAMHY*PDASTAFSSIG HITRDVHGT*IRYLHAKGASIFFICLF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
						LHIGRGLYGFAPLY*ET*NTGITLLMAT IATAFIGYVLPGGQISF*GATVTNLL
3549	17450	A	3572	3	414	SSGLAM*PHFISITLLTGLLNTLTYY Q*WRDVRESYQGHITPPVQKGLRYGI ILFITSEVFFAGFF*APYHSSLAPTPQ LGGHWPPTGITPLNPLEVPLINTSVLLA SGVSI*AHHSLENNRNQIIQALL
3550	17451	A	3573	2	423	GTLVLLPGA*AGVILGTALLTAEGLQ PGNLVGNDDHITNGIVTAFAFVITFFTVI PIIIGGPGN*LVPLIIGAPFPAFPRINN ISL*LLFPLSLLLLASIVAGAGTG*T VTPPLAGNYSHPGAYVDITFFCLLAGV DQPLQLQLRRKQKNCNPRGGGCS*F RLCPFPAAWAKLSLAKKKKKRIVE KYAQHDYITNVLGVVCRHKWLSLYMS ITKSIDKICKKAS
3552	17453	A	3575	2	394	ALANMDSQTSILHQYAVERTISLPSLIS KKHDRVLSQATQYLRGSINTNDVLPDY AQDLTVISELIPMLSLINS*LTNSLHH IPNLVYALLY*RDLFQEPRTHSFQDIM QNIDLVSVNEDITYDSFLS
3553	17454	A	3576	262	418	GWREWTELIIFYIFPFTLIPLAIYTR *GNQPERLNAGTYPLFYTLVGLSLP
3554	17455	A	3577	232	443	PSVQTFPCQPLSEGGWLLCVAMTPSPG VPVPTERALYSMECAPHPLFSLTSGACR LDYRTFDNR*VGLP
3555	17456	A	3578	48	410	GGLLHHRAGCWGHEADRRADQPDSSDPH SLHVAICLPPGAAARAAGAPSPA*TPAJA CPAPVPAPCSEHRC*PFGLSQRCLPGL PDARPGAAAHGWSLPTRLVLHDSHP EBAFRHED
3556	17457	A	3579	422	186	VYSKFL*SQLLRLRQESRLNPFGRGCR EPRS*HCIPAWVTQDSLSISSTSHET CGSHCSPGYLTWHICDQVPFSL
3557	17458	A	3580	442	3	GSATSRCTQESTYQTHFTFVKRGLRY GIILFITSEVFFLAGPL*APSHSLAPT SQLGGHWPPTGITPLNPLEVPLINTSVL LASGVSI*AHHSLENNRNQIIQALLI TILLGLYFTLQASE*LESPTTISDGMV CGRSG
3558	17459	A	3581	428	1	TRDIP/ASSLGM*PHFTPTLLTGLGLT TPLTIYQ*WRDVSRSTYQGHITPPVQK GLRYGIILFITSEVFFAGFF*APYHSS LAPTPQLGGHWPPTGITPLNPLEVPLIN TSALLASGVSI*AHHSLENNRNCLAA LE
3559	17460	A	3582	160	415	RCLSHCLAFMELSLTFTPSQLLSPPHY KNTFFFFPLNKKFNCVPAQGGQGNLI* LHPPPRGLKKPSCLRLTSS*NYGREPQP S
3560	17461	A	3583	399	2	STHLGLPKCNDYRCRPPFALLAVKLL CKTILVRNINNVCLPLLTGAASVIGLSA SLLFSVSPGTSIQLEAR*TFPWPMSST CWWRIFTSLGRAQPGHSDLOTCPRRDV DLAEPGLLFNGQMLVPPQRS
3561	17462	A	3584	215	1	KSPGLLNAFSRGSIYQASRANGA*LNQ RFWPGTVAHACNPSTLGG*GARINRSGD GRMSKDVSPGCGV

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3562	17463	A	3585	138	19	LNQRFWPGTVAIDCNPRPLGG*GARIMRSGDVIRNSKDEV
3563	17464	A	3586	262	3	GRPEVFTKDPFRGEPPPPPPFLPFFFFF FPPPPFVLFPPPPPPPPPPPPPPPPPP*Q VRLYLLEKYELFFFFLFPPTISLCCFGWS
3564	17465	A	3587	381	1	KKPTPPPPPRKMGPPPPGPF*RAPEPPPPFL GGGGGLFLFGGPPPPGGGPPPPPPPPFV FP*KSPPLPSPT*KKRGPPPPKRGGSFK TTPCPFFPKKGNPPKKKKKKKKKKKKKK GRPSSKSDAMVIRIG
3565	17466	A	3588	198	1	PKSPFRPLARKEFPNFFSKKKKKKSI* LNTNSLMDVAHICNPSTSGRGG*PHL RSGVURDOPOG
3566	17467	A	3589	373	1	GIYFPFFPKRGGPPPPPPPPPPPPPPGGBI PGGGGGPPNPPRKGPPFLKXKKGV*SP P*KGKKFFPPGGGVGDRGFLKGGPPPI IFFPPPPPPPPPPPPPPPPPPPPPPPP DLTCHFGTHPTH
3567	17468	A	3590	506	98	HTSRGPPPPFKKIPPTPRPPPPCQVWV FPPPKKKFFPFCSPKSLHSPKKKKKN FFFFKGGGPPPLPPLPPPLPFFFFFP PPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP FVLLIPPLFYNALTTI
3568	17469	A	3591	407	1	LVRGQITNKKLNFLQRELRBNRVRVVF LQQRLLFFPKL*LQ*KEIYLPF*MTCS RGAGFKSSLIFFPSPQNVLFPPPPF IFFFF*FFPPPPPPPPPPPPPPPPPP YLYISPPDLLEKKKKGGRRSRSS
3569	17470	A	3592	380	68	FRRGVGPQWPPFOKKGSPQKPPGPKRP PLKGGKLTTPPPGKPPPKGPKRPPPF FFLEGKTLFLGDPD*NLGKG*RGHK *GANRVPVPVFFPFEYSY
3570	17471	A	3593	394	45	ALNFTSQBGRQKHPHQKKASRGR EPRGVRKNYPPPKKSPKKNPPGVT PKKKKAKLPPRPL*GGPQRPPQKTAFF PLNFYPPKEPTKVLISFPFFPPPSAND VBLV
3571	17472	A	3594	402	62	AMIVLHSSLGKARFCLFKKKWAKDLN KHFSKEDSQMANKYKRLISLVIRNMQ MKITVRCHFLTRMAKIKOVNSKCRKE VQIPTLKHCWNECKTV*ILWNTLAARV G
3572	17473	A	3595	220	425	FISGFLNLQERERIAFFKVNIRLGAVV HVCNPSTLGGRRRIT*SPGV*DOPOGH GFCCLVNLQRI
3573	17474	A	3596	13	412	AEIAPLSTLRANDLCKRKGKGRNFG GDGQNPQIQAPFPGGNGKPTCKQKPHQ QWQGGHLLKGGGGGPKAKGVPPKKKT TIWGGTPLA*GVNPNWGHGTGNPGADP KPPGREK*SGQAQITGHTGP
3574	17475	A	3597	2	293	COLSP*ELGTPTREERERERERERER ERERLPPRLREKRAOVFATHENYEV CVIRHYRGCVVYTPLTTHSIDAHKMCV CVKKRPLYYKKKK
3575	17476	A	3598	243	9	ILLRQKQKQKSGRTRPQLQDQBOVNT*D RTWVWMPGAVTHACNPSTLGGRGGRIM



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/051,26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
						MIINLTITTTIPLGTITDALSPELNTTTF VIRKTLTLLTCLFL*IRTAYPRFRYDQLIH LL*ENFLPLTIALLLI*YVSIPTITSSIP P
3592	17493	A	3615	2	405	ARGLQEAGAVQNDPVSRLFDHMLQGH AHQMAIVTYQEPGETYIPKDKY*FLHE SQTYFCFLNS IPTPSMMEETHRRSSLEL LRISLLLTBSWLEPVRFLRSMNANLVY DTSRDDYHLLKDLSEGTILM
3593	17494	A	3616	328	63	PKSF*RPCLISPPPLGPGPPN*TPGFLK KKEFPFRGAHP*SPLLFRVRPGDPLNP RQGF*PKLPGPPFTRATEKPNFVQK KKK
3594	17495	A	3617	1	379	GTSVGIPGQGEFS*PAALHGSNVK*SA AAL*ALRIMLTPTVRGLTGIGLANSSLD IVLHDTDVVAHFHYVLIGAVFAITGG FIH*FPLPLGYITDQTVAKSHPTIIFIG VSVTLFQHFGLGC
3595	17496	A	3618	494	17	GSANPRPRRSCKTRETSPRNVMSLMS PMSPTLPMRPTSPGTPELITNSMGPMQ PNSSRPVNPASSATPVSPASPARPKPS CFPAQ*SPPL*SPERHGLSCLSVVK KCECTWVVMHIVEDRHSKPYHGPQW AHACNPSTLGG
3596	17497	A	3619	350	480	LGSDVYCKPPHLAVLL*QSPVLLPR LVINS*AVQVTHLPWP
3597	17498	A	3620	2	400	AAAEPHGCAKVLDEPKFLGSEB*NLIK QNCSEFQGLGEYKQKALLGRYTKVPQ VSTPTPLVSV*NLGKVGSKCKKPEAKR MP*ARDYLSVLNQLCMHEKTPVSDRV TKLLTSSLVNRRPCPSALEVK
3598	17499	A	3621	3	476	LGYSVHPQPLAQVLSPFLGCASAGNL LRMRGPPSPHPPTPAGLQAPAEALVPA RASPTTPCKLREWAPALASPERGSHSA VGG*RAPQMPKWEPRQGRQEQARALR TASMLSPLSFTHPVTLISLNFPTSLPPR NSPSWVSVVR
3599	17500	A	3622	40	390	MKGALTPGPRAGLGSQSONDMASTKPK SPDDQGSILHMGFPFLVSLLPPLSLSPS PPSPRHSVGTICAP*VLPRLGLALRVP HSSVPRPHAVPVVGTTRYSRGAWPLSL DFRGL
3600	17501	A	3623	52	475	AVEFHLFLQPLETINILSVOMDLFILA NSPK*NLQIICDLFFVFHIA*CF*DLPL EHVSVIHFWAE*FFFF*EGVSLFSPG WRAGNQFWLTKTPPHSPARLKGPSCLTL PGSWNRIRAPPSPANFFVFGKGFITLL P
3601	17502	A	3624	333	466	SITGKIRLWKNPWPWQVAAQCDPGLR G*GKRIITRSGVDRPG
3602	17503	A	3625	2	138	LRRGNPLNPGGCGSP*SRHCTPASST E*DSVSKNQKTKNSQMI
3603	17504	A	3626	3	337	LSLRPPLPFCPPRRPPTPGQHSGAG FPGRTLL*RLPPLDPPPSLGLSPGDDP GLAREBELKSPCWGPHPLCHLPP*CHA SSQPSINAYSWRKKKKKKKKKKKKK
3604	17505	A	3627	2	393	LGTDLSLIRFELGQGNLLGNDHINIV IVIAHAFVLIFFIVIPILIGGPN*LP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
3605	17506	A	3628	2	379	LIIGAPDMALPRINNISL*LLPPSLALL IASAIVEAGAGTG*TGYPPLAGNYSHPG ALVDLTIFYLHARVCST
3606	17507	A	3629	1	400	ODATYPTIESLITPHEALITICLCFL ALDALFLITTKLINTNISDAQEETV* TMLPAIILILIALPLCLRLIYITDEGNDP SLTIK*IGHQWY*TYEYDYGGLIFNSY ILPPLFLKPGDLRL
3607	17508	A	3630	416	1	SOLGYSGRVDRLEKATCLFSDILKHAGR TTPFLCAVRQGLHLQRPLQPPA*LCPA PRGGVYRGRQASLSCGLHPVRASWPLC LPTQFSAMEGAPPLALLPRSSISDYCA SNEQGSYVIGPSEPCIGYNLILVCHLL
3608	17509	A	3631	275	83	RWGSYVVLGILQLLSSSDSPALASGA GITGVSHCTQPKNVI*KISHLIVAGPAA DKTPQTPR
3609	17510	A	3632	186	3	FFFFFLLFFFFFFFFFFFFFLFFFF FFFFFPPFFFLVQVPLLCNL*HLVYLE YMWL
3610	17511	A	3633	3	235	GIISPLLIR*YARADANTAIRAILYN RIGDIGFILALA*FILHNSN*DPQIAT LPHPSDSKKYLYLSHLQKKA
3611	17512	A	3634	1	428	RIKKTILFNPDSG*DFILYQHLF*FFGR PEVITILLPRFR*ISHLITVYSGRNEFF GYLSN*AMISLCLGVIA*AKHITTV* IDVOTSAVLTATMTAIPAVRALS*L APLHRSNIK*SAAKL*ALRLIFLFTVGG OT
3612	17513	A	3635	2	129	PVIYSTIFAGTLITLSSH*FFT*VGLR INMLAFIPVLGFW
3613	17514	A	3636	2	422	DR*LFSITHKDIGTLYLYGA*AVVLGT AINLLIRAEIGQPGNLLGNDDHIYNIYVT AHAFGIIILFIVPIIIGGFGN*LDPLII GAPDMAFPRINNISC*LLPPSLLLLAS AIMEAGARTG*TAYPPLAGNYSHPGASV
3614	17515	A	3637	14	479	QNCRRNNFFMYFLPHQSEFFPKRCKQCN TICFRLSNQNTMKKTENELLLWIRKQ T*KQCKNSNGYTPSTPSRAKKKKKKK KKKKKKKKKKKKKKKKKKKKGGV LKKL
3615	17516	A	3638	2	449	IIITCFVGLCALVUTITTKLTNANILDA QNVET*ATLPAIMLVIALPLCLILYI TEWNPDSLIK*IGHQWY*AVETDYG GLMNNAYILPPLFLKPGDLRLLDGDNRV VLNPAIRIRIWMTSQVWHS*AVRTLSL RTDALPGRLL
3616	17517	A	3639	347	98	HFLLGGGGGGGSPFPKCKFFFLRGFF FGGGGGPNFPKKKGGFFSKKPGGV*TP PKKKKKKFFFPFGFWGPPGIFFKGPPD
3617	17518	A	3640	2	426	DR*LFSITHKDIGTLYLYGA*AGGLCT ALSLLIRAEIGQPGNLLGNDDHIYNIYVT AHAFVIIFFIGTPIIIGCGN*LVPLII GAPDMAFPRINNISC*LLPPSLLLLAS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AIVEAGAGTIG*TVYPLAGNYSHPGACAD
3618	17519	A	3641	94	294	GROGGGVAGGRGAMNSKGRQGRNGNPVR GREGRKSHPRKBG*KEGRKEPPPPPKKK KSRGEKNQRBG
3619	17520	A	3642	1	405	RTRGFDLRRFVLFDVAQMVESGYVCEG DHKTQNALIDRVSLIKRKRERQRIAVRE EQEKKQOBESLKKQVVBQSASQTGIKQ LPFADTGIPTASTTSAVSIVQVEPEDE AD*HEQLQYQQPSLSVLSDGTVD
3620	17521	A	3643	34	405	HLGRKQNKALFLAEAKKKKKKKKKKKG GPLKKNFGAIAHNGGKKIPSP*GVTK KTPILGPEKPYPSGGKGNANPPEKKIKT LKEKKKP*RGKGGKKPNPFWGERDESSS PK
3621	17522	A	3644	430	81	EPAQLSPQIKGPPSPPPNPLPSTLNGP FSPSP*KKFPFLKGLFVQGFPPPPSP PKKGFPSKNQLVPLSPFPFKKLPFLPP PLNFGPFRVFFKRPDPPEPPPPPP
3622	17523	A	3645	399	2	APFFTKKKKKEFPPEPPPPPPPPPSRVEF FLGGFPHFFPPQKKLFLKIPRGFTLP PKKKKTFPPPP*FLAPPGFFL*APPFP PPPPPPPPPPPPPPPPPPPPSPCSWCHQV FPHASNRHNPNSYPLQOY
3623	17524	A	3646	49	326	KKKKKKKKKGGPPPKTPGGAQKNPGG EKKFFFL*GGHKKPPRGIFPKKKPFFGGG KNWTFPPQKNKAPGGKKKFLGGGGEKPP PKBRVKKK
3624	17525	A	3647	327	94	QKKKKKFPFPFPNPTTSPNGPFFGGG GGPSPPPQKGGFSSNDGGVFLPPPKKK KIFPPPGGPGAPGPF*RGPP
3625	17526	A	3648	2	301	TSSVASTPIMSLEPTTIRCLDCEIIV N*H*ATTCTQILYSLPKLDYPSLIPIPV ALFVWPIIEVSL*YINSDPNINQFPKY LLFLITILILVTCG
3626	17527	A	3649	2	406	STNHKIDITLYLLPGA*AGILGTALNLL IRARLQGPQGNLVNDHIYVIVIAHAFG IIFPIVPIIIGGPGN*LVPLIIGAPDM EPARINNISF*LLPPSLLLLGCAIVEA GAGTG*TVYPLAGNYSHPGACV
3627	17528	A	3650	3	418	HAYADAWVHPSITLLILGLLNTLTIY Q*WRDVSRSTYQGHSTPPVQKGLRYGI ILFITSVEVFFAGPF*AFYHSLAPTPQ LGGHWPPGTGTPILATLEVPILANTSVLLA SGVSI*AHHSLENNRQIILQALLI
3628	17529	A	3651	526	2	WGGEKGRAGGAGEETPHOESRGGGAL QGBPLYPCCALHPPPLPLGSLLLPFS LPLPL*ANWPHQCGQGNLAGESTPR EKRLWGPPIPLPLWPPQTFPLSRKIG CPCPCPREVPTSPPPWAKPPLPGPPSEI AHLTTVRGGAALANVHNISDIDENKL NAFVTA
3629	17530	A	3652	464	297	RNSFHRVSQDDLLDLTL*SPCLSLPKCW DYRCEPLPASYIDVS
3630	17531	A	3653	162	467	NSKKQQPVLLEISITSVYWLHKRDLDSH TIIMGDPNTPLSLDRSARQKVNKDQIE LN*ALHQADILDIYRTLHPKSTETTFPS APHCTYNFLQSYFSSQF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						VGDDQGGHGET
3697	17598	A	3720	14	472	ESCARNPGLTHASQYOTPLFV*SVLIT AVILLI.SLPALAAGITILLTDNRNLTF FDPAGGGDPILYQHLF*FFGHPEAYILI LPGCAIIITHIVTYYSKKKEPFGYIGRV* AMISIGYLGFIYRAHHIPTVGIDRTRA YPTSATIIIAIPT
3698	17599	A	3721	3	298	EAAIKYFLTQATASILLIAILFNNILS QQ*TIINTTQYSSLLIIIMAILKLGIA PPIH*VPEVTQSTPLTSGLLLT*QKLA PSTIIQLSPSLNV
3699	17600	A	3722	86	505	AGAVTITVTVSL*KKDSFTHSNVC*A MRUNWES*GLSV*ARHIFTVGIDVTRA YPTSATIIIAIPTGVKVS*LATLHGSN MK*SAAVL*ALGPIFLTAGGLTGIVLA NSSLDIVLHDTYVVVAHFVLSIGAVL
3700	17601	A	3723	432	48	FKTSLFLPFLPSPFCPSFSPSLFPFSPS CFLSCPSSLSLFLFFLLFHPHFFPPTLL ISF*VFLF
3701	17602	A	3724	2	406	HHIFTERDVIDTRAYPTSATIIIAIPTG VKVS*LATLHGSNMK*SAAL*ALGII FLPTVSGLTGIVLANSLLDGLHDTYV VAHLHYVLSIGAAFAIIGGFH*PPLFS SYLTDQTYAIHFTMIFIGVNL
3702	17603	A	3725	174	158	KFFGGGPHFFPPQKGGTFPENPRGFF TPLLGKNFFPPPPVNLGPRGFF*GP
3703	17604	A	3726	2	392	LFSTNHNMGTYLLYFGA*AGGLGTALS LLIRASLGQPSLLGNDHNTNVIUTGHA FCIIFFTVIPIIIGQGNRLGLIIGAP DMARDINDISCVLPPLISLLASALA EGGAGTG*TAVDPLAGNY
3704	17605	A	3727	48	474	KKKKKKKKKKKKKKKKKKKKKKKKKK KKTPAGPPPPPPPREKKNPPPEGGQKDP PAH*KKPPPPPRGGQQPPPPPPQKNPPE KQKTWGAEGGTTPPKPPPKKNGSQIAD PPSNAKRHPTEPPQSQCIAPPPTP PP
3705	17606	A	3728	387	53	PPPKGVLPSPDPNFTTPPK*GVFSLPP *KFFSPKGLIFWGGGGNFPDPKKKFF SKKPRGGFFPPP*KKKILISPPREKLG PRIFLKGPPDPTFF*FFFFFFF
3706	17607	A	3729	1	397	PTRLQPLSPFKRFSRTPDVAN*VS LSPSPSPSGSFVFL*VESFCVWKKRF TMLARLVDS*PSDPANASQAGITGA SRLASLYIY*CFSIQIGLLPEFLIQYV QLLVIVPIIPIHLYLSVPHL
3707	17608	A	3730	407	0	TLKKTKKKKKKKKKGGGLKCTLSGPK *NCGRKKKIFPLKGGKKKQGTILKKL ILOGKKKKKPPKKKPLGKKKPKGK GKKMLMPGVIKLGTSSKKLI
3708	17609	A	3731	3	200	GGCSLRSCRCTLAFTS*DSVLSKKKK KKKGPFKVLRGKPSGNRGAKKIKQ KPCPFWESF
3709	17610	A	3732	3	380	THKIDIGTLFLFGA*AGVIGTALSLLI RAELQGPNGLLGNDHYNGIVTAHAFVI IFPIVPIIIGGPN*LVPLIIGAPMA FPRINNISF*LLPPSLLILLASAIVAG AGTG*TSYPLAGN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
3710	17611	A	3733	6	394	AMISIGFVGIVG*AHRIPTV*IDVNARA YCTSATIIIALPTGGKVP*LATLHGSN MK*SAARVL*ALRFIFLFTVSGLTGIVLA NSSLDIVLHDTTYVRAHFYVLSIGAGF AIIQGFH*PFLFSGYT
3711	17612	A	3734	27	238	GIPGSSHASAHIG*IIVLPHYINITLL NLITIDIILITTAFLNLNNSSTTTLLLS RT*NKKKKKRGOPF
3712	17613	A	3735	402	249	ASAHASAPLV*SVLITAVLLLSLPVL ARGITILLDTKRLNTPFP
3713	17614	A	3736	100	430	VTEKSDSTYEKICLLEPQTDLRALGF CLSTYKQKKK*KKKKKKKKKKKKKKK KRG
3714	17615	A	3737	158	306	FLSSVPSLVQVLFSSICLDNLPDMMQ LWSEIFNK*LYLQELSLQVY
3715	17616	A	3738	279	3	PQICFYNNLNFPYFQIFPQVFLANSGL LFLYQTLILLSFNIPYILYLIIQISIVFO SVIL*FIPSNYSWYGFVLCVLTFFBK KQTCADV
3716	17617	A	3739	268	388	HFFFFEMEADSVAKNGV*WYDVLQGF PPOVKRYS*LSL
3717	17618	A	3740	395	153	GWLMRFKRCGLQNIKV*GEASADABA AAS*PEDIAKIADEGSYT*QWIFPVGET AFYWKMRSPRTFLAREKSMGPKL
3718	17619	A	3741	271	386	TCFPFLKLWVYELGL*RRNMRQGAHA ACNPSTLKG*GGRI SRSGDR
3719	17620	A	3742	406	190	QLLKLRLQENPWRGG*GCSKPRSPFRP QAWVTERDFVSKSTKINQPKQNERKV FWFFFLRKEKQFEL
3720	17621	A	3743	272	408	GLAQANSL*YVDLAI PCNNKGHSSV GLNMMMLAREVLRMG
3721	17622	A	3744	211	407	KGRNII LGPVNITFCDTPTSCNFFR EEVSLDCGMSQTPALK*SSCLGLPTCN D*RRQPR
3722	17623	A	3745	405	189	CVSQDGLDLITS*STRLGLPKWDRKCK WTNQLFVNGQKSLNSFCVYSFNVLDITG FKEIVMLVHVLPFL
3723	17624	A	3746	120	362	LKA*EISWANGTIOTHOEKPEVONIL EENIVFLPGQDRIFECQAVTALPEKK ATVAGCSDSHLYPSTLGQDQWIT
3724	17625	A	3747	401	233	NSGRCGCEPRSLPCTPAWVTRDPSIK NRNKTNIQ*QKCKR*TKGVI PMTRSL
3725	17626	A	3748	353	109	LGLANFCTISRDGVFCWPGWRSPTPLR *SAHLSLPKCWEYRA*ATMPELLMFLI KALDFQCVCGRWGGGSDITIKLCQM
3726	17627	A	3749	412	221	HGLKCLVYPQWQNSNISLQGHFSEV AM*QRAHNHGIHWFYHDSFPRKIWINWA RRGSGCL
3727	17628	A	3750	1	355	FHVVSQGLDLITS*SPRIGLPKCWDYR REPLRPAENTVVHFSSWS*TNHSGKIN *TLQWKEQLPGL*ILRVFFFPSPISW NS*QKASITVFPCLWKRDIPLYHFPVS OTFRGF
3728	17629	A	3751	423	125	QVCEKVLISLITEMQLKTIVYHLPDVK MAFRQKTDNKNCRGVEKGTVPVHCWK CKVVPQ*RTANRFFK*RKLELPYDPAT PLLGI*PKERISQGV
3729	17630	A	3752	3	171	FQPIAPLYANSEQSGKRSESTSYSSVER



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		6				TPQIFSTGTTFKAGAGELLEPGGGACSEL RSCHCSPARATRVKLVKKFKKIK* RIRITQIFSTGTTFKAGAGELLEPGGGAC SELRSCHCSPARATRVKLVKKFKKIK 3749 17650 A 3772 112 406 FFFFFFFFFFFFFFFFFQGGVPT* K*FMPKKKLPPPPDAKLEFFS2PPP FFFFF 3750 17651 A 3773 24 197 IFSVEMGFCHVGQCQLDLGGSSNPASV S*SAGVIGVSHAMPLVKLVKRNKLSY V 3751 17652 A 3774 85 201 VNFPHLI*FVNKKIKLEKKKKKKKKKK KKKKINWKKKKK 3752 17653 A 3775 1 382 WENLSPGSGRSESP*SHYCTPA*VTE* DSVSKKKFNLQENKRLTLLLEKALF KNRGSPCFSIKWAGKCKICQWPFVATR MGDRSROTNLNGENLKSPLS*SIKIQ FYLLGKNSPSRNIY 3753 17654 A 3776 1 181 IKMATVTKATVRCVTPSKLPMLLPKL ETKILKLNWNLERA*TPKALLS*KNMG LSNS 3754 17655 A 3777 70 385 LNKMQTKTFDSDTHTSICPTLHFINTKL QTFILLAIFYLLFVNPFIFINFEEDGF CFDDLSSCLFY*CLP*FYFFSAFFRL HLFFFYRLSLTLDLFSFLI 3755 17656 A 3778 2 406 KDDRNTHEQVHPNASQDEAFDPYENF FEDSDSPKSSSTEPSPIHPVDIMQTI PHCADNFARQYTLAKLAKKKKKKKKKK KKKKKSSSSGGGPKKAGPPPPPRGEKN FFFFGPIIFSGGGP*NGGGGGP 3756 17657 A 3779 403 176 FLFF*LGFFLRQSFTLVTTGSGQRDLG SMQPPPRF*FNRGKKRLWGA 3757 17658 A 3780 3 248 GLNCTOLRLKLYSSHTHTG*TYAVLPY NPNTTLNLTITYLITLTTACKKKKKKKK KKKKKKKKKKKKKKKKKKGGGA 3758 17659 A 3781 3 330 VDRLRTGVQDHPGRHSESPSLPKKKKKR *KILPKRGGVYLNPHFFERLRGENNLT GGEGORETESPPCLPAGGNKIFV*KIK KKKRGGPFKGNKFFPRGGGKIFF 3759 17660 A 3782 399 187 FPPPAKGDFLPSHFLGLPPGFSPPVFK PRPRNLILGP*KKFYLPPRP*TWFL* NGPPPPFFFFFLDF 3760 17661 A 3783 392 11 KKLVNLPDHPAVPLGTFPKMKAGY* RAICTLMPFAALLTIEK*NRQNNLLVD K 3761 17662 A 3784 324 80 EGPFFFFFFFFPAKRGFFPPDFLVPQFF PPPLP*TPDPDFFLAPLKFFPSPPDA LNFFFFKGPPPPPPPPPPPPPPPPPP 3762 17663 A 3785 354 24 PPNKIFFSPPQKKYFPYKIPPTTFEFL SSFFFFFFFFFFFFFFFFFLC*MVH FIVYKRCRGRITLHTPTLRQLVLCC LSVILACCCIFYVTMCLCAKYLE 3763 17664 A 3786 3 369 SCGLVIVYQELLHPCRGNGTAVRWOK KKKKKGASPPREGAPGEP*RGPTQ KEPPLKE*APPVGGGGPPPNGLGGG PAPPFFNPKAFFKKGPSQEPGPLEK GLFWKFFP 3764 17665 A 3787 1 125 PRHFRSRIKXLDLIF*BARGLPKCNDY RREPPRPAHSIII

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3765	17666	A	3788	427	251	LTPTKRGSCSEPR*CHCTPAMVTEGESVS KKKQAKNRCSLRMKYRNEITSSPC
3766	17667	A	3789	250	2	GFFDVEKIKKNFFFI*KKPQFFFPNP FF*ISGGKGIFFLAGPPFFSFFSFFF* DRVLLCHSGRSVAQAQSLTATSTFR
3767	17668	A	3790	412	3	GSTPTTTPFGVGGLAPPGGVVPPFPAP PGGTPTFFFKKKKKKKPQNFPRPCSRYN GGLGRKNFTLRAGSTNPNFSPAPPPG GQNKTPFKKKKKSR*MTLQSFPRPGTA PGAAM*PVSPPEPCGPPAPALSTK
3768	17669	A	3791	10	187	GCSEL*LIHCTPARIWSETLSQKKKGRG KGGFKNGIPCFQKNGKKRFGKSPGHP STG
3769	17670	A	3792	1	331	FRVPLGRLSRGEHQQQQQQFFPPPPFP GPLPLAGPSRSGSFKIRLSRLFTKSC NGGSGGGDGTGKRPSEGLAASASLITDM GGSAGRELDAGR*DRPGAGRQTSFSW
3770	17671	A	3793	1	431	FRKSGARCAPKAPGADGVVWGHHRASP QTAQAPPVTCARSAGSNVFSHASGPQDR DLHSPPVPCPRGAPGTHSPGASGA*G RTVPVGGK*VAGVQQRTHPLGLAP*LVL PGLAVHITKPKGSGTITPGTVAHACNP NTLG
3771	17672	A	3794	342	48	KRENNPGVAINPSTLGGCNPSIVGGFCN RVGNPSALGGCNPSFLGFCNHNVCNPS LGG*GGRISRSAQDHPQHGECMSPK IQKISQACEARVG
3772	17673	A	3795	2	189	LNFGKRGSCSEPRSCHCTQAMATE*DSVS KKKKKSGSRPONTIPSAALPGFPVSGELI LAGPML
3773	17674	A	3796	1	401	LNFGKRGSCSEPRSCHCTPVVWSE*DFIS QKIKKKKKKK
3774	17675	A	3797	279	3	TLAATVPMVNSFLERHYFLFLVELCCFL QHVLYLVTFTTETGSGRSVAQAQVQHD RSSI*PLPHGLKRSFFLLSLRSDWYMET PPCLATE
3775	17676	A	3798	229	394	VFVKSLLQCPGMVAHCNPSITLGG*GGR ITMSGD*DHGPGHGVSTYNTKKKGGG
3776	17677	A	3799	380	206	AGHM*S*LLRRLRSDPLSPGVQSCSEP *S*PCPPAQVTVIRLSKKKRLHERDKSS AS
3777	17678	A	3800	450	3	TYLLRGRHSLHYSRSPFYSNRYGACSY MRPTQOATILGLRLNQGITREGPAIAHSP AVRPRLSLAHAHVRLCLDRPQAPAPFP AFFLPCLLVAQAGVVRRLDGLSQPPPPR FKRFSCLSLPSSWDDRRPPPLSS*FAFL VRMGFRV
3778	17679	A	3801	301	10	KKQPKKKKKRCFFPLFFPPRGFKGSPPE FFLTPPPLKRLPWLKALPQILRTFTFF FFSRSRSPVTCAGVLAHDLGSLQ*TP GKEMPSCPVLLC
3779	17680	A	3802	420	51	SASSPASPSTFFPPPKKILPSHPPFFFP PPPPPPPP*DPSPFFFTPKKKKILF PPPPQKLEFLQPPPPPPPPPPPPPP FFFGFVNCQFSLVLI
3780	17681	A	3803	253	73	CTTPSKRYSVLECCIN*ITCTKRIKLD PFLTLDLILIN*KSFADLVNRATTDITD KVKG

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3781	17682	A	3804	385	55	AGTRPVFAALAAAAAPARLLPLAPHGSA ATGFFPPFPHGEGLRGAPAASSPPLA HRSQTPNMVDCGESPIFDPPQFTLL*NGP PALCLPQGLETVNIVESLALCFTSHGN
3782	17683	A	3805	191	2	QRHLKALNPLPRCVCCVCCVCCVCCV TF*ACKICTCSDFPGSPRKYKLEFGTKI INIVDFN
3783	17684	A	3806	1	367	KLROVIYLEDLPTI IDEGSSYTKQWIFNV N*TAPYWKMKPLKTSVTREKSMGPFKA SKDRLTVFLGANVSDPKLKPMPITYNSE NPKALQNDASITLPMYKRNKACIALAH LFIWATEYF
3784	17685	A	3807	3	145	LGPGGGCSERSCHCTPAMATKGLCLL QEKKKKK*RLDPEAEVAVSRRGALALQ GQQRGNSVSRRKKKGRDKVSLCTPAGF
3785	17686	A	3808	362	86	NPPF*CSPPFFFLWGFQVVPWCGE* TPPGPFCELPPLPKKSKSPPGVWGPFF FPPPWGGGAKPFFFLPKMGFPQTQICPL PFGLGKKN
3786	17687	A	3809	245	377	FGYMPSPFETQSESVTQGVQWHLDSL QPLPGFK*FSCGLGLP
3787	17688	A	3810	3	268	KRNPLNLKRRYEFKTFANVFNSKIYNT PHLRSSTS*GYPLPLLLNLLKVLPNRI RQOEIKGRIGNKKKTSIVYSIMLSANT EKPK
3788	17689	A	3811	2	388	SAENCLNFGGRCGDLRCHCTPAWUTE RDCVSRINKRETEKYMKN* TGNMLTIID AGRRYMRCHQTIFTPFFFWRGSLIFLAP PFSQGGIFLPHPPENMKKVRITITPT FCPLRTDGFLLPGQGF
3789	17690	A	3812	292	136	PPTVIARKGKPRFKISSPQWQSAEOLG LPSFLCFEVCRCOCLLLPLLLPCREDE SICCPGWS*TPGLQSSHLSPFNWCDCR CEPLCRAIF*FFCLCTLLLPAPVSAVLL
3790	17691	A	3813	359	52	KKGRFFPFEPNPFGLVFKKKKKKTPFP PNPKKKKRGAPFPFFFFFFFRH*VPLCC LGMFRTPLGKSSCVGLPKPKMDYRHKPL PLTKDDYVYVGLFVSLQ
3791	17692	A	3814	382	1	GGGMRAPLGYHIKTFFPLKQKNPPGG GAKPVVP*PPGG*AGKMGLPFRQRFPLT QKGPPPPLOGKREPPQKKKKKRV TAN GDP*NSECR*GCHLRVQKEMRLPGLRNS PPHYIIPNRINDMCS
3792	17693	A	3815	472	340	TGFHRVSDGLDLNS*SAOLGLKCDW YRGLPIIIPNMGWS
3793	17694	A	3816	247	378	PPPPGGGXNGLLKLPLPG*REIPPP PPRGGNPPGAPPPPG
3794	17695	A	3817	25	465	TPFLGS*GKKFPRGPGGSPPPPKGNPP F*KKKKPRGGGA*FPFGGGRPKN FLPGKGS*PKFPDPPEGTCKRP PPKKKKKKKKKKKKT*AKAYKLCDC PIVPGDLKSDKTLAPPVSVGLPRPCTC LSPR
3795	17696	A	3818	475	147	PPKG*EHPPGPPFRGGRGNPPHRRFF VLRTPGYSFFF*KKRGGPPTFFFTLGGP FGFLKGPSPFGGQKLPFRPGGGGLK *IPFFPPPGKKKDFFTTKKKKKK
3796	17697	A	3819	461	57	TNQKKAAPPPLKKKFFPPKKKTGAP

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3797	17698	A	3820	1	418	<p>                     PRRKKRGGGKGGGQVTRKSPHAFSEG                      CAPPYLRGGLFFFFFFFFFFFFFTFF                      FFFFFFFFFFFFFFFFFFFFFFTFF                      FFFFFFFFFFHVKNILFV*DYIVILADL                      IQSLRHKKDQELLRR                 </p>
3798	17699	A	3821	385	1	<p>                     HAYHI*KPSF*PLAGALSTLNTSALAM                      *PHPHSITLLILGLLTTTLTIYQ*WCDG                      TPSTYQGHITPPVQKGLRGLYIILFITS                      QAFFGAF*AFYHSLSLAPTFQLGHW                      STGITPLNPLEVPLNLSVLLASGVST                      LQFFPFSPLHGVRQFPFSSPSCFWWG                      FVSKLLPLQLLGRQFPQKSLVSLQ                      FFFFTPLLIKIGHNENLCCGWSKTFE                      LK*SSHLGTPKCSDYRCFFPHFDPNDI                      CSYVPQLQSTHPLNLY                 </p>
3799	17700	A	3822	72	424	<p>                     KKKKKKKKKFPFKKGGAPAPLPPQKAG                      GEKLFPPRGLIPKKPKKAGKKKINLFK                      KKKKRGGP*KKKKLGKGGKKLPFKGA                      QKKNPGAGFKKGGRGKRGAPQKKGQGG                      SSS                 </p>
3800	17701	A	3823	154	2	<p>                     GHHTQRTPEQRLLNNSYRAELKHLNNTK                      NNPI*KNAKMNRRHPSKEDIQM                 </p>
3801	17702	A	3824	422	212	<p>                     MGSSNFSPTASWDEPTIGCQHT*PYVE                      MGPCHVS KAGLGLLGLRDPSPASQASG                      VAGVSHCTRLWILL                 </p>
3802	17703	A	3825	2	417	<p>                     KRVNTRGFPFPFFPKTPEPKIFMGPPQKK                      KNPSPPPIKIFFF*KAPSP                 </p>
3803	17704	A	3826	423	65	<p>                     ACGRGKRYFKSGGRVAFPCAVIDFPFGKK                      ANQPTFANPRKQKPSGRGNSPMGKPPG                      CFCMEKASQFVSFNKGVALATKDFC                      PIGKTA*IPSKKKKKSDPG*VKRGKPN                      LYSIYNK                 </p>
3804	17705	A	3827	285	136	<p>                     FFFLFFKFLFFFFFFFFFFFFFFFFFFFF                      FFFFFFFFFPSGA*KIFILATHY                 </p>
3805	17706	A	3828	425	316	<p>                     QDGLDLTS*SAKLSLPSWYRHEPH                      PAQTFEKQ                 </p>
3806	17707	A	3829	3	169	<p>                     LSN*ANNLY*LAYTIAPITKPLYLGLH                      L*LPKAVHAPLAGSIVLAVALLLKGG                 </p>
3807	17708	A	3830	6	452	<p>                     IGPQGGAKDFCSKKFORNVRVSPRGE                      GRKFLPLFGGGQKFPPLPPGWGAKTFP                      LKPPPKKKKKKKKKKKKKKKRNPFP                      VSPSSWSPV*APSEQRSGQLPSPRGD                      *VVRLSPSPRPDCVRSATRGNSPPC                      RGSQGP                 </p>
3808	17709	A	3831	45	387	<p>                     NRGVKVPS*LATLHGSRNK*SAAVL*AL                      RYIPFVPGKKKKKKKKKKKKKKRGGT                      PPGGKKRFPSPKKKKKKGLKNPQPKK                      NPFNGKQKKGKGTTPFWGGKKAPKKI                      P                 </p>
3809	17710	A	3832	463	288	<p>                     DGLDLTS*SVRLGLPKWYRHEPH                      APCILMATPQGEVLSFLETIVKSL                      LH                 </p>
3810	17711	A	3833	294	90	<p>                     FFFLFFFFFFFFFFFFFFFFFFFFFFFFFFFF                      FFFFFFFFFFFFFFFFFFFFFFTFF                      FFFFFFFFFFFFFFFFFFFFFFTFF                      TCAPPAYPRS                 </p>
3811	17712	A	3834	427	37	<p>                     SYHGRILRRADHEVRL*NRKGRFGAVT                      HACNPITLGG*GGRIMRSED*DH                 </p>
3812	17713	A	3835	499	53	<p>                     AKLMYQPSRNNVAKESYRNQKASWHP                 </p>

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						NQFAVLAGQCTTALAEVLNVK* <sup>1</sup> LSSYH CRLLVGMVHGCLLVSVTFPCNIFSGLK VH
3813	17714	A	3836	304	3	RLKTRTRNNNQTEINS*YIKDLNARQET IRLLEENIGGKPHDIRFAMLFWI*HLKK TKNIYKLOYTKILDPCISKDTINKV/KR* PLEWERIKFANHISDKG
3814	17715	A	3837	475	135	MEGLFCFAPMVHFP <sup>1</sup> IPPPILGG*GGGSPG PGIQTPPGYGP <sup>1</sup> PPFFTLKLPRRGAV FFFFPPLGGLGPKNVFTPGAGASLEPGW ASVFFPGGVP* <sup>1</sup> NPF <sup>1</sup> PKKKKKRLKIGWH F
3815	17716	A	3838	415	245	ETGFHHVQDGLDL <sup>1</sup> LTS* <sup>1</sup> SACLSLEKWH DHRREP <sup>1</sup> PHDPQVSEIRALFFTHGAPLS
3816	17717	A	3839	460	413	WDYIKLIGFCTAKETFRVKQETTHMTKTS AKYISDKGLKTRLEKQ* <sup>1</sup> KNTNLI* <sup>1</sup> NNV K* <sup>1</sup> LGRYSH
3817	17718	A	3840	2	470	GQDAPHTFDGVAARRRGSSLLRWGGQQA QGILTSQTFWPGRDAPHLPDGVTAGPRR SPHILRWAGQTRSSLP <sup>1</sup> RCDCGGRBEALLL TS* <sup>1</sup> VGWRPGRDAPHFPDWAARQGRSSH RRWAARQRRSSLP <sup>1</sup> RRGSGRAEAA <sup>1</sup> SSNA SLQRVSKVSVSCRP <sup>1</sup> GG
3818	17719	A	3841	54	332	QFGFHHVDQAAP <sup>1</sup> ELLTSDHLPSSASQSA GITGVSHRARPSLAHS <sup>1</sup> THSLAL* <sup>1</sup> PTTA HSLIHMLTHSLTHSLG <sup>1</sup> FPSCFSSPPSHIT HSLARPLGV
3819	17720	A	3842	208	468	ENFTPPFLWCFA <sup>1</sup> LV <sup>1</sup> EDGFSLSYLSA HYCIRVFLYCPVLESARFLMFLNLAHV CYEWHLSVSLS <sup>1</sup> FTVS
3820	17721	A	3843	406	2	PSSSSSSSSSPAA <sup>1</sup> FLGCGVFPSSPFF LKRAPGFFFWGPKKKNFSP <sup>1</sup> PRGVKFFF FKGAPPLFF <sup>1</sup> FFFF <sup>1</sup> FF <sup>1</sup> FDVLLCHPGW SAAHAS
3821	17722	A	3844	370	253	VGLLEPRGQGCSELSHST <sup>1</sup> PMATE* <sup>1</sup> D PILKQNETEQ
3822	17723	A	3845	369	73	LRODNGNPPGGRACSEPSHHT <sup>1</sup> PAWAT E* <sup>1</sup> DSISKKRQNSVFTESYFASEHCYS LTGGVAILLMEGPTGPDGAFMCHLRNL CRCSPILPLALQCDH
3823	17724	A	3846	198	388	FRKSTINVRVHVRINLKNIT <sup>1</sup> PTIDAQR P* <sup>1</sup> EKLQQLHMKYSITMNSRKLSPALR NL <sup>1</sup> * <sup>1</sup> KPS
3824	17725	A	3847	391	20	GFFPPRVF* <sup>1</sup> HGPA <sup>1</sup> NFLGPPK <sup>1</sup> KKPLF PR* <sup>1</sup> * <sup>1</sup> TWFL <sup>1</sup> LKG <sup>1</sup> PPL <sup>1</sup> FFFF <sup>1</sup> * <sup>1</sup> DGVSCL RPGWSAVSKN* <sup>1</sup> QTNK <sup>1</sup> SIIL <sup>1</sup> PRGK <sup>1</sup> NL FVHSLIKGPTCDLLIPK <sup>1</sup> NRVKESTKT IDHLSRQDMA
3825	17726	A	3848	227	2	KRNPFHIAALADSDGPR* <sup>1</sup> SKLKNFW RGFSLDAIKIPDSWVKISILTGFWK KNILITMDDEFGFNHTRGR
3826	17727	A	3849	373	2	SSGQKYKKG <sup>1</sup> GG <sup>1</sup> FP <sup>1</sup> PG <sup>1</sup> K <sup>1</sup> TP <sup>1</sup> PP <sup>1</sup> FP <sup>1</sup> FN APTKK <sup>1</sup> IF <sup>1</sup> FGAGREN <sup>1</sup> FF <sup>1</sup> L <sup>1</sup> AG <sup>1</sup> PP <sup>1</sup> PIIF FFFF <sup>1</sup> FF <sup>1</sup> FFFF <sup>1</sup> FFFF <sup>1</sup> FF <sup>1</sup> * <sup>1</sup> YNS <sup>1</sup> I* <sup>1</sup> DIKTHV <sup>1</sup> LLHS <sup>1</sup> VGF <sup>1</sup> RV <sup>1</sup> LVYK <sup>1</sup> RLYFT LYHS <sup>1</sup> FLK <sup>1</sup> NELG
3827	17728	A	3850	394	2	EACSVTQAGVONRNLSIQAPRRGSCPL RGSILSPQH* <sup>1</sup> EDRT* <sup>1</sup> HIGG <sup>1</sup> TOQTSMNE*



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
3828	17729	A	3851	3	164	MNLYLQWLCLPILYQLCSTSYT*EVIQLN LAPCVCLVGFPCFFVFLPFSTASQSPA* AGVONCHHSLOPQLPKL
3829	17730	A	3852	35	390	NHLNLGRGCSDLRLCHETLAWATEGDS ISKTKTVQ*RLQNNIPHEHTCKNL NPVSNSEFPFFFGNGAPRGPRGGGGQGN LG*GEPPPPPG*KQFSPLTPRGGNNNGG PPPRVN*GFLKNGVPPGGPGQPPDL GTGPPFPBGSPPPPGQFSKTKRTAPGQ PKGGPF
3830	17731	A	3853	6	437	PNK*KTPLGLPPPPFFYPFFPPPLSFL KPSFPPPPPPLPFLPFP
3831	17732	A	3854	1	236	PTKPLRLGRCEENLNPEGCGGPRSCY YTPAWAT*DSISKKKKGR.KSFTT SGGQGLPFLRGPKQSTGCAAP
3832	17733	A	3855	52	351	TGVIHE*QTTDVIYVVLHCTDPLLEDE PNKHQY*PKKKKKKKKKKKKKKKKKKK KKKKKKKRTTQKKKKKKKKKKGGGAPQ *LTLSPPPPLLYYFF
3833	17734	A	3856	72	420	NTYGGKKKKKKKKKKKKKKKKKKKK EAGGGGTTGL*KENSGNNGKPKIKKK GGKARGAPLGVSTQLL*RGGEKCLSP GGGGSEHKCTTPLAYPLGKKKCTQGGK EKK
3834	17735	A	3857	410	107	SSSSSPLARYPLGVAGPFLPFLTPRTGP RIFFLGP*KTSLPTPGR*T*SP*KGP PPFFFCRDVILW*PGWSENGJQSSC LCLQCNWRYKPPQLA
3835	17736	A	3858	419	239	TTRSQLLPLVENGPHHAGQAGLLTLTL R*SACLKPKMDYRRESLHLADA*GFYNG EDPL
3836	17737	A	3859	262	1	TANQENNGGPIKKTPRCQFGEVLIDPF KRPPPPFFFLFFFLFPF*RRVLPCCP GMS*TPPEK*STCLGLPK*WDYRHEPPN PAS
3837	17738	A	3860	357	133	NTTTPPGAGRNKNPLFPKKKPRGVPLF PPPRJAQTEWLYPGPK*PFFPPPPPG GKNTKKKPPQKKKKKSL
3838	17739	A	3861	253	375	TLSQPG*GGPFPFPRGGGLEAPFPFG LFFVPWGRGVSP
3839	17740	A	3862	3	482	YITDEVNDPSLTIKSIGHWY*TYEYTD YGLIFNSYLLPPLFLEGDVRL
3840	17741	A	3863	1	129	LANSNYRRTSRTITLSGGLTLLPLTA F*LLASLANAKRG
3841	17742	A	3864	289	372	NHLVRKAKDLNRHFS*EDIOIAHRHR
3842	17743	A	3865	266	31	KICRIFSPPQKRSVFPKRVFPQKRPP PALLFSAYFFPRSSSVTQGVVQ*CN LGSQPPPPPGKRFSCSLTGG
3843	17744	A	3866	1	395	NTSDFC*KPARYNESHEHMDWRRL*G KEDNLTLDISKLGQIFETSKAQLNLVS ETRAMKAVGSLTSLGPTVTKTIGNST INNVLCGLGASLVVRYIQQLRRDS DGRSOMMTWAVLSKRGG
3844	17745	A	3867	137	2	APLKKGECLRAVAPACNFSTLGGRRGE ITR*GV*QDQDQGETP
3845	17746	A	3868	1	108	ENRLNPGGRCEPESCYCTPAMATERD SMS*INNK
3846	17747	A	3869	198	302	LLNINHYGV*GCSSEL*SHHCTLAAA







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						LSPOKLNKAGKIFLRFVPLEKKGQTQLL *NRAGKIFLRFVPLEKKGQTQLL
3900		A	3923	263	74	LLSVNRIPCAQKKRKKRYCECPILVF VFDLSEENSSYIFKPILCVVCVVCV CVCVM*VGNPKRS**SSDSKTKTKKKH SHSYLFFLSFFCAQGILOTERSHELLPHL EVSIFKE
3901	17802	A	3924	3	129	TGPHHIGQAGLKLITL*SACILGLPKWWD YRHEPFPAPPCD
3902	17803	A	3925	281	10	NGLPLGADYIPASGGGSCNEMRSCHCTP AMVGAAPLRRK*KKKQNLKTSKEM GNPNMYILDKITK*PLYPKQLISLFLM GELGVK
3903	17804	A	3926	110	1	QLGAVAHACNPST*GGQGAHHRSGIQ DQPGKHGK
3904	17805	A	3927	180	358	EINFIITNYITLLEPNQGLALSPRL*SG GAILITHGTLLHLDSEPTSDS*VAGTS GTYHHA
3905	17806	A	3928	92	2	VRPGAVAHACNPSTLGGGEG*ITESGDR DH
3906	17807	A	3929	2	146	HLNLGGGSCNLELHCCTPAWATE*DA SKKKKSKFKITSAPTCQIVML
3907	17808	A	3930	221	3	KERATMGTELNMVSKIPPI*LRQRNL* PPNKKCYNNLLRP*LGPGTVAHACNPST LGSRRGRIITRSQDQDH
3908	17809	A	3931	1	102	GGRCSESSSINCTPA*VTRKDSISNNI NNKIVK
3909	17810	A	3932	351	69	GQGGGRFIQDPSSRGRFPFPPPPFIW G*RIQPPPPRANFFFLFF*KRGFPLGRE IEFFPPKQVPPWPPQNGFGQGGAPPP PPFFFEFFFT
3910	17811	A	3933	401	94	EGPFFLNPFLWEKNHAGPKVGG*KKPP PTKKKPLPS*KTIFPPGQPPFLPPPR GGKPKFLYPPIKFRPREPKGPPPPPRG TKKKTTPPKKKKKKKVS
3911	17812	A	3934	184	2	LKEPFFSRNRSVLSHSNF*HLFI*LIIT YFFEIESYSVTLAGVQMSDLSLQPRPP GLKQ
3912	17813	A	3935	2	393	KILIKVEIBGTYRKITNAICEKPTANIV PNRKKLKAPFLNRGTR*GCPVSPVLNII TLEVLARVIYSEK*IKGTIKQISIAITME NSKKFPQKTENKTTICSSNSTTGICISKR KEMHISKRHLHSFVYCN
3913	17814	A	3936	291	2	FFPPQQTNGPKSSSRHSPFGPGPGSTT GAR*PFRPLLLVRASLRPPIGLPTPTPG TGGMRPEA*RTPATDKQNSRRGP*GA WGRPGCRGGA
3914	17815	A	3937	382	1	QNLAQTVSWQNELLLFLCKHPPPSLLP PSSCRPHLATWTPAFPSHPSLTKAH FGSGPSSPLLITSFMPPEIQTATG* PASSLITPVCSQHGRFPKGVVRAGRS SHLESQHFGPEAGG
3915	17816	A	3938	398	2	FPPLLLNKIQAKKQAFPCSPGPRKIP CGQKTKKSVFPPFRV*DKSTFDCFLCPI VYVKQIWLAPLHCVSPGRVAGSGKSP LCLSLPFFFFFEMESHEVTAQGVQMRD SPQPPPPGPKPSSCLGLPSS
3916	17817	A	3939	240	385	KLLFLFLFIYFF*DGVSLCFQGSVAUVO

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3917	17818	A	3940	230	381	TLTTEPDAIPGAGGTPVSEI LISSSYRYLAKDLRFSSKQS*WLCSE FRGLGAV/HVCNPSTLGGQGRW
3918	17819	A	3941	1	107	CWPNVS*TPDLKOSTCLGLPKCWDYRQA QPHRNLL
3919	17820	A	3942	2	95	DLLTS*SACGLGPKCWDYRRKPPRFALF AFS
3920	17821	A	3943	163	404	CRHKAQWLPOI/PHLLISEKTLKYSPEK GLRSQH*KLLFLFCFG*TESRSVTOAGV QWRNLGSLQFLAAGSKRFSCLSL
3921	17822	A	3944	3	200	GLDLLTS*SAHLGLPKCWDYRREPFRLA YTFI*KKKKDGCCELLNLFNSCMDTAH VSPHLLGG
3922	17823	A	3945	423	2	LFFFFSEV*SHSVAQAGVQNYNLGSLHS S
3923	17824	A	3946	209	413	TTTIEQCNKTRRLGAVAYACNPSTLRG* GRWIT*RSQVDRPDQHGTTKNTNISTT KSKTKNTKISQA
3924	17825	A	3947	425	3	SFSQGLRDKTIFISLGQSTWGKGQWMAQR QOT*TSNPDGSEESRSPTTFEQQLSER SSSAKGQTNSSSGSLNSVSPDWETPPSR SQQTPTHTGELQLASGRCSGMINLPBGT DSNLCCSATHAS
3925	17826	A	3948	299	3	ASOTTFRGGCTLFFSFFISVCLFVCLFE MEFHSRCPGWMBCNGDRARLHLACTITT TIEIVKDDTNKWKIH*RLFNIKMSILP KVIDILFNAIPKI
3926	17827	A	3949	331	374	NAPKSERASKAF*ATLEENKEKLPLDIN FVVHPHGLFKCVAPPHCLGWDL SAVFA SHALGFPPQPNASAHVARSASAASCLGT AVTSAGSGVLGTPNKMPQKYRERARLFW R
3927	17828	A	3950	439	69	TNOKVWVPPREKGLFKKKOLRPRVGGPA FHSPPLEGGQS*FP*GQRPKRPPPPVVK PLESINPQINYPGGGAPPPPPSPGG*GG KFPPTPKAKVFFIQLSPPPAQAGGTQV PFPKKKKKKSH
3928	17829	A	3951	422	3	CFFALGIGPPEHPKRVG*KGGTPPGLFL FGKFLKEKNFGKNFGPGQGGPFPKKQ RGP*NNRPGVKVKKGAGDGPVVPKKPP RVPPPPGFFGNPPGAPKFFFSPPRGED QKRKNFFFFFRLWSPTNEAAGVQWR
3929	17830	A	3952	223	3	ALFPWGRGTLPRVRGINKGGGGGFFFF FFF*ETESHSAQAQLQNHDLG*LQPPP SRFKPFSCLRLGSSLS
3930	17831	A	3953	1	388	EKGVSPPGRTCSQRQCHCTPVWATERD SVSKKRGMSNNFSLILRSMNNKGGGTY PQKFLIYPCSTAKIGHSYINCKIFK* NLSLFHWTVQVNRILILQKLDQCHWD FVFLNLQCCGLGCK
3931	17832	A	3954	1	396	KLRFKDOTHTPQGSATUVFVPSVVF VKSISEILFFFLKKNFPLGPOLGRRGO ILVGNPCPGKKKFPADPPQRRGKKGG PPDPQFIFVFLKKTGV*XI/GPGV*TPA LGIAPPPFPKGG*RGDPP
3932	17833	A	3955	2	199	FGGGGCGEPKTRGCTPAWATERDSVSKI NK*KLKLKNNWLYAKSLASSPTGR*EE WGCFITIEH

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3933	17834	A	3956	393	2	KEFPLFPFGADPWPPLSGPSPVLEKFKCG GGVVPGINTPPGGGFFPQGLWAGDFFP* PLFSPQLPFFKKQKFFFLPREGGLWAF FPPFGGLPFSQNF*KTGF*GGFFFFFG DGVSLCYPGWSAVAHSA
3934	17835	A	3957	278	390	LVYIFKRLRTCPGVAHAQCNFTGLGG*G GRVTRSGDQ
3935	17836	A	3958	385	311	GPKNPPASASQGBETTEV*RHAWLIFFL FFVELMSSHVAQAGLKLPASSDQS*TL Y
3936	17837	A	3959	410	119	SPPPRYKTPPPEFIRGAPKKKFFSPFPR PLMLLLKKPPLFFFFFLKAPKPHLNFV FPPQKKQV*INLYFPPKKNES S*GK HFALHNCNPSCISK
3937	17838	A	3960	77	400	TALPLKPKKKKKKKKKKKRGGWKKKK FKAPGEEKKNFFKGAPEKKKFRGRV*KTG ERKKPGGNKKKFTGKKPPPPRGEKKKKP QA
3938	17839	A	3961	2	194	CL*SOLLGRLRMEDHLSNGN*GCSEP*S PHCTPANVIE*DPVSRKKKKYFVNQZL RGFLSPA
3939	17840	A	3962	52	409	NSKTSORKKRRVIRLSLRSGVD*TV NTRRGVFGWHLKQLPTTLVLKMKEL ETYFMTPLDLDPHITTSYFNGCQLQAKV GGTITDLIVF*IVSKNIAAGLSLNNVN AKFNLL
3940	17841	A	3963	382	96	LSSQLLEAGERNE*TGWLQQLQMLQH KNPCIEPRSYCTPAMATEQDPVSKNQ TNKQTKNSLEL
3941	17842	A	3965	3	169	DAWELSRHCPFAH*QSSETPSKKKKKG KKKIFRFLYLFNKRCKFLNGENGLVIP
3942	17843	A	3966	1	121	AGFHRVSSDGLDLTS*BARLGLPCND YKCEPHLAENS
3943	17844	A	3967	200	2	PPFRLYWGVELTFLPLRVKPKFFKQWF PFCLFFFFFMESRSVAQA*NQWRDLID SLHPPPPAFK
3944	17845	A	3968	471	440	MELRFYHVGQTLKILTS*APPVMAQS AGILGVSHSTW*EAPNSLATFLSHLS PROP*THLGC
3945	17846	A	3969	214	2	EGOPECOLQAGDWSLNLVCSGLEVRA WREAPRLWSFCLFFVSEM*SHSVI*DR VQWHNGSLQPLPP
3946	17847	A	3970	53	398	GDLFPKQQQKFLNFCFQLLLYARLFGP IFLV*HLATYNNKHLCEVGKVMINCOA DILNKMEISKVGAQKKKKKKKKKRG PLKKKK*IPRGGERNFFFLGAPKKKGTG GFK
3947	17848	A	3971	396	160	KREIRKEKEDNKKKKKKKAGKKKK KEKEIRDRESKESSNLLQBELSLCCP SGGIPRSSL*DPVYATGELIC
3948	17849	A	3972	416	3	FFPFRVPEGVGGGEGVFPFGFKSGGVF FPRPGGCAPI*KPPPPCGDPPNFF* KTGPPSPPGQAPAKRAPPFPFGGGGG KIFPTLKKGGLFPFGPPKGGVFPFGPKT LFFPKKKKKKKGRPPRSHASANDS
3949	17850	A	3973	232	381	YKTSLLIF*LFFRRDRVSFCHPDRSAV LS*FTVASISWAQGLLLQPLK
3950	17851	A	3974	396	141	CEFFPPPKRGFFPTIFGGPFGFFFPF

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						F*NPPPKIFFGAPKKKKIFFPPGGKNTFF FLKGGPFFPPPPPPPPPPPPPPPPPPPPPP RKLQISPHSQDNSKQKQSWRHHAATCLQ TILQGYSNQNS**APIARTILSKKNKAG GITLPVFKLYKATVTKTAWYWDQK
3951	17851	A	3975	286	422	GPHRVGQNGDFLLTS* SACLGLPKMDY RHEPPRPAP EGPRTCSFFDTEVHSVTQDGVRRNRNLS LLPFPFGIK*FFYLSLPSNMDYRLPPR PVN
3952	17853	A	3976	3	116	SFSPSPCFFSLVDLGVSLYCLGWSQTLD LKSSLSFSPFKCWDYRQ*ATTGLPVYF FFPVVTF
3953	17854	A	3977	223	399	KKNLINFQDQGRREKSSHCAPAWYTEK DCLKKKKKTSVCVCVCVCVCVCV*NHL SSLGLFPFVGLN
3954	17855	A	3978	227	422	TIYFGDGVSLCCPGMLKQSFCLSLPKC *DYRHVP RPRTSFHLTNIGVLQFLKIQ ATLSFTLL
3955	17856	A	3979	519	313	KLTPAV*DY*EKLLLSLASLTQAALP PEHFTYVISNPGSPANYIFTLSSGTFH QFYAKS*CVTYE*KKNLNSPPTGDKFN *GRSQTKIKQTKY*SELCPFVHLFETGS HIVAQAGLELLSSRDPTTSASQST
3956	17857	A	3980	217	414	SVLPTPLNLK*KSCKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKK GGACSEPRSCPCPTPAWATERDSV*KNK QPNKQKNKIDLL
3957	17858	A	3981	2	409	TNANKLNDLMDRPFLETONLLRNNNE TSYQMRPVTRREE*VIGNLLTEKKNGP PQGTGEFTYQTKELLP
3958	17859	A	3982	234	416	AFFFFFPGRKQDPSIVLGGKPGPS PPPVFKTRPNTFFLGPKKKYSPFPGP IQMW*KGPPPPPPPPPPPPFKLGIEV IS
3959	17860	A	3983	414	291	GRFPGSNFTSAGLQFQXXGXGPKPTIS RFGV*QRGEWKNPGVNNLFPALSTSPGR W
3960	17861	A	3984	192	415	EEAVRVSNLYTKLDESQ*VVKQLNVE RLKK*ELFLQDLYRKVPLKI*IP*VKNL NSFWPDAVAHACNPSTLGGRGGWIT
3961	17862	A	3985	403	145	HHHTWTFKFKCKDGVSLCCLSNARIPG LKRSSCFRLTKWDYRHBQLCPAFKHFF LY*HNTMSTERMQE*HNS*YPSPTVPK GVTFYYISYICFILLLSAITYKVFHTY IVSLNHVCSNEAPLSLNI
3962	17863	A	3986	255	425	ETDRRLKSGGSLSKTLTKMCTCFVFRD GVSLCCPGWIQTPLGLK*SSCISLPSND YRHMPPCPA
3963	17864	A	3987	247	2	TRPYNHATPYTLPFYTNLNLGKKKKKK KKKKKKKKGGPPLKKKILSPGGERNPF FYQPKKKSGRV*ZGSGKNPQAPQHK PLGNLPLPGGKKKKKPRFS*PPPPPP SPGKKRAPTKYVAGLIP
3964	17865	A	3988	1	394	KGGLFLLPRGKGGKGTWKNGLNLEKNK NPPA*PSKEGKKGGPHQAGKILKPGGK RGLNKGKGTGOKLPGGIPPPGP*KVGE KKEKPPAPGQGLFFKRRGQKNP
3965	17866	A	3989	208	402	
3966	17867	A	3990	2	408	
3967	17868	A	3991	81	406	



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3968	17869	A	3992	396	64	YSSPPPTKKIDDSDASRGPPFFPPPPER RGFTENDFFWVPPGFFPPDPGF*TPPPVF FFWAP*KKIFFPPDPRE*KFTFLKGPPPF FFFFFFFFFHHQLVLIIC
3969	17870	A	3993	367	193	KLWERKKILWKRQ*GETKSCHTPAWAT RVKLCLTKKKKKKKKGGEIGFKKRSF SFLGQKKKRGPAFF
3970	17871	A	3994	188	2	KRANTLPDFRTYYRAVLKTLVWRKDK HRSKQKQ*ESNEVELLYHNRNKLMD HRKQ
3971	17872	A	3995	2	147	QBNHNPGG*GCSSELR*HYIPAKATE* DSVSKNXY**TSHFSGDF
3972	17873	A	3996	23	329	RNSYIRSAFNSVINKVLFSTSEKKKK KKKKKKKKGGRGREYLRGAGGNNKYF YK*KKKKNTQG*KKKGWGRKREKKRL GGKKKFFPPEEGKKKPG
3973	17874	A	3997	164	392	KPLGRAGLWPCLCSSPTGFLM*KTEPCS VVQACVQRHGLCSLQSPMFKRFSLLS LPSSQDRIYRLLRHPNSNV
3974	17875	A	3998	396	3	FFFFFFFFPPGKMGISDSQPQLFFSGVKNFS PPPPPVNNGRLVWPPQKNFFFFFF*KKV FSFTWGGPPNPFFFSILLGGDDPPPIF SGEKIPPSLFFFFFFFEMESCSVAQAGV R*RHDGQLQPPPPWLIQF
3975	17876	A	3999	383	2	VPSPEKVGIKKIQPLDFFF*FLGDCQRK KKSPS*RPMPPEPGKKLN*IRLNGPPFN SKKEFF*KP*AFKPPFFPPKGEGI*GFF SRHSFNNQALPFFFFFFMESHSITQA SHQWHLRLSLQPPPL
3976	17877	A	4000	213	1	RGONKTLPLTKENOTKFNQTKFNQTKP TTFL*SVIRIRVKKKKYTKRKTGNPTT SLTRSLGRYKSPTRP
3977	17878	A	4001	412	129	GLSSPRLCESGTTFAHCSLNLFGSSSP CTSAPRVAGDE*MGQACMPCLPVPNFFF WGGGGILVETRSK*VAQADLELLSFSDP PASASKVLEL
3978	17879	A	4002	411	293	RDTRCLFP*LDNFVFLVENGPHRVQAG LELLTSSEIA
3979	17880	A	4003	46	392	QDFFFFFFFLKGAGPPPPKRGOTPPFK KTKKGPPGPPLEPPPLGPOPEPPG GDLKKDPWPGQTPL*KPKMGGGGGGP P*TPGTGGGGKINPLTPGGGKNGPPPP DPG
3980	17881	A	4004	360	1	KCLGPOFFFFFWNICILFISQLSASQV QKSEIQNAPMSIFFRRHVSFKQFOILEH FGNIFILGMLSTYKTLILLKLN*RNA MDILIPVITFMIDKLILKFTWKYKPR RVKAILRH
3981	17882	A	4005	152	408	NKPVSHPTWGNLRSPTQTT*QSFCH VRLDSVF*YLYTRKILIFPAKAPFLD AKYVCVCVCVCVCVCVYFGIGGNLPS S
3982	17883	A	4006	411	67	YLPPSSPTPGVFFPPPPKKEFFPDPF ILGTPRFFPDPF*KDPPKFFLGPKKK K*FSPPRGKIFFKRAPFFFFFFFFFFF FFFLLOCSLFMYHIIKTKY
3983	17884	A	4007	217	2	PLFFFFKILKAYSVDIHISPAIRLYLL F*DRVSLCHSGNSAVARSWLPAGQNTF

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3984	17885	A	4008	235	406	ITTKQEAIVYLLAIPRV GRHRVSNPISIRRRGLSLLPLECSG VSLAHCSPDLPQSDPSASARLLGLRLR Q
3985	17886	A	4009	833	237	SLUNNARPCLVSPFIPIKGRSIAERQAD GTTSPDPFRLSRRGHPIIPS*RGWERKS QLCSHLQSSRDPSGLGRAGCQGGDLAE SPGTTFGNGGSDLPVPTAPIPIEPQIC QATCAVMKLSFDEETRAANLGECPRS SGKPSSPRTGGSSAAKGTQAGSSELG LGIGARRGTDLSHSSSTSEHWITVLGL SP
3986	17887	A	4010	276	2	VEVKGNNSFSQSITLIPNPKQPKET DQPLMSTYAKIESPGKPSHDG*LIPOK GAKIIQ*VKNSIFNKWCNWDQFVKIM NDPFTLI
3987	17888	A	4011	188	27	REKFOIYTIQNDKGIITDITTER*KLIR DYIEHLYAKLENLEEMKLGIGIP
3988	17889	A	4012	1	202	CLHQKVIISN*LA*ATTQTQLSLSFKLD YFSIIILPVALVVTWAIKFSL*YINSP PKKKEAKDLN
3989	17890	A	4013	1	403	CLDQKVIISN*LA*ATTQTQLSLSFKLD YFSIIILPVALVVTWAIKFSL*YINSP PKKKKKKKKKKKKRGAPLKNRRGGP NFWGGGNLIFFFPGGDKKPPRAFWKKP LFLGGGNLGGPPPPQKFTPWGKK
3990	17891	A	4014	67	439	TELTIFYIPFETTLPLGAIITR*GNQ ERLNAGTYFLPYTLVGLSLLPLIALIYTH NTLQSLNILLITLTAQELSN*ANVLI* LAYTLIAPRKKTCKKKKGGLLKDPWGGQ ILAGREKIKFPF
3991	17892	A	4015	3	260	LIVPTIILLPLT*LSKHHI*ITNTTTS LIISIIPLLFNQINNLFSCSVTFSSD HLSDPILKKKKKKKKKKKKKKKGGGA F
3992	17893	A	4016	258	3	LKKIFSPPTINLFFPPFLKFFFLSL *PFLGVSPFFPPPKIGFFPKIPGVFF SPDPKKKKFFPPPPFFYAPRVEFKGP P
3993	17894	A	4017	287	2	EKQKRNIFFFPNLSFPGRGAFFPPLFP ILRGKGDDFFYPRGLKALGNQ*NPFSR F*IPFFFFFLRRSLAPVTQARVQWHD P GSLQPSPSGFK
3994	17895	A	4018	228	487	SYDVQKQKNGI*ASKTWAYVFSSFLS FFFFPFKKKNFFPCQGGQGNLSLRE PSPPGVKKLGLNLSKSW*QNCPPPI IF
3995	17896	A	4019	35	228	EELNHLNQCGBGCSQRSHHCTPARATE *SSQKKNKFWYIHPCNIVITNTMT ESPKHYAE
3996	17897	A	4020	2	402	ARGNLATTFPDPAGGDDLLYQLFL*FF GHPEVYLLLPGGGLISHIGTYCGCKE PPGYIGMG*AMISIGPLGIV*AHIFT VGIDVDITRAYPTSATIIIAITGV*VFS *LATLHGSNMK*SAANL*ALG
3997	17898	A	4021	1	420	TRGATRLIILLIVETTLIPTLAITTR* GGQP*RLNAGTYFLPYTLVGLSLLML IYTHKTLG*VNILLITLTAQEL*NS*AN NLI*LAYTLIAPTKIPFYGLQL*LPKJH

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
3998	17899	A	4022	409	3	VEAPLAGSGLAAGLKLKSGYGLIRLTL LEWASCLATIGNNNPPFQIVTCDKRWI LYENW*LPAQWLH*ERASKHSRPNLHE KKIMVPVW*SAQGLIHYSFLNPGCTTIS E*YAOQINVMH*KLQGLQTLFINRKGPI FLNNNTKLHVAQPMQLKLNELA
3999	17900	A	4023	464	374	HLPPWEDKARRHLPARTFLAFLASRN VRNKPFSLQATQPLVLYASSTKITKPLK TNQKRLKKSQSLNNWTPPIKRNICICI VGLIEGKEGKGAERIPEEIVPQTP*NL VKDK*KVQ
4000	17901	A	4024	58	323	RAKLLCBIVKKSAAVLTREMQIKTLK YHFLLVIAKIFNLHP*RSVGYTLQ WAGRNAKS*PWRIRSOYLTKLYVCVCM YTHS
4001	17902	A	4025	480	150	BNSLLRRRLRQDMSPGQCGCSKL*LHH CTPAWVTEQDPVSKKKKKKAYDPDIPK KTDKSNKGKQDPDSRQKPEKNSPPFPNQ RSTAPRGRAKSCPTH
4002	17903	A	4026	204	1	KKKPGALPPFFMGLTLPLRLRYR*WCD HGSL*P*PPGSSDPPTSUSQIAGTMGVH HEFT*RSQVVLK
4003	17904	A	4027	116	472	MPPLPKPVSGPRPHSCSPLGGPQLSTPL TGPRPASLSLPSREGICGICITAILWAVW YLVQLMGLSLPMA*RGAGSSCSRHKKW WLGLASPSG*TFPKNRTKGRARMLTPVI PALWEAB
4004	17905	A	4028	355	444	VSYKKK*SRGAVAHACNPSTLGG*GGR II
4005	17906	A	4029	410	181	ASILLLVAFVSNILSGQ*TLNNTINQY SSLIIIMAILKGLIAPHF*VPEVTGQ TPLTSLGLLLT*QKLAPCF
4006	17907	A	4030	49	474	PXRXKPCHTVITYSGRKEPPGYIGW*G MISIGPLGFIV*AHIFTVGIDVDTRAY FTSATIIIAITGVKVF*S*LATLHGSNM K*SAAVL*ALGFIPLFTVGLTGIVLXN SSLDIVLHDTTYVXAHFYVLISGAVFA II
4007	17908	A	4031	274	427	PPF*EMESHVTOAGLLGRNHSLLVPOT PGLKRSSLLSLNSQYRSQFHT
4008	17909	A	4032	205	393	TWGGPKNPSPGG*IKKHDPNEMPLQN CWKILFFOGGFFTGISPRAPPINGNII LWVGKK
4009	17910	A	4033	2	386	SEPLSRKRLYLISLISLQISLIITFTAT ELIIFYIFFETTLIPTLAITR*GNQPE RTNAGTYFLFTLVLSLPLTALITYTHN TLGSLNILLITLTAQELKKKKKKKKKK KNIQGPPLRAPSGAPN
4010	17911	A	4034	3	169	GLFAMHSGPDASTASLSIAHTTRDVNY G*IRLVHAKGASTFPICLFLHGRSL
4011	17912	A	4035	3	317	HASADAWAFIGVLP*GCTISF*GATVIT NLLSAIPYIGTDLVO*I*GGYSVDSPTL TRFTPH*ILPFI*LAALALHLLFLHET GSNNPLGITSQKKKKGGPF
4012	17913	A	4036	446	194	KKKQPGGPPPPPAFVVGILKKRPPT PGKKPKFR*KFFPPKGGFVRDPPPKG CWREKKKKPLNNDKWLVEGSEAGLF
4013	17914	A	4037	213	1	GKAKVKARFPKRGKRGVRLNPPWGGKF

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						PNSGTEKTPFFFF*DRVLLCQPGMSAVAQS*LTATSTFWQAQAI
4014	17915	A	4038	307	36	RRGFFFSRCGEFKRLPGPPLGGWYLRLLFCQXKKFFHDKPFGPG*IFLPPPKIFFIFSFEMEFSCCOWSANGRPRLTATSACWAQANS
4015	17916	A	4039	2	372	NDTSLTVKSIQHONE*TYEYTDYRGLVFNCYILPPLFLBEGDLRLDLDNRVILPIEAPIRIINTQSDVLHS*AVPTLC*KTDAIIGRLNQTTTFTOTRPEVYQCSSEICGAHRRSMLIVLELL
4016	17917	A	4040	107	279	LILLFFFWKSLALAPRWECRGKI*GHCKLRLSPSCSPA*ASPEAGTTGWTYGC F
4017	17918	A	4041	3	351	GSHYTAQAGHKNDSGSHLPSASANSAGYTGVSCHANLKIFFKESVSDYS PHLNSRKNNAVYVSFFPPWKKS FVFPVQAGGKLNLLGSLKFSPLRLKQSGCLTLPSS*EYGLAPPPP
4018	17919	A	4042	1	385	RPRRPDL*QERRTOEVLQAVAKVKKEESQLPTGGPKNVLPVPRAKAERPKQA EASGLKKEITDVLKVDQAERKTEPTQGGKGGQTTPESEKAPQVTEI*SSSLVTTQAEITLAGVKQEMV
4019	17920	A	4043	3	282	TAILIOTF*SPGTAVILLIHAHLTSSLLFCLANSNYERTHSRIILSQGLQTLPLL IAF**LLASLANLALPTINLLGSELVLTTFSSVDA
4020	17921	A	4044	2	407	GRLEINSRSGIFPPTLELFDKNEPPEPYREALPTLKLSDSLYGLIEPEERVSG*ESLEESCFATPTTSKIDEVLKYLYLRDG*VSDSDVKQYTSRDHLAKHPQVDEKFEKGDKHKEVILH*RDLCVGVMDERGR
4021	17922	A	4045	4	380	ENMLTIIRQAMHEADRNNTTFFDPAGGDDPILYQHLF*FLGHPEGYILLILGPGFISHIVTYYSKGKPPFYIGMG*AMISIGFLGFIV*AHHIFTVGIDVDTRAYFTSAT IILAIPTGVKVS*LATLHGSNMK*SAT IILAIPTGVKVS
4022	17923	A	4046	2	94	ADRNLTATFFYPNMGDDPILYQHLF*FFGHPEGYILLIPGPGIISHIATYYSKGKPPFYIGMV*AMISIGFLGLIV*AHHIFTVGIDVDTRAYFTSATINAIPTGVKVS*LATLHGSNMK*STPTTILIFRPP
4023	17924	A	4047	376	138	LLARQREQNGVNPGGACGEPSSRHCTPAAWAT*DSVFLWREALLTQTAPNRLQLLALSSFFHRIILVDPHSG
4024	17925	A	4048	145	226	EPIQACSSRRVCV*EPIQACSSRRVCVCTPSRHALPGVCV*EPIQACSSRRVCVRAHPQMLFPACV*EPIQACSSRRVCVRAHPQMLFPACV*AHQMLFPACV/CVCDPIQACSSRLVCV*ERAHPRILF*ACVVCESPSRHALPGVCVRAHPQMLFPVCVCSPSRHALPGVCVPSRHALPGVCVC
4025	17926	A	4049	2	414	ADRNLTATFFDPA*GVDDPILYQHL*FFGHPEVYILLIPGLGIISHIVTYYSKGKPPFYIGMV*AMISIGFLRVIV*AHHIFT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
						VGLDVTIRAYFTSATITIIATPTGVKVF <sup>S</sup> *LATLHGSGNMK*SAAVL*TLGPIFL
4026		A	4050	472	228	LTRDGGACFFSKLPRVRQKPNLVIGE <sup>*</sup> SCSEPKLCPCCPAKKTQDVPVSKKKKFF IWIINRTKIPRKRKQNKAYHKVKYF
4027	17928	A	4051	238	3	RRHGSFAPLPFGLPLCTSYIWLPTITLC NIIYLYFETGSRVYVQVGLKLLCSSEPP PGTS*STEITGMSHGRPHINP
4028	17929	A	4052	225	172	LARYPFHIGQCTNMPSNKSITSKESDN GPGAVAHACNPSTLGGQGGITKSGVRD HFG*HGLV
4029	17930	A	4053	471	30	GFQGIKISGALFPLNKVAVPVVFFRPP LIPQKAVPQKNGPKGFRIETRRR VPPPPGVFVKSGLPLSPVPPV*STA VKTGEPYRPGQVPPRGLVPPKKCKSVLN RPDLMSGPQPS*SLPLPGPSPVSHAGCL PQANRG
4030	17931	A	4054	425	41	NWGSGLTLCFQKLGVPFPPPPGEGVPGA PPPARLLVFFFF*KGFSFVGRGQFKFLP PKNPPPLFPQKVGIPKGGPRAGPIFSPP QLFFFFLFTWLTFSFRLBCSGALLAHT PAWETQDSSISKQTKK
4031	17932	A	4055	312	1	IRNARAHLLPGSGFPPPLPIPIWIIETIS LLIQPIALTVRGAANTAGHLLMHLGS AALAISTIIIP*TRIMPTIIERTILSI AVALIQAVVTLTVSVSLWLA
4032	17933	A	4056	648	123	DFDPVFSARGCVFSGAPGRGAQLKKAND GALA*LPPCLCAQELPSPSLGTQKPAVG LSVNSBRGRLGRVSNIAETVAAPLKG TOSRRGINKNPLPQREPSRYCLGLGGE SSAQGTSGLTQQRV*QNSDLPFLASGDD KQGRSSQGGAVSQSSPRGRQIPPSPPPA ALENFL
4033	17934	A	4057	135	464	QHNSRLNQQAQKGVTVLAKVITLDLYEDE ISILLHNGKEE*AMNTGEPLGCLLVLP CPVINVGKLRHNPGRITINGPDTSGMK VWVTPAGTKPQPAEVLAAQKKNKCG
4034	17935	A	4058	3	575	LRSRFLHIIYLSGCLLVTPRSLSPFPPFQ RLRLCRPSRGAIEFFFSRLTKLHATLP LRIEBSKTL*NCC*LYEGC*IS*IHGG LFDVAANKIIEEVEKYDKQVRGKELLG FATYKTFEITVHQYIQ*LVEPALSMQK AMETIQQAFINVANKHFGFENLNQTVQ STIEDIKVKHTAQAEYMIQLQVR
4035	17936	A	4059	389	3	TPRGPKVFRYPTFLPCPPPPRGVFSKNIX TPPPPPFGVPPPERKIEFFFLGALPLP SRVTPFGLKRGFFLSLTPPPFPFPPF WPPPPFFFPFPPFLKRSFALNTQAGVQ WEDLG*LOPLPGPKR
4036	17937	A	4060	397	1	KRKNNFFFGKGLSLEI*TPRGPFLWFF F*KAPKGFCAKFPFYPPLPKENGKTH RQKTFPHFQCLPKNGFNVLHAPSLGDF PARVMGPPFKRFFKIGIFKEFPFPGSPPP KGPKKKRTAARDLELADAN
4037	17938	A	4061	38	410	AWIST*ERPFITLVVRPNFLAISGLLES YFRINFLVQIIHITFFRKLFLVLSYVPR FTDVKFFFYILPFPFPHLEGMICSYAA L*FFITVFCFLPFFNGVTS*IGLEILLI

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFKKPTFGFGG
4038	17939	A	4062	405	81	GGANVFPQKSPFPGNKKGGHFFSYKILN NDGHPPFLKKKKNAPGGGNPWSPKWK GAL*PKKKNPPKKKKKSPFPKGGKKNCP FPPKKKKKKKKA*GDNFDMGTGN
4039	17940	A	4063	415	239	RPSFFFFPPPKGSCSTTTTTLSPGFFF PPPPFTTPPTFTTFFPPKKKKYFFPPPG KKFFFF*PPPSLFTTTTTFFFTFTTFF TTTTTTTTTTTT*GLTSPHKQLGLVLA FLALASKITTHASLPVPSPPSKKKKKKK KKKKKKKKKK
4040	17941	A	4064	95	241	SPCRSPHEWVNS*ANSLI*LAYTATFTV KTPLYGLHL*LPKAVVEAPTAGSTVLA VLLKLGSGYIIRLLIILNPLTKHIAYFP LVLSL
4041	17942	A	4065	28	288	YFDI*VEARSPYVFGLELLIGSSNPFA SASQSVGITGGSHCAQ*VTILETTCTL HVNG*I*CIKKLHNTFILVISLQYIFG FFL
4042	17943	A	4066	338	134	FGGGCEPSRSHYSSCTPAWQ*SETPSK KNKKKKKITYSVKNWGIRVFIELILNSF TTVRP
4043	17944	A	4067	26	365	WVSLMTSALAMRVDFYITLLHGLLAS TLTIYQ*WRDVTRESTYQGHHTPPVQKG LRYGILILITSNDCHFAGF*AFYHSSL APTQLQGHMPPPTGITPLNPLEVLLNT S
4044	17945	A	4068	491	174	TQLKTH*GSTTDNRTEVRVEPRVRINYK DLLKFL*SKGYDPSSEFTTETIAKLKVKY MYDNRESQDTSPTTLNERVIQQLVLSHI FKDNYANINAELKLSN
4045	17946	A	4069	210	402	NVSKGLRKPSTQ*VINISCRPGVVALA CGPSTLGG*GG*ITRSVRDQPGQNGET PSLGPGRV
4046	17947	A	4070	202	1	DSATALQPRQ*EQNSVSKKTYRTIDLR SEYFARNSFTLAARAGVQRNLGSLQPP PPGFKRFSHAS
4047	17948	A	4071	412	143	FLGAGV*FRLGPKG*TFPLLQKQLIGH GGGALYSQYFGNGGRNRSFNPGKGFTN QNPPPSLQTWGKGVSPSKKKKKKRRKT KMGGE
4048	17949	A	4072	2	324	RRIKFCWF*SDRVSSCCPSMS*SPGLKR SSCLSLPKCWDYRFEPFLYLARVIMRCY STHNTYIMYQMQRLFCQHRYLSVSTSS ATRPLYLNNFFFCNKNVMPCCG
4049	17950	A	4073	2	326	RGRRLPRTGPRGNDAGQPGKISLVD* LITLYLFTLWTSKSHVAGGQNRNNGS LCP*PFLKSSSRQSGARVKKGVKCARL LLDPLSVGKPYTYKKVDRVVSFEA
4050	17951	A	4074	422	116	EIKOKKNPGVFFFFPPAKRGFTPTPLI WGPPGPPSPFLKRRQGFPLGL*KN DPVFPKPKVFFWAGPPFFFSFKKKFFF LVPQSTFTHFTFH CYIL
4051	17952	A	4075	3	294	VFCHVGQGLELIDSSNTPSTVQSGAGI TDTSLHT*PDLSCCKTKFD
4052	17953	A	4076	60	389	PSAQLGSKTHRWAVOP*PPSPPELLHL PKMLCPHSNHTPPFPNPGTVCTYSPR SSPAFFQKGPSSGEGGLVLSFFSSPPN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
4053	17954	A	4077	93	385	HVHDAPTS PESGGRGRGRVPRHGAYV KFLFAPGVLFPGGPGPKREKGGGAQGGP KKFSPPPPFFSFPFKTLWVAPLQSTQ GLRLCPFFFT*RGKGALF*KNGGRFKP PPPPKGLLGPPTP
4054	17955	A	4078	2	363	RVVGRVS*DEDLRLTLLRYMYMLNISA AKDLLYRRTKALIDYNSNKALDKARFK SKDLKSDCAHPRDC*RA*APYPLFAKNE LVVPTGBQRHFLQDVPLIVQRTILRLTP DRTSLPLSL
4055	17956	A	4079	6	298	PLKIMGFFTLAETNRTPFDLAEGBSEL VSGNIRYAGGFALFFIAYTYNIIILIN TLTTFITLQTTDYAPRP*LSPLFYIE DPSYPTPWSTST
4056	17957	A	4080	414	154	FIPATRSRGKAGSLNPSGRGCKNKRGRH CTPAWQKGTTPGQKKNKLLALKV*SI FHLMB* KYLKPFGSLDKLLTVITYFDL FRC
4057	17958	A	4081	347	1	VLKPRFGNIIFSPKIKKCNLPPPGNYF FFFPDPPFLFFFFFFFFFFF FFFFFFF*RGGLLLFLKILQPLTPHP YLSNLTLRGNVPGEGSCWSESGRGEDCL QDH
4058	17959	A	4082	1	354	STFIISLPTTIFMCLDQVEIISN*H*A TTQTTLQLSLSFKLDYFSIIKKKKKKKK KKKKKKKRGGGGLKGGKFGGGGKKF FWGGKKNMGGGVKKPGGCKRGGKKK KGGGK
4059	17960	A	4083	384	85	FFFPKVPFGCPRFPSFPGFLTPPPQLV LETPIKGLSPDPPLGNFFFTTPPFF FFFPFFFFFFFPPPPPPPPPPPP FFFLPM*AKKPLSNR
4060	17961	A	4084	1	122	PHRFGRGLDLLTS*SAHGLPKNDYR REPPRDAFLPOP
4061	17962	A	4085	223	401	NGKLVSVPFGFCFCFEM*SRGVAAQARV QWRISSLNFLPGFERISCLSLLSRD YRC
4062	17963	A	4086	160	408	ALFPRRGGGGAFSPNCLFPFG*GKG GYGDAPS CRSGLGQHGETAAPLKAQKSF GHGGRGYQVRRRVGPPGGGRQKLNEG APPPPHLGKAAAP
4063	17964	A	4087	261	81	YDIDRIFCQKLESSHYSPGAVAHACNP SPLGG*GGQITRSGVQAHPSPNPPEVNG LQA
4064	17965	A	4088	428	140	QPLKNPPLGGRAPPFLRGKKLPPPPQG EPPFP*KKKKKRGGGGPPPPPPPRGE PKLSL*PQGGGKKKKKPPPPQKKKK NPPKKKKKK
4065	17966	A	4089	1	205	FLRQENCLNPGGGCCSELGHYCTPAN VTQETLSQKKNFW*KTFRKAKSTGNF HMENTSIQLEPI
4066	17967	A	4090	154	410	ITGCSITKYVYAMKRRKESGVGYPPSS SINTPLRHRLSDGLDSRTISLSTHSPA PFIKSKNRPGTVAHACNPSTLAG*GGR TK
4067	17968	A	4091	428	67	LPHPPPPPPPLSSSSSSSSSSSSSSPP PPILLPGQRTILTRPLAPAGQLGSRGS CGAPPSSLGASLHVA*NLGRQ*RAALS

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						TPHGLTGPSAAMRRERQDLLLLCS
4068	17969	A	4092	431	3	APTSNKGSTIFTLQIRKLRAFPSSIGP SPSTLPVKLEL*SVLLPQQWLN*SPCHP FPRPKCSNRPRYTLFVVKLPSSGLPPRP SPSQQVIAFPPLTSRKEPSSPTPASDA FPFPPAPVSARRQEVLCESIPSVTMBE
4069	17970	A	4093	151	1	SIMPWMDAAVAHCNPTILGG*GGNLIK SGVRDPDQHGSETSSPPKTKQL
4070	17971	A	4094	35	363	LQSKIYCTFFFFLGRGFFFSFVRGPGA HPGLGAKTIGVGNPP*P*PKGGDPQGV PPFPQCFWFFFLKGQFFLLPGG* NFG KKKXPLVWP*PKGGLKGSTPGPPPY
4071	17972	A	4095	376	1	LKSPFPFLGAPFFKRGSLQFLKQFP TDP*LGSPPLKSLPGLQGNPNQKWK KRG*PKQGGENPP*FFFFFTRDQASLC CPWNPQT*PGLKQSSNLSLPSSWDYRCLS KSLPKENTETLAS
4072	17973	A	4096	65	446	FFFLFPLNKGLPFT*KRQKQKPNFF* PCPRKGINPPPP*GGEKRGPPPPGK FFFFFPGERGFPQGVFLDLGT*PLGFL KGGEKGRPPPGPGPKKPL*KRKANSPP TGGERGRGGKKHCLP
4073	17974	A	4097	34	387	IREADEYVLTIRACVFGDNEPLSSPHR LHTRIGSSPSTTCCTPACPCSSN*HGAS VIPSQTAYEDWFTLKNVLTSLVLLM GLLDQVGASHQGHFWTDNALEKSKAN VSMHSSGVYFFLIPYYNSVVRHQSNL CFLPCNKERGF
4074	17975	A	4098	80	422	IGHVLTICLLCFVLS*LLMFVQNYI LRVYFTCLILCLRVLTICLYMCHIR* FTCLIALFAGLS*DSPYHESL*SEFHEA DISLCRCVITDQINFICSLIQH*ELRMA QF
4075	17976	A	4099	74	402	IYLLSTHLHYQFSWLSITFDLSFFFFF LKKEISLFPQRRGGGGLGLLKPDPG SPFPDPPIFRGGGKQPPPPPWVIFFPF* KKGGSPIYPGG*IFGDPDPFPF
4076	17977	A	4100	3	335	DWASAWTYEYSVSRRKKKKRGGGKK KQFPKIKGPRGSLFKRGGKPLSLKT* PPPPF*F*KPFPKKGASPEWFFLKPPF CLKDRGGAPKIYFPNPPGAPRGAAFIK RGGK*GPGGGLL
4077	17978	A	4101	406	1	RPFKPPPKPKMSKALFK*KGFPFPR LLIGPPPPPKKKKFFTLFAKVLPPR FF*NFNQVSKRPFTPLKVGQ*PPMVL QKRPTRGFPALPKKKGSSLVRLIKRK FTWRHILTPTRWAVHSGNRC
4078	17979	A	4102	2	183	VMPGSGKSEPI*CLCT*AWVTEIDSVS KQDADNDKQALRSFPLGFPFPLFLHPT SEAF
4079	17980	A	4103	119	391	DNLQCFPPFFFKRGLPLPRGGGKSTG PFS*GVGTPPPPPGKGLTPKPPPPG *ILFLEKGDPLLARV*NRQKKKNPP SPPPKGG
4080	17981	A	4104	413	64	GFKPPPPKDPDPDPKGGFMGRPPPR PFAPLSPPPPPGGGGLF*GGGGAKK PHIWPFG*KKPPPGG*NSGGQINPPG GGKNPPKKKKKKQPTANIWFCLLI



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4081	17982	A	4105	2	196	LGSM RGRVGRVLIISLPTDILLNLCTIICPHK TQ*LCNG*CHSRMKVCVCVCARVCVCV CVCERRRD
4082	17983	A	4106	1	335	FLVET*PHPVGLAGLELLTLQDPPR*ST LGDPKCWDYRCRPLDPASVSFFLCLKL IFVLKLFKFFFKPPPLYSKLTRGRDNNYN YFP*PNPGFIPHNRAKSTITGNRRLI
4083	17984	A	4107	1	148	GENGSEIRSCHCTATNAE*DSYKKK KKKEPKKFFLAGFSGGKICFP
4084	17985	A	4108	331	41	GLNFLAQKFGSRFSPPPGRRVPLGPKFF FPLGKPPILLEGFPGP*KVFTSPILPPKE VLTFFSPGEGKLGPPFSGGACSGFFPKG AKKKKKKPPSN
4085	17986	A	4109	137	3	TKKERNTNKPQGAVAHTCNPTLGG*SG RITRSGRDRHPQHQH
4086	17987	A	4110	3	269	GPHRVSQDGLYLLITS*SACLRLEKQWDY RHEPFPHGGLGFCEFFFFRDSVQPGQG SENPSHKKKKDRGPFWKAGAGKIFLFXPN SSAL
4087	17988	A	4111	196	330	GAIAQRGRNCDCT*GSVGHVL*NDPTLN CILQDQDTLYSGIMINBYERASDAMALL PDEQLPEBGDQIVIA**A*DMSGGQHR VSLARAVYSGADVLLDDP
4088	17989	A	4112	426	241	LLKRVRHSTLFTIRGKGFSEPRSPFCTP ANATERISVSHKEKKRVLVRP*VDLSN SSLVL
4089	17990	A	4113	394	1	GPVFPSPGCLYHARQYFWPHKKKKYF PHPGQKNSVFLKGRPLFGFGFLIFFFF LVEMGCCIAQAGLELPTSNPLTSAQ RAEIKDVSHRSQ*FFVFLFETGSCSVTQ A*VQCNHSPSTGKCF
4090	17991	A	4114	328	2	KQAMFTMPDZGIEVSPSPNIRFLGA PESTFFKRNLPQGDLEKPNPYCTFFQG VTTTPFFLFPFPPKLIFFFF*DGVSILCR PGMSAVARSQ/DATTHLPGSSDSP
4091	17992	A	4115	220	3	FKKGFGDGFPPVWGLGAVVWVGVGFFP ERHSTLMTVQVQVQCNFSSSLPPPRGL KSFSLSLFSS*NYRH
4092	17993	A	4116	342	2	PINFLYLSFNPQV*RSNFSKILHFCF KILSFFYTLAFPLFSSQLIRQSFRFVYL INTICPLQDLYLYLINLQILYLIFFHL ASRLDFCLFFVFIVLCLIPGNSTVAQ S
4093	17994	A	4117	124	352	TSGPT*TRNKSKIPT*RSFYIDLEAKM KEKFLKAARSTQLITYRGTIQMPVDPS WRKTEAQAQWNLMEVLKKNCTRSLSH PATMSFRNKGKTFMFSDEKLRDSVTLP LKD
4094	17995	A	4118	11	387	KNGKILATSPKNGIMVWVSTECVVSF FLVSXKKKKRNLQKLPKPKPCWVFK RAPTPNH*KAVGPCKTPP*KOPKKQIP CRPPKGPFCI*PNNGINPSPFFFEKIN KGAAPPKNSKK
4095	17996	A	4119	2	407	NTFQDQSGSSSSNREPLRCRDARDREL AIGGVLEABQIKNNREYKVAQITSCIS RHLECLSRSEWNLVEQVDLIYQLKESTL QQQAQQLYSLGQGN*LIHOLECTQNKD

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4096	17997	A	4120	157	2	LANTQSVCLERLGLS/TLKPEFST LTGSHSVT*AGVQWCKIGSLPLPLGSK RSSSLNFLVSWDHRGPPHSANF
4097	17998	A	4121	3	168	LALKSGRRKVDIRELGHVVCPCWMS*TFEL NQSTCLGLPRCWYRRPEFWLALNNP
4098	17999	A	4122	2	376	ETGPHCVSQDGLCLLTS*STRLGLPKCW DYGNREPPRPADGFINIRDFNPLLESTST CCCHVKKNTFASPPFTILVSLRPPQPCR TDPIQNTLPLVMSPVALLGCDSPFAFP VLMNPLPSSDCTK
4099	18000	A	4123	11	221	GTQLLRLRGEDLLNLGRGCTEPLRH CAPFWETEPPDV*ERQAAKANNLLLA ALLKTVKKEDEAVM
4100	18001	A	4124	2	125	ALTKKTSNRW*GCR*RGMLVHCPRKC KLVOPL*GAARL
4101	18002	A	4125	425	152	TPVTLALWAKAGRSLEPRS*RSANATW QNPISTKYKK*GGRITSWGG*GNGL *WCRSPASATETPSQKXKK*EKNLPT LILKVIK
4102	18003	A	4126	3	99	CGAGLEMLTL*SDSLRLPKCNDYRCEP RFA
4103	18004	A	4127	396	58	ENCNPLSWSGITISQLLWVGYSNKFPS FLWCLLPVIGPPTAGPSLWPGTQWHD HSTL*TSQTGPGSLVPGTKWHDHSL* T SQTGPKLSSRLSPSSMDYRHKPTTPEA H
4104	18005	A	4128	51	349	LQSYLLALLRLKCFSPNQVGDLDISYIN IBGITATTSPESRGCTLWPGSSKHLEPT ETSPSVYPLSERVETAPP*AHQSPNSP PSWGGSPNLNLPFGGGGFEKEQSPKRRS FTLYPLGPPSEBSHF*PSLCPFPFGQ SPPTGIPSGDELGF*TTGPDKK
4105	18006	A	4129	97	362	RR*SACLSLPLKNDTRHEPPEKXSC
4106	18007	A	4130	376	279	DQDDLDTLS*STHLGSKNDYRHEPP HRAS
4107	18008	A	4131	133	344	ITYFFFF*NPVLQKGGQGNLGLSKLPPFP GLKQFLGITFGRSMDHGPTSPFRANFCI FRKKRVLLCCPGWS
4108	18009	A	4132	164	3	MNEVSYESSLDDHLLKQ*NQCLASSE PSPPRLEQFSLSLSPSSWNYRSTK
4109	18010	A	4133	355	2	GKKQNRKTYGFKTHSAPPPPKRRSSS RATQSWMENDFDRPEBGFRRSNYPEL REDIQTKGKEVANFEKNLESCITRIPNT EKCLKELMLKTKARHLRECRSLRS*C DQLEE
4110	18011	A	4134	193	357	HHCNPSLCQNDLFWHLVLSPPIGVQWYN HGSLLP*PPGLE*SCLSLPGS*EYRH
4111	18012	A	4135	357	104	LRRL*YENHLNPEGGGCEPNLLRCPA WATEQDSISKIIII*CNFLH*QNMQKI KQNPKNSSKILTEIKISLGNLRLRS
4112	18013	A	4136	179	381	DTSLHIIQMRSLISKKL*FLYFY*DR VPLCCPWSAVQVS*PTAALTSLKRSSC LSLGNWDCR
4113	18014	A	4137	89	318	CLISCTKIQDYLTRYKTLGKVKFC PNK*NTTPEWQAKVSLLKISFLPLRIYR LRIIPVRIPAGIFVSLKFG
4114	18015	A	4138	315	60	KRLPAELHAPLAEATD*ALPKACETH ASVQAPTSQTPAAKATITAEASVKVQP

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4115	18016	A	4139	377	51	FPABEASLAKFPFAETQPPADQERGSBDI GPTSPFFED*RIPLGLFSCIGNTIQSPHF RNTGVSVPFPPGFFFPQBMRVLLCCPG WSQTLGLKPSCLSLNSNVMVRCAPLVP GMP IP *LSCFLAIGLSEFVIYIGY
4116	18017	A	4140	413	175	NFGIFCRDGVLLCCPGNS*TPRLKFPSSC LPKCDVYRRRPRTVGLPFLFINLRKDG NSVLEITYLEYKITQITVQRLLVL
4117	18018	A	4141	1	394	BTFVTKRMSGLGVVAHNSFSTLGG*GG QITRSGV*EQPDHGGSPERRGLKERRGL MVMKATFLGLRHHLEHIVGHRSLRDLN NSKKKISSHPLSTPHVPTVLKPCRLIL CFKHCQCPVKPNSPSTYR
4118	18019	A	4142	22	376	LUNKKRTTFVFKKSGVLEPKKGRGLN TVNNGSINFRQGNPLA*PKKKPOTKGG HNPGEI**FFGKKKA*QCGPGSGGIPGP RRPGLTLQKGGTYGREPSPLPGPTKEN PRLTKT
4119	18020	A	4143	161	1	PIPAKYSHFCFFVSLF*DRVSLCHPG*G AVV*SQLTASTFTQSSDPLTSATP
4120	18021	A	4144	18	159	KHLDGGGGCKREFPSCHCTPAWVPIAKL HLKK*K*VELEKSPSVIHT
4121	18022	A	4145	383	109	LFYFKTQNTYTGHGSGCLTIPFLQRVKQ NCFNPGGGGCR*PKLVPCPTWGKQGF VFQKRLKKPKPKPKPKNWRGLFLPFPFS KRPKKKI
4122	18023	A	4146	374	164	QQILRLSLRWEDCLSWGG*GCSEF*SCP CIPAMVIARSCLQINKSLFAETVIPSLEY NQLARQ
4123	18024	A	4147	25	375	RKKALF*QYGGSQPPSNLMDPPFPGE KKLSHLPLPKKKKKP*KKKP*KKK KNPFLPKGRPPPGGKKKKKKKPTTPQ KGGFLFAPPPKK*IKKSPHPKPKKOK NFWQR
4124	18025	A	4148	376	202	HYNKVFPQGPQNSFLPLQALSTFFPA APIPIFWLHSLKIFFFF*DRVSLCHPGWK LR
4125	18026	A	4149	3	144	LFCFDWITPTGLKQSSHLGLPQCMDYR *VTVVGLPISGVVFFFPF
4126	18027	A	4150	3	188	QLQSQLLSSLEPDEHNLGVRGCKLSL HHCTLA*MTS*DSIS*KKILKKCF*KK HSFLY
4127	18028	A	4151	83	358	GWARWLTPGIPALWEAKATKSLSDINA* A*CTYAPG*ESLHPIMNTLIRDPPVVT SPRVTVDTSTLARHWLFCWLLQASIGH LILTGP
4128	18029	A	4152	162	1	TVWYHNKNSNQNKI*FLELDPIITYK HLVDYKIGINHWVKDALVNTQCRAG
4129	18030	A	4153	369	20	POLLARQKQENGVFPGKAG*PKSRPC PFAWGT*DSVSKKKKKKSCFPVHRIG KLREAHISLGSNLAQRLVSCCHKKLC LGISIPDPYLPQKMPVPPSKPLTQIDW VOLL
4130	18031	A	4154	117	2	QIFFFFFFFFKQSHSLAQGVQVHNLGS L*PLPDRFKR
4131	18032	A	4155	369	217	FFSDVPPFFKPPPPKLLFPD*KKKNPP PKKKLIFFFFFFFFPPFPQTP
4132	18033	A	4156	214	283	ASPSRQQLSSGP*GLIN*SDKPSVTHS

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						P K P H C E T A * G G T S F L S S S G S S P Q A P K S P H H G P D S P L S D S I P M V I S P P E P P L R A K G C P Q G P P G A S W G T T
4133	18034	A	4157	319	712	Q D F V S K Q H S Y C L K N L K S S S L T Q V A M N R A Q V C L I S S S K G E R H L Y L I K V S R D K I S D S N D O E S A N C D A K G N N F I C I M Y K I I H L N * K R L N K * H W T A I * L K I Y P S N K M K F S N I N L S S V I N S F D V K K E R L A N T L N
4134	18035	A	4158	183	369	L K R K Q Q R G E V N F L K V T Q P E C G K A G I L F I Y Y F F H M S H S V G Q T G V Q W C N L G * L Q P L P E S S D
4135	18036	A	4159	190	336	D P I S T K N F H P G T V F L L E T G F L H V G * A G L E L P T S G D L S T I A S Q A G I T G
4136	18037	A	4160	10	390	Q G I L L P C F S S S E R E G R Y I S N T F S F F F F F W K G S P I N P Q G S Q A K K P R * R E P S P S G L T P Q R P G N G G F P P P Q Q N F F F K K G G * P G G P R A * T P G P R G T T P L G P P K A G N K R G G P R G R A K N F L K N Q N G T
4137	18038	A	4161	53	376	Y L F A F F F F S K R E A W Q G G Q P M E G A K K F M A P * P S K G G G G F S G L T P N Q W N P R A Q P P P R G E L I L I L E K K R P A P N A Q P G P N T L G P R E P S P L A P Q G K G N S E N P W P P P P
4138	18039	A	4162	1	356	G V F I L V S F N F A P F L S F F F L G K O I L V I M Q P E S Q Q N L A Q N P P P P * R G F P A L T P P R T G N K G M A P A Q P Q F F G F L K K G G F S H G Q G G F K T P T L G N L P L A P Q G I G N N L G P W P P P F F F
4139	18040	A	4163	345	26	A G F K P A L G P P G G F F S K K K S K N L F G L R G S T L Q A U G P F F L G S * G K S L K P P G O * A S R G F G W G P S F P P G O G N * I V S E K K E R E G K K K G R E K K K T T S N L L I F L S F
4140	18041	A	4164	18	284	T L Q G T S G I F P G R N F F F F L G T G I S L Y C P G W R A W G D H G S I Q L * P G S S S P A S T P L G R S W D Y R H V P P G W A S F F F F K I L P N G V T Q A G L E L W G
4141	18042	A	4165	377	30	F S G K K K F F O L G W G C G P P P L I P L M G W * F Q Q P P R V G G F N P L P P W K N V F V F K K P Q P G V G G A S P Y S P F L G K F R P I P F T L G P E G S G * P N F P P P P P M A P K G N S P K K K K F Y N C L W
4142	18043	A	4166	305	1	E S R Q V L T S R L T L L S T H E F N Y L L N N S Y T K H I T S L P I N I R O Y G Q D L K T L K K T K D I N K * G N I P C L G I G R I N I V K S L L S K L I Y R F K A M P V K I P G E L F L R N Q A
4143	18044	A	4167	394	78	B G K Q K R K K G R E G S * B G R R E R E K T R * K A S K E M K G R K R K K G R K S G R R K G R K E G K R K E Q Q G R D I G G W F L S L D T S Q L I S P A S O P K H R A S S I V A S I C L
4144	18045	A	4168	1	431	C N T C V A * C A V W C * P C G E R L C W C V S C N R V C C V * V E R V C V L V C S V C W C V C C C A R Q C V S V C H S R I E S S R P S S G P V A P S K C Q T H L Y I P K L S A P P A A G L W D I P S E A T A S L S G S L C Q P S C P R T R S F A T L V S S M Y H R P V T G E L Q S I T
4145	18046	A	4169	3	423	Y N A R R E I A A Q R D H A T A L Q F G Y R V R P C L K K K V L K L Q A W M L A * F * N F F F E T G S H S V P R L E C S G V I S A C C S L N L P G I V
4146	18047	A	4170	118	402	Q I C T C T P K P R M V K K I T M L S N N N Y L Y T

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						HLAQDI*DLIDL*NTADNKLDELNKR EIHCLRI*RLNIITKSILFLKLPYRVHAI PFKISARSEVE
4147	18048	A	4171	404	285	RGCGEPF*HICTPAWVIE*DLVSKNNK QNDNLSHLSLA
4148	18049	A	4172	274	431	ESLVGQRNIVAKYFYRITAPGRAQLRMP AIPAPWEARVGGSGLEIETLL*NNSSR PGAEAHACNPSTLGGROGRITRSRD*DP PQGH
4149	18050	A	4173	24	366	FLCLFHITCVLAFPVQQLCSVGWGCKVEN ADREEQPCDSQAKREEPLRCRGFNAP NINTEHLEFFVCLF*TGSHSVTQAGVQ GCHSSPQQLPGPKRSSHSLRSRSDWT GM
4150	18051	A	4174	397	1	TEFVLANTWQPNDRGELGQLGEPENT DNSHAVGADQLLKEPPFPLSTRSIMEEM SLNAWLDSPHREMQAGTFLSLCGDTYET QVM*SWGIRGILFQQPKWKGASLSLTAS LSLSFAHTLKEKHETHHTLY
4151	18052	A	4175	90	387	KGRNLFPPQGGERGHNG*TAAPPOTGKE NPPPPPKDRGKANAPGGIWIYLN GFFPIGQGGEPFPPFRGPPFAPPKGE KRGGPPIRPGKLLK
4152	18053	A	4176	398	280	RRLKWDPLNPRV*GCSKP*SHRCTEAW VTE*DPVSNFF
4153	18054	A	4177	253	395	LFNFFFLVKGSGRYVAQAGLKPLA*GNP PASASPRAGITGGSHITQP
4154	18055	A	4178	366	48	PWASPGISLSFSFLIKTPTIVKVR*YRVG PGRQPCPSHAPPAACPFMSFPANVSP GSAASPPREASQVQATASPPPAQGLG APANTAGLGEKQLAARVGT
4155	18056	A	4179	44	413	GDGVNGAFFFFFPLEKKWVTPPGGEPK PEFGFRAPPFPGVKKIPGFTPLRGT* RPLDPFGKGNFPKKNQSGPMWPGCV* PSDPKGAPPFGPKGGE*RGEPVWGNFA LLKERRKPLFKE
4156	18057	A	4180	396	235	HEVSLCCPDWS*TPGLKYSSCLGLRWG DHRCRNHGPGKTLQEGHRQVAGLSR
4157	18058	A	4181	85	408	YTCSLRITQDHFFFFFLFKGKIFFFPP GWGAGGQILTSKTPPGVKGIPLNPF GGGPGGPPFFTLPLGF*KKRGPFGGQ KPRPKGDFFPLFPKGGGLKGGPTP
4158	18059	A	4182	1	149	NHLNL*GRGCSBPRLHHTFANVIE*DS VLKKSYYIHLGQNPTRVKLL
4159	18060	A	4183	310	3	ATAPSGQIRIN*RNHCYIRVQSEASA NLETAVNNPENLKKIMDEGG*MKQIWK RMTSRITFVKSMPGFKTSQAQALILGA NIAVNFRLEKPMLIYLEN
4160	18061	A	4184	1	359	PTRPLVLDREPPFFFLGSGKKKNPGV FLYPSGQWTPPKKKSLGSGGLKGG GGVFPFKLPLFAGGPFPLKNSGGVKKK RAPPP*IKTLP*KKPPPPPPKLEKARG PW*KNGEPPFPCPPPSPLKGGPPKKE GV*KKPPPPPTTPPPNQNFPPFKG STPPQNIKKPLGFFSSQTPKKKKRAADR DLRLADAN
4161	18062	A	4185	1	362	HFITYLFISC*K*ALCWNQDCCKKGP MNTNVIQEKATSLYGSLSGHEGPKAG

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						EFNASKGWLNDNFRKSGFGPIGVKITGEAA SANKQKADKFPDAIKKILREKGYLPEQI FNAGESAL
4162	18063	A	4186	366	47	AALFLVDPPGRGGVKGPPPPPPGFFVFF QRRGVPPPLSGGFFFRPPNSPPGPPKGG GGSGGGPRGPA*THGVFLKNPNPCGAG KKKGFFLKKKKKKPVVPSVK
4163	18064	A	4187	394	112	KNTNFKISWAWHVSMSAPNEATGG STEGTGCSKL*SCHCTAMVTVRETLSPR KFFKKRANYLITPRI*KVCSLYHRKTGNS FKKKTQGRKF
4164	18065	A	4188	230	372	KKMFLLFPNPAILLGLYLKEYKSF*HKD TCMMPITAFITFKYKQW
4165	18066	A	4189	149	2	NBSLEFMRFKGSSHLPI*VQGGKAASAD VEAAASYPEGLKKTINKGST
4166	18067	A	4190	2	159	MHQPWLLRRPKQENCLNPGGGGCSSEPRS HHCIPA*AIERDSLSSKKKKKGGA
4167	18068	A	4191	180	415	LGLFLQLLFFVGRSMFIFALETSHGWLGS SLSF*PVCVQOSSLSLSLSSNDHKGMS YPANFCIFCRDKTLPCCLGWAQ
4168	18069	A	4192	424	41	PLDLRAPPKGLL*PKNSFFPGAPP*IPF PPKKIKIKFKFTPGGGAPLFLFLPROVZA EGSLPRRVFGPPPPFFPLPLSPLGAKPN PPFFFKKKKKKRLHKSSLFYSAHFVLC LKYSLSFFYQSVKTK
4169	18070	A	4193	105	424	ELKRLVIRKLIRGIPKGRQAQCKEIQKIA QEVKGEIFMBIGSLKKQ*KIQETLDTL LKQNALESLSNRIBQVEERNSELEDKV FKLTQSNKDPQIKKKILYNV
4170	18071	A	4194	3	240	LCLQSOLLGRLEQENPLMLRI*GCNEP* LHICTPAQVTERDPSKKNKGSFIPMKI GKLYSELTNMRNCNCKNSEKENV
4171	18072	A	4195	385	1	KYKILTKKKEIKHDEKELQKTEVDLKI ENNTTRARLANNIKKPPSESEKTNKQNH TKKSL*DDQIKKETRPQKKKIPFESR*V RHRNRILNLESRRNGKINPSGVQKKRDS VPTLITQTOETWNWCF
4172	18073	A	4196	3	272	LFPLINALKHKSSDVGNENIYAKKLES ASFKERI*KSYYVEAKIYGNKEYCIYEI VKKEK*IMHSYRVQYTLQFQTSLEVL RIPHG
4173	18074	A	4197	236	379	GGRFKGSNFTSPGLQNSFFMGPPKLS RAGV*QRREGKNPGVQFNR
4174	18075	A	4198	375	1	NFKIPADPPQNKGRPLRGVTPPLFLFSP GSPPKSFPAKAWARRDPF*NPGETLQ G*VFFSGRFFFFFEDRVLCLCHGWSA VAQSRITSSDSRVHTLILVGRGCSEPR SHHCNPAWTVK
4175	18076	A	4199	1	270	PSRTGPIPRPRTRSNCPQGLGF*GCG SPRSRLCTPAWATQDSISKKERGLLV FLKGFHTYIRLLINLFAARGKRVLVLA GGRBNW
4176	18077	A	4200	388	1	PPGIINLFDGL*PPPPNMGDPDS*KL ISPOKKKKVPPVPVPIINISGPPPPTL VWWLFFVSLKROLIL*KSQVSAASLV RHDGAPRITSSAGKGHAETFPQRPPTH RNACSFVLIHIQSYKVF
4177	18078	A	4201	298	158	FKVITNFOPLTPIFAPSEGRGG*GRGR

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						LRSCCHCTPAWVTS*EPI*KRKIKGKKRT EQESRRQNLA
4178	18079	A	4202	128	358	KLMTFFSPQPPPPRPGGRRGGHPDARENA PSGR*GAPLPGRPY*EKRIPIARTPPRL GGWPSMSLRTHDDNGGVNE
4179	18080	A	4203	406	1	FFFFFLRQSFLLVAQAGVQ*RNLSGQQP LLPGF
4180	18081	A	4204	322	2	KPRPKRTGPGFPPT*GGRGAPPPRGGAP KGGSP PPPPPPPGGKKGGKKNNPPGG *KPMGGFFFFPPF*TPPKRGLFLKKK KTQNP KKKKKGGRSRTRTSRV
4181	18082	A	4205	3	127	GPHRVQSNGLYLTL*STRHLPLKC*DY RSEPLCLACFLP
4182	18083	A	4206	1	216	GRKRVGRGLLLDTS*SAQLGLKQMDQC GR*PPRPAHLGCNSNAKEPGLPACPLLS GHMHRVAVVNRNATATL
4183	18084	A	4207	427	0	LFFTTNFFFAVRFVFLDPF*NDPPGFF FLPHKKKKNNPPDPGFF*FFFYADPPFF FFFFFHHFFFFFHHFFFFFHHFFFFF PVVLKTVVSC
4184	18085	A	4208	2	404	PRVLGIINCKERLFLCYFFFFLGRGCF LAQGGGPGGNFG*RAPPPGGEKKIPPPP PRGGGEGKPREPRGRKIFGLKKGGGPF GPGGVGPPKKGPPPPKPKGNGYGGKPP AQKRGFFFGKKRAPFFNWNVG
4185	18086	A	4209	40	412	PLFCLSEKRPYFEYATYLMLSLKFLSC IMSVNSSAVSASVY*W*KIEREPLTSN TLKLOPEVPHQKFAFT*RAKAILRKKN KFESLTLGFEFTHYKITIITTVVY*HKD TQIDQNRRES
4186	18087	A	4210	219	392	HFFFLANYNFGKGVSFQFQAGCGGRNLG *LHPFPPLKQFFCLTLRNMRHRLVPP PP
4187	18088	A	4211	409	2	LERKTVFSSPPPIFFPAVFFLSPPFYT PPPLYIFCPDKKKLIPPPDGKIFPFKK GDDPIFFFFFHHFFFFFHHFFFFF*F FIMYQ IVFNISYMLKVDSHLYLFKDKKILLCT ISSDAW
4188	18089	A	4212	24	399	ADAFSTINLHGLGPDLFPTPTQWYNLS MAILL*AGAVNIGYRSKIKNALHFLPQ GTPTPLIPILVIETINLLILATATLVH LTAITTAGHLLMLIGSASLAGSTISLP STLATVFTILLIT
4189	18090	A	4213	411	197	SWLTAPSFIRFSCSLSS*DYRLPVPH PDNFCIGSRDGRMVISIS*HHPDPASAS QSVGFTAPKVLGLQT
4190	18091	A	4214	218	126	KKEPELIFSSNSVGAIDLNVMRVLII KSCTPGVVAHTCNSTLGRGGQITRSG DRUIFG*HKSALGSCASCFYLDWLLH IYFE
4191	18092	A	4215	1	332	MAPELCLSNKKRG*PGFGGAPGIPGR QGQHPKRLAFTKPGPPKGLKGLVLK TPPPKPPFFLSPKGALKTESP*TKKK GGAEKKPPDGEKRLPGPPCKKPDWG
4192	18093	A	4216	1	185	KLYLSILISLQISLITPTATELIITYI FFETTLIPTLITIT*GNQPAFLIYLLV SPHEN
4193	18094	A	4217	1	388	LRFCWETLFLPLYNPFSIFSFLFFSFS

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4194	18095	A	4218	3	195	FFFFLGGKFCFCQPGGGGPNLNRDPP PRG*KEF*APPPRRGGNGQSPPPPPNQ GGF*KEGGLNHGGGGGFPQKKPPPL ASQGRNKGGAAPPILKF VIYSTIFAGLTITLALSSH*FFT*VGLET NMLAFIPVLTKINPRSTAAIKYFLTQ ATASHIPA
4195	18096	A	4219	261	1	EPRRRERKERKSKKGATPSRICMKRER BERFS*ERRRERGERGERGERGERGER EKERSERERERERPKN*MLNGRGRER TRG
4196	18097	A	4220	5	375	DEMLHLKFTVILN*LEKTLIFPKVNL YN*DFLNSKVGQTPPPPPSRPPSSSP DPPGPPAGAGRRARRRGRGSPGGP PAPPAPPFRAGRAAGGRPPAPRGG GPAARPAAGGG
4197	18098	A	4221	258	267	GGGALKKKIKYGGGGGNTFF*SPPPSFF FFFFFFFFFFFFFFFFFFFFFFFFFL IYFIFILIF
4198	18099	A	4222	127	330	KKKKKKKKKKKKKKGGGPKKKKFLPR GGKNFFF*GGQKKLGGVKKGGGKK PGAKKKKKRGEK
4199	18100	A	4223	1	377	RRPHLRRENLEQKRTNMGIFFFFVGAP PGGGKSTSPSFFF*GNTPTFTPPGG GGNLVGENSNPNPPPRDPPSPSGSEK I*KKTTPPFLVGPNTKNKGHFGGGSPK KKTLLPPPLDPP
4200	18101	A	4224	223	431	IRKTLGFLRGGRNPLKRV*PPPLTFF QKGPFPFPQKPRFLFKFKRGGP PRKVLTPPGLL
4201	18102	A	4225	173	2	RCRLHCLFFPTATITR*GNQPRNLNAGT YFLFYTLVGSLLPLAIYTHNTLGPTR P
4202	18103	A	4226	11	377	FLTVVFCISLGRMLGI*FFNVFCEL FFHAFSFLIKTDLIFSIDLLEIYAH VCHICCNLIFSIFYFVFNGLSKYIKC* NLPAIILDFAVSLIFMRTGKQNDN QFSLKILIGF
4203	18104	A	4227	1	412	KNSKVRNATDLLKNASEPSHSRTDEARE RISELDRLFENTKEETK*KRKK*SM PTDLNLSIKRANLRVLGKEKVGEL*V GSFFKDI*QNVNLEKDNIAQASAYTT LSRFNPKTTSRHAIKLSKVKKR
4204	18105	A	4228	373	163	IGVFIAGAPFFFFFFFFFFPQGPGRGG KGGASGKTG*GGGGLKGGKQGWPFF FLKWTFTFRAGL
4205	18106	A	4229	392	3	PCF*NRAGFNAGPPFKLYSSPPDRK FSGKGPFFFSADPQKPKS KGGCL FPGAPOF*GCPGGNYPWQOFP*DSH PPPSNGPKRAAFSKKKKKRKGWGE GEGQCSNHLLEGYQI
4206	18107	A	4230	211	400	VALIWLICLNHYALISVFWCCCFPLI FKFTYVFINILLFLAF*IVLCILKVNQNH SGSLISVSYFPLLEACRFFLPFLF*NL *MICNMVLYFKQLCSALSVFLVFLF FNF*IYLCIFKPIVFCELRNPTLAQA GVQNHDLGA
4207	18108	A	4231	69	386	KRIFFFLGPRGGGKRWVNGNFPPEKG



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						GNFSA*FPQRGGPKGPGKPNKVI FGFKK KRGFYGGQPPNGLKGLAGPPKGGRK KTHPGGKFYAFLLGGGLFSKKNN
4208	18109	A	4232	394	287	PKKKKKPPPPPLFSPPFF*KRGGSDPLF SPRGKK
4209	18110	A	4233	442	112	LLGRIRWEDGLSPQGRSCSEF*SCHCTP AWATQ*DPVSNNTNNKNPNQACSSLN SLPWTAAVWRTLGEHCNCGREALPARRN ATKAPVLITHHIQQTVRTISCALLFH
4210	18111	A	4234	415	58	SLQKGHPFPQGLDFQNRGRSGASVLP TSLFPLSLLFRF*FNAGVLVSYKGCW EWPAALVLLFLRDRVSLCFSLJSTLQ LKRSSCLSLSSWSYRRTTPHAST**FF Q
4211	18112	A	4235	406	168	HGETPSPLKQKLAGRGTL*SQLLGR WRQGNMLNWGRSGSVIYTEKITVHTQQ SVTT*PFMSMOTLAYSPLSKSS
4212	18113	A	4236	247	397	TVCFSVVIYITELLFPQV*FFCLTLPS WDYRSVEPLPAYFCISFRDGV
4213	18114	A	4237	36	405	RLYCFIKGLVWENKFKRIVFFFPFLNF PFGPQGGGKGANSGFPEPLALGVKKGR PPPPGGGE*GAGPPGNGFGLKKKGVP RGGGGGPKPTQRFPPGRFPQKGNPFG PALGKKVFF
4214	18115	A	4238	407	3	KKKKLLIRPGGGGPPSPLEKRVQKGG NPGGGFSKKKKSPPPPPPRGKKKKPFSK KKKRFLSGNNTGKRLGKDPQS*PAGNA RKKPGMERALAKGRAPNTDRKPKHGL DSGQSGTQEQSPNPPVKH
4215	18116	A	4239	144	405	PTVKLVLYLVLLKRVAVSLR*SQLT V*QQRQLWKKRLNTEFLYLQSGWGH LVL*PTVNTLSLKSQARMVTPVIAL WEA
4216	18117	A	4240	369	40	PLLQTPASMPRWGRGDRPRKEG*LP RETRVPPALHQPARAGVSL/SPGPPFW LSLQRLRGHSSSDSLPAVCQYSGSWRE KAAAEAPALTPALCTCTICSVLTVL
4217	18118	A	4241	397	1	ISKSLFFPIFPWKKKKKGSPFLNFGG VFFPFFFLKIPFLFLKRPFFPFLQAG FKIFKYPFPFPRGFKTPPKKKIFLNPFF KKKGGGGALFFFFFETGSRSVTQAGV KWHHGSLLQ*PPRLK*SSDP
4218	18119	A	4242	230	393	ADRRGSPPLSAPETGSHLAQTGVQ*HN YGPS*PLTPGLKSSCLSLPNCWDR
4219	18120	A	4243	434	104	KQPTFQSTTGGSPAGRPFPFRACKKKP PFF*KKKKSGNIGGLFPFPFGGEKK NLFPRKRGSHKTDSSPPH*RGKKNNL SPKKKKKKPCWDRKRLCPATF
4220	18121	A	4244	2	425	FVFKTLNLSLQENLQFKIKKTHD LNKPKNKTKGNITKQNTBILKNSKSE IKNTVSKPNRNLNQAREFISELEDSPF MTQADKKKKKGRSLQDVLVYTMK*TNIL WSFQKKKKKKGLQNLINKVIAENFDSL
4221	18122	A	4245	12	424	IYKTLNCT*IF*FGALACFHFPYFP IHYGVFVSPVYFLSHVLSVWTSGLL YSLGCPILSLFIFLLKLFHFGYLTQV GIYVWILFVCLFLSNSFINI*FTYHAI IPYIPLKVYNMFPYSLTTPK

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4222	18123	A	4246	215	425	LSIQTSQIRNLITLPTINIMGLAKRK *GTSDAVNQITIFLRPRTVAHNSCNPSL GGGGRITKSGDRE
4223	18124	A	4247	413	2	WEVESFSLOKAPWSCATNPGFHPKPF LLFTMKAPPPMRVGFQDFNKDGRPI* PRTPPCPRARGAKNNSVSKKKIKIWK WPPTPLPPGNGGTRKFPSSPPPPPPPT TPKITTPOGERQL*PQRAEGAGDTK
4224	18125	A	4248	61	281	ITWKDPDSFVLRVSKAPHLALFAPIGN CIKCHIRMGITYPEEKFGNIIKCYLILEID VCGH*TWKKIIFLFFLRGRFLFAQAG QQWLLSLQQPPPGGKRSGLSFLEK* DPDSFVLRVSKAPHLALFAPIGNCIK HIMGITYPEEKFGNIIKCYLILEIDVCGH IRLGKFFPCFPF
4225	18126	A	4249	23	13	RVRPFASPGGREVTVCGGLGREQERRL RWIRKFLFLAATSQAVFRSVTPSPVTS GSADGQSLVAGAGTLATVGGLELINS NDPPASASQAGIAGVSHRAMP*T
4226	18127	A	4250	182	342	KGFFFLPPGGGGGGF*FNEPFPVRVG IFPPPPPGKGKPPPPPPFVGVFVF
4227	18128	A	4251	2	219	PSLRKMKQIKARHGQFLWSQLPQRIRRE DCLSSGGRSQTHGSEL*SYHCIPAWAT GDGVPKNTKFFFFFF
4228	18129	A	4252	223	324	LGAVAHICNPSLTGGRRIIR*GVRDQ PGQHGE
4229	18130	A	4253	165	336	ESDAQGHQVAJRVSHVLEKDALLVFRSL CKIAMKPLGEGPDPK*ADSSSWPVSQ
4230	18131	A	4254	3	233	ETAFCHVGAGLELLTSSDPPASGLQHA GITTPATKSAP*WS*VSGPHLGAFDSL MLAQDQWALLSAGFFEL
4231	18132	A	4255	394	44	AKIFEPQVKKFPASTFPGQKKKKQPP PVNFPFPKKGQGFPPHGGV*HFAFINP RWDPKRMGFKGEARPPPKLNLFFPG GGKNFFGKKKGATGGPPFFFEFEH CRPD
4232	18133	A	4256	152	2	YNSPFYCRSCCIRQTVARTCNPSLTVG QGARTFTRSGVRN*HQRGESPR
4233	18134	A	4257	404	190	AQLIRGWRQ*DHLSLGGGQCNFESSCHC TPAWITEPNQSLSQTKQKMLIN*YG *TVSPFKSHDELQFS
4234	18135	A	4258	288	407	ENCRPRAVAIACNFS*ENCRPRAVAIAC NPSAPGGRGEQIPRSGEQEQPVQHG
4235	18136	A	4259	406	163	GWGVQTHPGHGEITFLFKKK*VGGGG PTRYSPIGGVGPGQNLNPGGGSKNPK LNPLLPWQKGVVFFSKKKKKKRD
4236	18137	A	4260	101	276	LTSIVPSLWBAAGAKRLGGRPACKRS LCHCTLPNVTV*NLVSKKKKGAGALGF FF
4237	18138	A	4261	2	414	WVAATPNLVFVVRGNGQWFTGPFITRG GWGGLFPVKVYIKGLAFPSGPIPIR KNGKVGQGLFENKINPK*NFVENKNT RRGIKNVPEKKKKPKQKIPLEPOLNEN QIWGDPDFPFPAKKKKLINSFLGWA
4238	18139	A	4262	337	382	RDARFLRCSLV*LTIT*LGKEFFVFGQG VQWYHFGFLQPLFSGNPFCECLSLLSRW HYRGPPPSLGKFLVGLKAGNLVFTKFW FCWPGNRALTGFVPAITTVQVAIFI

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4239	18140	A	4263	406	184	QLLGRLEQENCHLGGGCS*LRSPFCIS AWATILDVPSEKPKTKNQKPTGLOGLNQ GPASLLKKIKRLGKKRPG
4240	18141	A	4264	233	440	LPVHNGWGLSRKLTTLGKEANPSFFTW GQQGKAKQKQKQPGAGPHACNSSPLGG QGR*ITRSGVQDQ
4241	18142	A	4265	2	230	GARL*SHLLVRLRKENHNLKGNCREL KWPCHTPAWGTICKDSARKNKQLPPLPK GVKSPPQREHGLIVTCMFVQ
4242	18143	A	4266	1	349	HKTNIHFKLVMSNVPTFFFFGKGFSFC APGGKAGPLTGLVETPPGRKAPFGPNP PRRGE*EMAPPCPKILVP*KKTGFPRG LNFPPGGPPPFGQLRGGNNGNPNPQPE FWP
4243	18144	A	4267	2	375	RSQFAGSASSNFGSLSTRSGCGGCTG SPNSASPPALCSISRRMAAFPRGRARD LQPMNPDPPTHSVSGCAKPPR*ADPPA PRRPVPSITTQGLRSAGAQGTGRHLHLQ PQCRHWWKPG
4244	18145	A	4268	377	3	TPAMWTRDCIWRRTSAPGGSWFSGPV PSPGAQ*RPSPQGLGLWAAAAARC*T APGPRPPHGGPSQGSAPPTPRPCRP HPRAGSAGPTGATPPGTSQQRHRS HQ LPHPGHRVALG
4245	18146	A	4269	1	254	LEDWGRGARAHYDGSLEPESDEYRLR LQYHGADGDSLSWINDKPFSTVDRDRD SYSGNVALYQGGCWTHACQ*ILDVAVY ATGPKQVHCEALH
4246	18147	A	4270	2	218	TRTITLLSQQLTLLPLIAS**LLASLA NLAPPTINILLESVLVTTFS*SNITL LQKKEKKKKKKKIFP
4247	18148	A	4271	32	443	LHSDVDQLAGLVFPQCPNPLASPARAP AGPNPRRAAAPP*SAPAPRLAVSAGSP ANPPST*GLPAPAAVVASPASAPSTSA RSRS*ASPTARRCRPGGTAAPTASRQ CQWRP*PQSRPPSGTCSAAAPT
4248	18149	A	4272	434	57	HLSPFPASAPKPLPQASLWSSPSTIV LAQVPPMTDPCQPSA*PASELSPMP PARPOAPPNNHSP*GOGAQTVAFLVPG ATPAHRPASPSVTLVPLTAGHCFPLY TYQIFLKFHYIKR
4249	18150	A	4273	288	424	GLSLVAQAVQWCDLVSL*PPFPRVQK FSCLSPPRIWDY*HPPP /
4250	18151	A	4274	1	429	NTRGACGPPQMPHPPRASAFENPCGRK N*QVSGP*ASGSPVIOAGPAGTWRKG GLWGPTRVVRGPRRRPGASGYARQK GGHGPGPPSPRRRLSVPAACLCPGQTS GTAGLAVWPQIGLCLIAQGARSCPRDH SD
4251	18152	A	4275	253	3	PHQNAVILYFSPVSRCDDNNALYSFV IVVLCPVKIGVSVYRQGV*WHDHSLQ P*TAGLKRFSSLTILSSWDYKSTPPCI
4252	18153	A	4276	406	3	HWSSQGVCAK*QAPATPREGIFPRSD TQVVRVQVQKYNMGLVDFDQYNELHLP AVILKTLRLRLRPLLTLDLYPHVVGFL NIDBSQRVATLQVLQTLPEESYQVLRP QTAPVLQISAHSDQNMINTCI
4253	18154	A	4277	373	3	DVSLCPGNSAVAQSWLTAFL*ALOPT

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						FLFPVGGTGTIVLANSLLDVTLDHTYVV VAPFPYVLSIGAVPAIIGGPIH*PFLS GYTLGQTYAKIEFTIIFGVNLSFFPQH NLGLSGMRRCI
4254	18155	A	4278	71	176	AGGRGCNERSHHCTPAMATE*DSVKER KKGLEFFW
4255	18156	A	4279	2	379	SPFVPLQSSLGKNSSTPSSHGKRRKKR KRTDENOP*KHPIARPGPGAPRAQGA QGSQGRGAGPCKRLVHRGRTGNPKREP GLI PQQEGRSLGIHPSNGCHKPCPSGR P PPRPKQGRGRQGN
4256	18157	A	4280	2	338	CWPRPKLDLPSGRNTLGFVCVVMAQTS GLK*SSCLCLPKCWDYREPLRPNVYF KLWHP SPWKGLFPYSPVFPFLCLCTTA SLFCSCLPPCCSRVTLVGSESSCLWDAG
4257	18158	A	4281	407	1	EEEGVATGHTAERGRADNEERGEREVANK RGREVOPEARRMTTATGTTAATGAR T*TAATTATAPVTRTAAPATASSTRRL RTPRARTASVLMARCSRWSATRSAR TCDCRTASHSRPTATRSRTARMA
4258	18159	A	4282	367	225	PCDSACLGLPKCWDYREPPRPAVLEL *ASPS*OSKEVYVCKLTHA
4259	18160	A	4283	452	1	NTCGLQSVCRGTQGGPKRCPCHPRRW DLGDEQSSSEKRGPGREVGQGGILGAT FGAQGSH*GL*AEAAMSSGHALPGQVP LTPLSPSPNPHRRPRAGRASRQSRST EAQRAVPSQGAAPGWETDWGSSHWQPC QAQEGRTGR
4260	18161	A	4284	436	22	CHVTGTQPIKVS*AKCSREIRSGGRYQI SYLENSAILTLVKVDGDSQYTCYAVN EYVKDSCATQINIKERLIPSPFKRLSE TVEETQNSFKLEGRVPSQPIVWYK NNIEIOPTYN*EITFKNCIAAARI
4261	18162	A	4285	301	403	LSIS*PCDLPAIVSQSAGTTCMSHARP RVKSLI
4262	18163	A	4286	380	2	AQVLYSSREORRQDLPEQVQAEQ*V KASACQLTFEDEFAMESGPAALDKDQC TRKHIFAEVQSGPRCMSRYLVDSGPCPT FARAQNVCS*CCENLWISIAFTFILRI QWCTSTVHQVCI
4263	18164	A	4287	453	3	YIVEGSIIMEPRKVPFKDGLGHCQKF QG*RNNSYNNHVRVGTCADEGVRLDLS SLQSVITKPBQNIQELWKGFKKKEPAE NHIRTLEASLEKIMAKIHGQLEKLK SQCDRLTEELTQNRNENKELKYQCLK DQLEBRDV
4264	18165	A	4288	52	400	LDLFPFYKOCIALSPRLGRSSAILAHCN LKLLSGDDPTASQSKETSMRYHI* NL*NSMC*NCVDTTHRIGENIWESI* *EIMQACRIKPTQQQKTHPQKQSLH SNLQ
4265	18166	A	4289	2	263	THGAHLWSQLPGLKWRMSRPSGRSCS EL*SHICTPVWVTEGDPVSKKRNICQ NINEKTNLTVDTPRHSPTHKISLNHFQ MPL
4266	18167	A	4290	3	142	YLGVHRLSIDGLDLT* SARIGLPKCW DYWRDPPRPANFYILFK
4267	18168	A	4291	324	19	EMSKRIEOKPHRRLOQMANHVKRTSLA

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						I R E N K I E T T M K Y Y H T P L Q M A * V R N N D T S Q V Q M H T L Q V A S P L V A E V G W G N E A R N L R L Q I V K M V M N S H C T P A W V T
4268	18169	A	4292	2	204	I H F C R D R D S L C C P G W P F T A L K Q S A L L G L P K C W D Y R H * A T T K P G L Q S V F L G L K I F L I L L V R G V D R Y L
4269	18170	A	4293	427	3	R R K T V T P T R T G E R G I L S N E D N G L C K A V G N I P G S P L C N V S K L N I M K H A P G G H A R F C I W T E S A F R K L D E L Y G T W R R A A S L K S S Y N L P M H K M I N P D L S R I L K S P E I Q R A L S A F R K K I E N R V L K K N P V L R P L * R I K L T S R H K R
4270	18171	A	4294	24	372	F T C P L Q D V Y I C S D V T S C V T K I L A T T G R R L R D D S V Q F S F F F P G K G K S L L A P R V K E Q G Q D L G * W N F P P L R E F P G L A L P R C W N G L A P F P P L I L V F L E R K R F P L A G M G L N L L E S R
4271	18172	A	4295	1	332	I H S S Y F F P Q S * F F G T I N T S D K P L R I L I K E K K R E G T N * H I M H E P W K F G I D P E D I I K V K K K Y Y K Q L C T H K F D N L E R M V H F L K K K T I I H L I * N R * F E * L Y K Y R N
4272	18173	A	4296	407	30	W S V T Y G E N * E S L G W G A H P S H V A N I R V T G L R Y L F S Y G R H A L D N L E S Q D N M R S W W V S Q M S S E I D V D N L G H I S L C N A V Q * I R N L N P G L K T S K I E L K F K L H K S K D K A G S E V T K E F I E V Y H E L Y A V G
4273	18174	A	4297	350	1	Y K I V V M N K E K * Y V G Y N I E Q E Q K L A L K T T V L D E W T L P D G R I I K V G G E R P E A P E A L F P P R L I N V E S V G V D E L L Y S T I Q A D V O T R S E F Y K H I V L S G G S T M Y P G L P S R N E R E L K Q H V
4274	18175	A	4298	623	1	S R R G C A A T C D G S I T A M P F Q R Q A A Q G K P S V H S K L E A R A K P T P G D H A A S E S T G P S C L G P G G V H K T A H A H A R N P G D S N T G S G S P A G R R W E A R G S A P R H H P T Q P D W T H P D A L R Q A M A R N P A S S F * S F * R C T A A S P P V T P P S P V L M R G P V P G G G G Q G K I R P L Q E A P P P S S P V V L S R * P Q A G T P S P A V S S L Y H G G L S P T G R Q D R W G R
4275	18176	A	4299	469	3	P V R N C L G A R F R V S G R A A H H A L * Q S A S T L Q G D P R T K R Q A I S A * S S A F D V Q D V S H V T L P F Y K P R A Q S K D L I K A I L D N D F M K N L E L S Q I Q E I V D C M Y P V E Y G K D S R I V K E V D V G S C V Y V M E D G K V G V T K G N X L C P V G P G K V Y E L A I A H T C R P C I
4276	18177	A	4300	506	321	K P L S L I K I Q K L A G H G S C L * L Q L R R V R Q E N C L N L G G G C S G L P K F W D Y R C E P P C P D C W P S
4277	18178	A	4301	454	1	N G E K P T Y S G K K Y V L F * N T R R P I L P T W G K T N * G E R P R S S V Y S C S S X R L S S S L G R S * N S V G S I N I L A T L T A Q E L G S N S * A N N I I * L A Y T I A F I V K I P L Y G H I L * I H K A H E V P I A G S I V L A P V I L K L G G Y G I I R L T L I L N P L T K H I A Y P L Y
4278	18179	A	4302	3	463	A V S I L P L P R F R G L P P L R V G V V C P L R C H I L R T Q R L E G A P S R * Q T G A K A G V W E L E R S R I S L Q P R L G R I R P Y S G D P G Q V T D S S G A L A S S L E R G C Y P A A L L V G E G E M Y L G P Y

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						HPT*DLKRLSLAKPPGGTFLTRSHQT FWGGLPPSAVCL
4279	18180	A	4303	469	2	FFFFFSETESCSTV*QAGV*WHDLSGLY
4280	18181	A	4304	194	3	FFFFFSETESCSTV*QAGV*WHDLSGLY
4281	18182	A	4306	517	254	VVEETAFLRLTGKTLGLVTSGLDAAASYS QRGGMTGVSHCNKREFVLGNLIWMSSGL TFLPSPDEV*GS*GLSLPSPALNLTG LRN
4282	18183	A	4307	276	3	KIRMEGIPLHFPNPLVNLNLGLFLILAT SSLAVYSIL*SG*ASNNYALIGALARAV AQTSISYEVTLAILLSTLISGSPNLSL LITLV
4283	18184	A	4308	234	398	KKFFFPFPLEGGSP*ITTSWPELP*RE SPAPPPPPGGIKGLAPPNLEFFFLDKA
4284	18185	A	4309	403	100	SGGQKAVGEPKAKPGLPGKTNKLGZPLP QPSTEGGAFW*PQGG*PKTGLEPLPQ*LN PRNPDP*WPPDP*PPENRKSOPHTSP TFLCGPPPKNRLPFFF
4285	18186	A	4310	399	85	WKPFLAPLAPWGVTRFRALPPCRPLHCP TLKLTAPSVIHT*VIDMGFLVGVSLSV FLERESCSFTQVECSGTKLALRSLELGL VSDPSISAFQKAGTAGVSHHA
4286	18187	A	4311	230	2	WTEEDTRCLVLESPFLSPFLCPVLRLQ RPACCPGSAVTSQSLVASTSLAQAKR SSHLSPPQRS*DYRHTPQCI
4287	18188	A	4312	1	420	NTSGVGLSLIVIVINLLPYWLPKG KFFFPQNSRFPSPAPPHSSPPGLRSDFSH SGGLFFHLEVLNGLPLPPPPPPASTHVR RPLGTQQCP*LAWYIHLISASYQKQANVA PQLSCLQQCIRSKGDLILPFFFTCLIS
4288	18189	A	4313	403	207	ESSSE*LNPLAHAMRYKQCPKQVREK SEFLIKSIQVRKSLNTRMSLLQLDFTC RYSRCVCFY
4289	18190	A	4314	469	328	TSEGGGFNELRLCHCTPWLK*DSVSI SQRLKKNLTKQSLVVRCP
4290	18191	A	4315	1	212	NILPGVEVLRRLREMSLNP*GGGCRFP *SCHCTTAMATEKDPVSKKKKKKKKPPGG FRPHSLSQPGPPK
4291	18192	A	4316	63	359	SNLTWOCFAVAVETPSSLCGPVPSPST SSATPKPIPS*AACTPPEDCALAAVRAL PAAGRPFSACLTPOPNPCVLWCLWD HSPTSCTPGSS*APHSCAFLVPVRLGGG MTTVHPTVHLPIHSSLTFAWE*PSPDAC LTAPRPTGHCLLSVPPSAVSSSSPS
4292	18193	A	4317	135	405	PAPPSHPKMDVSVCLVPS*PAPPSPH PKPDSVSCVIPPSPRVAGSGLPENTILLE PRGPCPPRVFPTSPPVG*AWPHPPARR ASGRMDGRTDGRGRHLDLRSTHSFLTP
4293	18194	A	4318	413	1	LILVGR*SFHRSFPGQRIHPGGKPYD CKKCGTFLSLVIGRHLLTHGVPYK CKVCGKAYVRLFLRHSRSHSGDEYE CKQCGKAFSCSSYIRIHERHTHGDPEYE CKQCGKAFSCCKYIRINERHUGGV
4294	18195	A	4319	479	342	GVGVNDGGLVLGATNFWLDSATRRR *DNTVNLILFLTADVSR
4295	18196	A	4320	400	26	HSEAVTVRSHSIPVGHHSLSNAPPIVA LTP*YNNPINIEV*ARAQIKQGFITH IPIHLLIVITRDTSRACVVCVVCVVCV

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						CVYAYIYVCMCVIYVVCNVIYTCNYTFI PTLVILPINKMY
4296	18197	A	4321	370	1	SDRGQGGAGQATRLGRSTQDEDKGTE KSIPSWDKGPVNNFEGKSVNVSSNLVTQ EPSPEETSTKRSIKQNSPVKKEKSKC NECGKAFSYCSALIRHQRTHTGKPY* C NECKAFSRNV
4297	18198	A	4322	342	82	GLGLTINWLTOKSAGRCAPSSGGLWL AVGDSVYVYHRETBGGKPSGGRPCC*PS* AGLAPPSVPYPCGCEAPGSCCLHYRCLL TNH
4298	18199	A	4323	284	3	TKKFPRIYGGGCFSPFPHGLSKXNGLF PSGALSTSLIPGALIPGQAGVSSAKE KKKVLGRKPVVAHACNPSTLGG*GGRIK RSRVDPQPV
4299	18200	A	4324	365	3	QVEVYVVENHPPRELESTYQ*CRLEGAT SVAGBQISEYNTSMRASDGSPPLSTET HITLHVIDINDNPPTFPHLGSAYIYPEN NPRGASIFSVTAQDPDSNNARITYALT EDTLQGVY
4300	18201	A	4325	253	3	PSFLSRD*SHIKRRLCSOMISADYNLH LPGSSYPTPSQVAGTAGPSMSLQGR ASHDITSSSRSIGAKRLRPADHPQCI
4301	18202	A	4326	307	95	FLFLRKDKILLSPRLCSGTILAHCSLK LLDSSYPYAVAS*VAGTSGMCHYTWLRN KNLLSPGIGQCSGI
4302	18203	A	4327	371	2	WAPNHSPTPRSGSTTRIWAIPFPGNSP RPCQDQGHRTDPWYPEEFLINPDPPR ADASWSFPFQEKRLHFPALPCP*HLDSS LGPITLFSFSPFPPTSIRPSQTNHSGT PPLSYAQHDCI
4303	18204	A	4328	409	1	RLLEARQPELEMAALIFPTLRKYHVERE QKYHQLQDEYFTSAVVLTLILAALFGLV YLLIFPQSVVVLVLCICFLVACVLVY LHITRVQCFPGCLTIQIRTVLCIFVVL IYSVAGCGVVG*LPWANSSKPNLY
4304	18205	A	4329	262	2	LHGAYLVLDITGAQNRPEYSPFMRVQ FFFLVFSPRDLSLTLPRLECSGTUMAH HLDLLSGDGPPTSAS*I*GTGAYHTQ HV
4305	18206	A	4330	1	399	NTP*FLKGMGLNVNPIEDNLRKLYVSN LOIGHTRYATTCNV
4306	18207	A	4331	408	3	SSVGIVRTHTGKPYECHKCKAFSCH SSLRHRVTRTHSGKPYECNQCGKAFSHA QYPQKHVRSHSGVKPYECTECGKAYS SSLRHRVTRTHGKPYECKCGKTFTRYL ASLQAEVTRTHGA*IKYKSGV
4307	18208	A	4332	110	426	GLSPGTWSDITGGPVTAFPTCLTLGTHA GELLIDGIDAKPLHLSRLSIIILQD PFLPSGCTIR*APPPLRPTQAGSGVSPD LHKKEGSGVGGQDDPRGVSCG
4308	18209	A	4333	133	1	EPCCPSAJAAPEVLGPEYDKSCDMWSL GVPMYIL*VPSPPPLY
4309	18210	A	4334	165	1	ITLTFPKNEKRVVLAQYV*KNR*YDQ WNRIASPEIDPHE*SLISDKGAKECI
4310	18211	A	4335	42	440	SARRAGDPARGAFSPNNASLPDPREITG RPAQGLQ*GNCPAPPT*QLPSPSVSRPV SGRGPYPSPFSDPRANPRPNKGAQV

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						LTVMQGEPTGIRKANCPLSNAMITFGSLPEPKRTGPQIQGPPSRRG
4311	18212	A	4336	1	160	NTCGGGAQL*SQLLRLMWDLNSGSGQCSRLRSHHTAA*ETKGDPLSTNEY
4312	18213	A	4337	236	1	QRSLICYTMEIRTVAVRIVATKGVSESVYLAMSEEGTVYAKKCNFYGIT*ELVLESHYITTAARAVLRPVCCIESKVS
4313	18214	A	4338	408	3	QSSVSKKKRTNGAQNPAKQGNELRDSIEQPOEYYRQLRYHQHLEQKQQRH1*QOMLLGGVQEDGRDQQQNRNEQFLNRSIQKLGEINIGMDLGNBSVLSALIQCCNOSKNGSNGLA*YNSFDTPPHV
4314	18215	A	4339	363	1	RQSSSLKSPKXKISVFAKQGVPAQTSDT*GVQPSNG*RWGASTATQKKPSTSIATESLKLTPDKPLAQCAVVDLHADDSRISEDETERNGDDKTHDKGLKICRTVVRRYSINEV
4315	18216	A	4340	1	353	DVFLDTLARPLRHSNFFLCYLL*DFPKFIPQPFYWMFYFDYIFISRNFPYLLLTHFFFLPLFLVIRIQLHLFFSFFFFFGKGNPFLPPGNRAKQFVWNGSPLELVNALLP
4316	18217	A	4341	376	3	LELRGGFLPHTADEVREERSPALDDRAGRCQGGPRQVCLTPKSNLFLAPHM*TECHLCQCFSTSL*PIEIRTLH*DGCVCMAYVCICVHMCMAYICICVARMAKRPLESIHSTCT
4317	18218	A	4342	158	2	LAFFFFCETQSCCQNHDLSSLQLPLQRFRA*FCSLSLSPSSNDKXHTSPHPTCI
4318	18219	A	4343	145	2	TFQEQWFDYRKFFSFP*DFGASLTQAVHYVPM*SVTPCHDPRV
4319	18220	A	4344	1	434	ESLIFRATAYEYRYTCADLKLPAKRSKSLQGLPKWDYRIHPPLCARFTFQWITFAYKLR*KHYKSRQSLPSRSGSC*CACDTFVSDPSHWGTMAQTLGGNITLQVQVORSC1ADQPLPLPLPPTLAPCL*NDVLLFFFQSQ
4320	18221	A	4345	4	475	KHSCRSLEHLDRPLFPALQETCPVRAPL LLVRINASGGLILRMGAINRCLKHP1ARDTPVCLLAVLGEHQSGKFLNLHLQGLPGLVRAGRGRREAGSKDGGSCGLGASGIPVQGDKEPTN*CSFSPPLQESGEGGRPRGGEASLQGCRRANG
4321	18222	A	4346	313	442	DSTLNFFFFF*TESYVAQAQVQGHNLS1LKPPPPGFKRFSCL
4322	18223	A	4347	437	338	ARVQEFYGDYIAVNPPLFSINTLGCCQG RNDPDAQLSKITQGLTALLSLKKCPMI1RQLSSEAKELACVQVITKEYELPEFRHTYVPELLLLDRCDAITLLRNQWTVQNMVHLLGINNRDLSEVPCCHRPL*RIHEGTILERSIRLLEMPSSSNTWA
4323	18224	A	4348	409	118	GLHDASFVAALPSTQVYVFFFEEDASEFDFFERLHITSRVARVCNDVGGKLLQKKWTFPLKAQLLCTQPGQLPFWNIRHALLPADSPAPTAPHIYAVFTSQN*AAQPSGGRNSTSAAAFRRPRISCRLL
4324	18225	A	4349	2	418	YTLDPFPHIPLHSLHRCLOSRTASTYQSPGACTPISQIHQGRSPSCSSSNPAC



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						*SSSSCOSTGFRCPGSAHPGCCSVL*MG GR*RSSQAPRASPIAQCPRASAPAGRAGH PALPSPLP*GAPFPFSAASSPGL*SPA
4325	18226	A	4350	401	276	DPLNVGGGGYS*PRLCHCSEPTWVTEDL VSKNTHTNKKHL
4326	18227	A	4351	446	277	AQDFVLKIDGIVIGICFRMPFSPQGFTE IVFCAVT*NEQVKVSAAPRPQPOSTAHS
4327	18228	A	4352	408	3	PKSSLPTRSPNGKSKSTKRPAISLAYSN ENAAQSWNGDQADAGPLLVERPRDYSTEL SVTLAVGASLLFLNVLAFALYSRKDTR RQ*PLQLSPHIGIGASLEHAPQ*BLP ALLLPPIREHCEAGPHTDLPV
4328	18229	A	4353	62	280	VRIGCLTSVEKASSQCLPT*PGCC*PLG TLPCKSRRTKSPSRSRRTQSRSPKTY SPGRRRRSRSRSPPTTP
4329	18230	A	4354	364	3	PVGREGKSLVPKSPVEEKKS PVSQSPV EKAQYRVPKSPVEEAKSKAEVGKQDQK EE*EKEVPQAPKEDKVEKKEEKPHGVPE KKKAEVPVKEEAVAEVVTIAKSVKQLE KETNEECI
4330	18231	A	4355	3	558	LQPTLLWRRCQKVPKANSPLPTSLRRTL RASPGSPRGPLFMQAGSTPMTLPRSTP SMS PML*MMWPPTAVPVP*KPLMMAPEA PIVLLVITLITEIQEPATPAPLTQF*KPT SLMVSRPVPVVOGERTTRSTLCATTIA PSHATLAPGLSTTTSPMLWTLSLLBGO ASLPKG*NTSITLPSVS
4331	18232	A	4357	258	1	LQFHDGPGAGWSQPHGGRSAQAQ*PPQP PTVPRTSLADVSDAPLPQCHSRPQHHP FELHITSFSTPGLSAVCLIVHPAARVSR CI
4332	18233	A	4358	97	343	DRDLGDEYGMKQVHGDFRPS SHPLIFS SLIGSGCQIPAVSLIIVIAMIEHLYTE *VPTLNCIMSLFLNLSFNHNLQS
4333	18234	A	4359	182	2	KDYPGSSVENGGEEELKEDQLGQYSVI *ARDDDEDDDDDDDEDEDDDEDD DDCI
4334	18235	A	4360	88	2	RGSRTDTG*RGSDRGTG*RGSHTGIR*R GSRDTGTG*RGSRDTGTGGRSRTGTGGRG SRTGTGGV
4335	18236	A	4361	2	250	ELRDEGRASSAQRIKACGLQGFGERAF KAWAVARLSQRFPKAEFAEVS KLVTDLT KVHTECHGDLPGCDREASAGLAKYIM
4336	18237	A	4362	169	456	EQLLCAGQGLSCPEHLHLPSCPVGPPTP AHRPGRMAPGPSFLSPGSPCGGLAIP CSCQFWAGVFDHHLFSPPMGRAGLSPS ERSAGEGVIWPP
4337	18238	A	4363	1	419	PEFKLQKLRSSQNSAFLDIGDENEIQLS KSDVLSFTLEIVIMEVQGLKSVAPNRI VVCNMEVGRKELQTDCAEASRQWGTG DPTTTHPRPVVKYKLFITSTGTGLALEDK KLGRVILYPTSNSSKSAELHAKVVPKN
4338	18239	A	4364	375	448	PGAVAHACNPSTLGGRSGRIMRAG
4339	18240	A	4365	1	444	DPLTNHYHLPLTAGSLTGLGTAVQLY SAYKENNRITFLAAVKRNHNQYVNP SGV ATTFESIKRILLRQSGVKVSVVDHDSCV HGPCQNGRSCLRLAVSVLKSRESLPV IIVANEPLQPFCKCLPGYSDSWCEIDI

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						SETPQNNVGIM
4354	18255	A	4380	214	410	LDRLPHTPSPGTGEIEVKWPEAVQTGLPW CILGAFFGPRLGAQSLQ/LDS ELIPKA VQNGRIAPC
4355	18256	A	4381	2	74	IGDSGVGRSNLLSRLTRNKNPLGL
4356	18257	A	4382	290	119	IATVSLNIVRMPRLPRATYRFPNAIPFKI PMTFFTEIDRTILKQWNNKILPGNSPA H
4357	18258	A	4383	2	423	LERVCWIKDIIVAVTGENEMVYKSIQK YQHKRISLVEAGVTRHRSIFNQLKALAE DQINSKLSKPEVVIIDAVRPFVBEQVL LKVTPNAKEHGAGAAIKPLVSVTVSPSA DGLDYSLEAKHARASBNQAFDFVY
4358	18259	A	4384	356	1	WYPCCLASLCLVFRGLFELSCLVFRV VPVLCIQFPGSLGLSLLPSLLRQQLAL WPRLECSAIRAHCSLELGSNDSPASAS QSAGITGMSQCWPLSLLSVSPRPVGLS SVPLIF
4359	18260	A	4385	1	125	SGSKTKLRSLSLEPTTILDIKPHRESFF YTHLINFSGKRYC
4360	18261	A	4386	53	215	WQLYWTWCQKISRNQGLAHVPRNECSS MIIAHCKNLKLGSSDPPASASQIDPS
4361	18262	A	4387	2	390	PSLAARVLRAGYGNFVFFVLMKRNDRM HGECAFNVSVAVSTSHTTIGGGIRGGG GGYGGGGSYGGGGSYGGGGGGGGR GGYGGGGNYGGGCGSGHGGSYCGSSS GGYRRGGGGGCGSCNSGG
4362	18263	A	4388	2	441	IKTRISVTHKEEFGLTPIEGAYEDMKK TLQLAFAINQEPSSDAKMLQVLRGSGEA TVNQGPLEVAQVFLAELPADPKLYRSHN KGLCLNFPIMKCGAENKRLITVDQ MEYQQLKKNYNKLENLRPMIERKPIE LVKPIF
4363	18264	A	4390	242	24	KLINFLLGGCVKESPPVPGGNCWPDGFS LQHPPSRFKQFSCPTLPQNNFENAVPLR SGKFFFSPVFLVETGY
4364	18265	A	4391	1	244	VDQMQRNLFTFGAHLQCANQFQFDI ARTEYLSNADERLRWCASSLPADDLCE DAIMLKRFTRYELQCGGEAWEBCOW
4365	18266	A	4392	2	146	LDLLSQPCRAVYIFAKKNDIPFELRVD LIKGRSSLGFGEPKSGQEDR
4366	18267	A	4393	204	489	GAASEHPIPROESHGTSRASSLCADAGP AGHFASVYNPLAWTVITVILTVGPGV RVTEAGHPVPSQVSGICRCLQGMKAPP VTIVSGEKG
4367	18268	A	4394	2	171	LSDFQFPRSIIIFASVAGQFGSVGATE WLEVFIIIPSHIGHELVLGCCPVMFL
4368	18269	A	4395	2	197	WLELLKFTYTLDCAREYVICVRIQDILT RNNNNPKRRIATIGEMICCSIFVEYFI CATHYLQ
4369	18270	A	4396	2	285	TVDFPPOPKQCOQYNTKVLKCLQKVN GILESPTTGKTLCLCTITLANRHLRD GISARKIAERAGQELFPDRALSSWGNAA AAAGDPGPS
4370	18271	A	4397	366	461	TSNFSCLVLEERASDYLEDITIKNLVK KYSQ
4371	18272	A	4399	157	3	DVLRRNFARSAYLFLFTRVTLQNAFRL ECSGAIIAHCSKLLGSDNPPTS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, /possible nucleotide insertion)
4372	18273	A	4400	2	343	DDIDFKYHDFSSVFNPNELVALYGGSSIQ RQTKFFVHECIKTLKLYRQGFAPKSVIA IIGHGWSGLVARALLTKRNFKDLINLL ITQATPHVAVPMPLDRFTPTSGWGLKDH G
4373	18274	A	4401	214	430	ELGHNLTNVVMEBAEALSNKWFNGQAV HGEISPVPTDFRESCCRQVMEGCTRGGF CNFMHLEPISONLQRO
4374	18275	A	4402	3	227	LTQVSPQTHAGINTAQKSKMKNVLEK KHFOYFLPNRGLSLRVRMRGNGPRGLPLF FLLSPRATHAKRQISF
4375	18276	A	4403	158	313	NRDEFCHVACVGLLELGSSSPPAATVQS ACITGVSYHVRPTLSNKRGCSSL
4376	18277	A	4404	3	628	HCIREGGQGVPSNKDVITSLDWNSEGTL ATGSYDGFARIMTKDGNLASTLGQRGP IFALKMWNKGNFIISAGVDKTTIIMDAH TGEAKQKQFFPHSAPALDDVMQSNITFAS CSTDMCLIVCHLGGDRPIKTPQGHITNEV NAIKWDPQTNLASCSDDMTLKINMSRQ DVCVHDLQAKKEIYTTIKWSPFGQPTN PNANLMSLASL
4377	18278	A	4405	35	180	NCVDYHYFFCLLQPNMNNPQSAVETPT QTNGSNVPPKPKRGREFFSGK
4378	18279	A	4406	1	438	DFORPDEHDGVDEWEKVLITDCSNLQ DQTYILYLIVLVKPGSWITNLGQQNGVT VQNTLLGELYGKTGLNQEWGLLPYISLFL RKKVDVLAEAKTDLSDQKQSLTVGLSE PREKIIVAPLPRKELTKLIVASGGDII IGVLTV
4379	18280	A	4407	1	428	TESVNAZFKGADPTKCIKVTGDMTMSF PSGIIKVFPTSNPTPAVLCFRVRKISRLE QILPNAQLVFSDFPSQCSDNITCDFWMNQ AVTVYLLKLSEQNPASYSNVDVLKYQV SLNGIQSTPLNLATYNKCSASTDLRDV YK
4380	18281	A	4408	174	383	KSNMFGAVAHACNPSTLGGKGRQITRSL YRDHPVQHQEIPLYLKLTALAVTLFGLL TGLHDLVLTNLT
4381	18282	A	4409	1	288	LMAEKSDLPSTTHAVOLLTAGKNGSRV PLGRPLPGMSGPGFVPLASRPLGTFAV GSSGLILIFGSLDSTFPQPRVGRGIRSR LQWRPEGFPAIP
4382	18283	A	4410	292	422	LWISSCFQVSSKILELARKQRQWNTDIR NIFCTIMTSEDFLDA
4383	18284	A	4411	412	238	FFSRHRVSONDQGLLELTLTSLDALAS HSAETGLNCHHAQPLITNPNKYCISLQ VH
4384	18285	A	4412	1	405	VTSSDKSLLVLLDAEDKVFVNEIRNEHFS NVFGLSKOKANLQAYDRRRGMIDIKM KNFVSGLEKLQREHRLLSLHGAGCESI MKKTKDQFQELIKTEHALLBEPNIRE TSYIRHLDHQVSDLESLALACL
4385	18286	A	4414	2	149	GHVHWQAGLEVLTASDRVLVASQSQAGI TVGSHCAQLRSDPKFKRSSPA
4386	18287	A	4415	1	366	DTCHIRKLVKCPSSHASTNRLVQVQVSSI TASIRPEGLPNVDLIEFQTNLVPYRHR PFMTAPAPIVSADAKYHDEQFSVSDITTA CFESSNQLVKCDPRGLKGYACCLLYRG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Value, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
4387	18288	A	4416	1	164	VVPKEVNAAI RRRCMSSTFADTLILVPTISVCTALLAE GITWVLVYRTDPFTGLAGEGPGGRY
4388	18289	A	4417	2	141	DIATPCNNKGAIHVGIMVWMLAREVIRM RGTISREHPWDLTSSVMG
4389	18290	A	4418	136	1	EQTAKFQQLKVLGMDPLSKMPPKAPKN ENPVDYITVQI PPKDPMQ
4390	18291	A	4419	1	280	GNVCKYTYGYRPSCEGRRLRVLPKPNFR GRDVLVYLCNVGHILTSIACKGPPSRKV GLDIDSLRIHSARQNRIRHTLSEELRLLP QTLRGDPGA
4391	18292	A	4420	3	446	TVTSQVRQNYHRDSQAATNRQISIELY ASYVYLSMPYYFDRDDVALKNFARYFLH QSHEDRDADKMLCKNQRRGRSLLQDM RKPCDDWESALANVWALHLDKNVNGA LLRLHLKLLTDDNDPDLSDYIETHYLNQ VTAINELG
4392	18293	A	4421	6	182	DPSFCSEPRSCHCTPTWRTQDSTSEKK KKRNILKNNAKNYITLESSEKRSKQRS RR
4393	18294	A	4422	1	456	GPISYVVMPPKRRQALVFEDVLAGCNA VNYAADNQIYIAGHPAFVNYSTSQKISR LGDSDSRSVNSVLLFTILNPIYSITTD VLYTICNPGPVQRIVIPRKGQVQANVE FDSVQSAQRAKASINGADIYSGCCTLKI EYAKDTRLNGSK
4394	18295	A	4423	2	257	FHHVGAQGLKLLISVDPPALDSQSAEIT GVSHCAQPVLCILANQICAKAVLSPDSHP YPPKSGRHEGQVRBQIGSPCSYIYFKRT V
4395	18296	A	4424	106	259	CCCFKYFFSNKICPYRDLKPENILINE DMHQITDPTAKVLSPSKQGV
4396	18297	A	4425	3	364	WETKQITQVERQDPSCEPLRSRELLDE KEPEVLQDSLDRCYSTPSSGYLEPLDQ PYSSAVYSLEEQYIGLALNDSEYLVTK VISIHLVPOIGVIFLPQVPLTDPRDVIA AGRTYGR
4397	18298	A	4426	2	241	HHVWLTCFVFFVCTVGTGCHVAQVGLER IGSSDLPTSVLSAGITDVNNHAQSKPS PSKGTGMNRPGLRVGKGVWSRL
4398	18299	A	4427	2	438	TRLIGPNCFVGMNPGCKRMGIMPGHIN KGRIGIVSRSGTILTYEAVHQTTQVGLGQ SLCVGIGGDPFNGTDFIDCLEIFLND TEGIIILARIGGNAQENAAEFLKQINSS PNSKPVESFIAALTSSTGRKMGHAGQLL AEEKV
4399	18300	A	4428	34	427	AGMLPAVGSAADEEDPAEEDCPFLVPM TTHSEEEKSGLGAKIPVTII TGYLSAG KTTLLANYILTEGHSKRVAVILNEFGEGS ALEKSLAVSPGSELYERLELINAELCC SVKGLIALENLVQKSE
4400	18301	A	4429	330	8	YSDRI SHNI DWCPCKYITFGPVPHPHS TYLITAINLVAQNYENSHIDEKGA YQRKEKCCDDPMGAARIHPLCFPFMGFR SVSQAGVVPWHITSNQOPPRIK
4401	18302	A	4430	446	222	LTSSDPVSAFQSAQITGVSHRPPQPTWG VSIQLYFSGCPDTPQGRILTRHCDQD GEOGGPCSEVAQPCIDHNS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, -possible nucleotide insertion)
4402	18303	A	4431	3	243	AREDSADVFVFPPDFWWTLDLDFSLDL EQPLTGTGTSQKDNFILRLCIRKFTS LIRTSRSYQSDTVSVASSRGAR
4403	18304	A	4432	433	0	PPPSPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPSSSS
4404	18305	A	4433	25	185	ARWVACSELRLRCCTPAVATEPEPVFKK KKKVOQQGGVPGGLTPVSYRFGRLT
4405	18306	A	4434	2	329	VRDIEKELCYAVDFQEMATVEPSSSL EKS YELFDQGVITIGNERFRCPEALIQP SFLGMSQGMETTLNSIMKCDVIDRDL LXANTVLTGGTMMYGLADRMENEL
4406	18307	A	4435	2	374	WVTFISLLFLFSSGSEGGFRDHTSE VAHRKULPEKPAKALLAPAHYLEQC PFEDHVELLENVTEFAKTCVADESAEC DQSLHTLFGDTLCTVATLRETYGDMADC CAQQEPEPNEC
4407	18308	A	4436	2	352	KVRRIDSLAEIDRETRNPQTSQOLYS PSLFLGAFLLFFFGFFPPPYLLAPKN QFNPPPLCTGGVPVRKPPFPWPPEPRP APPLFSPQWDLGFQIAPFLWVINGGGPS GGRA
4408	18309	A	4437	2	369	QSCETLFHSWKDVEVCSSALSCLSQSV HIGGLSFLILPGMEVQRDSQMAVES LEYVREGISKAVADPTTNKTHLLTSQ GGNQMLDEGFRDPSQMEIATRAILCA IQNLEERKNE
4409	18310	A	4438	2	231	SDTSRQLPCBAARERFDGFLSLRPLP PFLSQVINEQIDHLLERKGLAIRDPD KGVVQGLSFHQWDAWVG
4410	18311	A	4439	1	365	MAHNMERVKKGLPKXEDICHEQFLEL SYLNGVPEPSRGRGVVRGRAPPPPP VPRGRGVGPPRNALVROTPVRGAITRGA TVTRGVPPPPPTVVRGAPAPRALVAMQR I PLSPPPATK
4411	18312	A	4440	92	510	LAALPDGGQELHPPSRAGPAGELSNV VGTGALSSLSILFGMARCRWPPPLRNS PLOGVIFNVVPLVAIPASLFSGLSDH LINQGYRAITVRKLMQGMGLGSVFLAL CLIGHTSSFCESVVPASISIGLQTNIR
4412	18313	A	4441	2	266	PDHPLPELGRKNECPWQDCSSAAVSF CEFSPHSPCKDHEKGLVPSALEGRGCC SEHDPMAVPSPEYWSKIKCKWESQDHGE EVKE
4413	18314	A	4442	2	279	KGAEVLFLPSNTRSLMTPLDQGVVTFK AHYAGYSMERIVSAMRENPGREKIMKKL LKLSG PGBI PAGEKLCFNDAMDPTLDD RVTHIRNE
4414	18315	A	4443	2	371	KVTFISLLFLFSSGSRGVPRDHTS EVAHRFDLGEENFKALVIAFAQYLOP NPFEHVELGNDVTESAKTCQADESDN CDKSLHTLFGDTLCTVATLRETYGEMAD CCSQPEPCEK
4415	18316	A	4444	2	372	WVTFISLLFLFSSGSRGVPRDHTS VAHRFDLGEENFKALVIAFAQYLOQ SPEDEVKLMNEVTEFAKTCVADSSDDC DKSLHTLFGDTLCTVATLRETYGEMADC CAQQEPEPNEC

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y-Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, = possible nucleotide insertion)
4433	18334	A	4463	1	338	SRHS DGT P Q P D C S L R T G R S V Q S V D T S S C S Q L S S S S G S S S S V A P A G T W L Q A S Q C S L T K A C R Q P P I V F L P K L V Y D M V E S T D S S G L P K A S L L P S P S V N W A S S F P L L S K
4434	18335	A	4464	2	343	I I D F P L G A Y L K D E V L K I M P V C Q K T R A Q R T R F K A P V A I G D Y N G H V G L G V K C S K E V A T A I R G A I I L A K L S I V P V R G Y W G N K I G K P H T V P C K V T G R G S V L V R L I P A P R G T G I V S
4435	18336	A	4465	1	371	I N S T L K M S F V C H S G S V I G M S D W E K D E P Q C C L E R I F F A L A S S L S S A S A K S P S L L Y G S K G E P C L Y C D K D I G G S P S L Q L K E K I M K L A A Q K S A R R P P I P R A Q V G S W N M L E S A A H P Q W F I C
4436	18337	A	4466	246	12	L C P T P L F S V I L F P F F T K S S A S P K L E C S G V I T A T S E V I L L G G G G C S E L R S C Y C T P T W V T K L D S I T K K R K R K K D L Y
4437	18338	A	4467	2	355	W V T F I S L L F L F S S A Y S I G V F R I A D T S E V A H R F K D L G E E F K A L A L I A F A Q L Y Q C P F E D H V K I A N E V T E F A C T V A D E S A E N C D K S L H T L A F G D K L C T V A L R E T Y G E M A D C C A K Q R P
4438	18339	A	4468	2	361	E D H V K L V N E V T E F G K T C V A D E S A E N C D K S L H T L F G D K L C S V A T I R M Y G E M A D C C A K H E P E R N E C F L Q K D D N P A L P R L V R P E V D E M C T A F H D T D E T F L K K Y L Y E I A R R H Y F Y A P E L L L
4439	18340	A	4469	1	373	S S Q F S P S E E V S G T V S V S F S S L P S S F C L S L S V C L L A C V S L S M F S L P V C L S V F L C V S P R P H S V S H A N P H R A S A L V N C P W P A P T S A P V S F Y K P Q S P A L K T Q A S P H P H P F P T S P M Q S Q K K
4440	18341	A	4470	236	371	K V L G A V L K E K G G L F C F V F G D R V S L C H P G W S A V V S Q L T A A V T S Q A
4441	18342	A	4471	345	201	A M T A L H F W A M F T F Y F F S T A Q K K K V F K T L L L I D N F D P L M D S K G K L
4442	18343	A	4472	1	144	A G F H R V G E A G L L G L T S R D F A S F C K R A G I T G L N H H T W P F S V I L Y T Y Y
4443	18344	A	4473	3	333	K N I L E A S T G E R P F P F D S F S C P H L L S S N Y H S L C P L G G F S E T G S A P S P R L E C S G V I A A H C S L K L G S T S P L T S A S W V A G I T G M C W L Y S P A V S P R S P D L T C T S Q L E N I
4444	18345	A	4474	288	1	T S A V H R I S T K S Q A D Q A T E Q K L R D Y S H Q G I Q I L A W Q F K Y K P G R V I M D P E D C I L Q L A K K K K E Q E E E E E E E E E
4445	18346	A	4475	3	124	P R L E C S G M I A H C S L D L L D S S D P P T L A S Q V A G T T K I S L H
4446	18347	A	4476	196	2	S C Y E H P R I V Y G L F L R Q D L A V T Q A G V P W H D H S L Q P L P P E L K R P S G T S H L L S S Q S Y R R A Q P R R
4447	18348	A	4477	3	162	L I E R N K K E L G S L Q Q M Y S T I R E Q V Q E I E V R A L H V L A H T P R G P I L G L C V I C N L E
4448	18349	A	4478	167	2	A C G I S P F S L S S S C F G V R H A S L P L A P H I D C G F P R A S P A M L P V Q S P Q L N L F I K Y P V
4449	18350	A	4479	195	26	W V S M L D I H D G P H E V A V I C P V C F L S Q S L A L L P R L E C S G V I S A H C N L Q P G R O S O T P S
4450	18351	A	4480	175	1	N R S A T K C D W G E K R T S Q E L N L F P W F T V C L



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
						FMESHSSVAQAGVQWNNPGSLKPLFPFRKR
4451	18352	A	4481	122	357	YHAFLYQWYNLAKREKRPRCSLLIIPLG GERKLQSIQLWNISHYIQRVYVLSIPS GLGVAHAACNPSTLGGQGWIT
4452	18353	A	4482	137	2	FYSYLKILRRMGPHVVPQAGLELLGSRD PPDSAYQSTRILGMSHH
4453	18354	A	4483	347	208	GQAGLETLTSSLPASASQSGAGITGAGHH TRPRIYFLKKYLAFLVGS
4454	18355	A	4484	411	268	RLNRRGGGCSSEPRSCRCTPAMATQNSI SKNQOQKTKLPCLCRILL
4455	18356	A	4485	2	102	PCLRLMOQLAGHGGHLLCSQLLERLRCF LHSVF
4456	18357	A	4486	1	113	HSAMTDLGHAGHTSLFKCWDYKSEFPR LAKFLNTY
4457	18358	A	4487	163	353	QVAATLNNLAVLYGKRGKYKSAEPLCKR ALREIKVKQKKGAVVFEIFVLCVQGF FFFKRDP
4458	18359	A	4488	408	307	RGCSSEPRSHDCSAWILTERDSVSKNN KSPKKQ
4459	18360	A	4489	337	179	YGINFALILIFLPLVGLVWAAIINHYR LHQLNNKLLIMIMWVSPRLSCG
4460	18361	A	4490	229	345	LENBTLGRARWLPVPVPLWBAEASRSR GQETILWNN
4461	18362	A	4491	180	365	ENNLKTLVALDMSFYFILFLFYPTLPFF ILFYFLRWSFALVAQAGVQWRYLGSQP LPPRFK
4462	18363	A	4492	269	385	GNLQNLKRVFYKIQHPMILKLNKLVID RTYLNIIKAY
4463	18364	A	4493	103	336	QLLVSLINLFLQAFKLQIDCGHTCMHPW RQNLCLLPPTLPTPRNLTLSPLSCSG TIWAHRKRLPLGSHHSPASATR
4464	18365	A	4494	305	379	YKIBNFCLGVAITCNSTLGGG
4465	18366	A	4495	47	224	ETATKTRRRMETALVQEPHPLAPVIV VETGTNSTIANFLILVYLSFLFLVYSC IQO
4466	18367	A	4496	3	129	YPLNPGGRGCSRLRSCHCTPAMATERDS VSKKKKKFPPPP
4467	18368	A	4497	396	112	LPLEPEAAVSHDCSEFLQLGTQSKTFL QKKINRIINNNSHSAISLLGIYPKEF KAGTORDICTPMITSLPTIVKROQPK CLATNELVYRM
4468	18369	A	4498	1	152	LSLPGSQTWARALIVATWAEAVQGSPE PRRSLQVAMITPLHSSCGRRG
4469	18370	A	4499	92	2	KRPGVVTHACNFTLGGRGGETTKSVVR DQ
4470	18371	A	4500	116	1	AGTAGNCLHAQITFLYFIVTRFCHLQ AGLRMLTWS
4471	18372	A	4501	99	1	QGTPEVRHWKCKLQVPLWRIVNSPIRV KIDNS
4472	18373	A	4502	140	288	RQPHYVAQAGLELLGFSNLPAITSQSAG ITGASHINQITSRFLKSKKIG
4473	18374	A	4503	330	181	FFFFFFFFFFFFFFFFFXFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFF
4474	18375	A	4504	171	2	VETVSKSSRLICLQIDIRYFFETKQHS LAQAQVQNHVQGSLLQPELRLLQSSRLS
4475	18376	A	4505	345	74	SVERTCHSPKPLMLPLFLVQARDILN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, -possible nucleotide insertion)
						GSHPVSFEKACEFGGPOAIOFGDPHEH KHKPGFLEACHFYQTASAPASALTDFPA SRTVQK
4476	18377	A	4506	258	102	KNIRELWPGAVAHACNPSTPGGRWAT RSGDWLNLRTCEHVLQKQKFRFLIS
4477	18378	A	4507	1	67	GLPKCWDYREPPHARNCRYF
4478	18379	A	4508	339	180	ANFPVPFPEENGFRVAGTGLEVLGSSDL PILASKAGITGISYVRPQTNT
4479	18380	A	4509	174	3	NEPKVVIYITPGDPLFFLLFFETESH YVQAGVQWHDLSLOLPLERLQRFSCV
4480	18381	A	4510	84	3	ARHIFTVGIDVTRAYFSAITIIIAI
4481	18382	A	4511	127	2	LLIKIHQWPGVVAHACNPSTLGVRGRI TRSGVQDQPBQY
4482	18383	A	4512	109	345	EITLIQHIESSCLCFLEGSFNCVATGF PHVTWLLITLSNLPTSSYSRAGITGVSH HARANLFCGSGNSGHTGOLF
4483	18384	A	4513	290	13	EDLNPITQKSGPKRHITAIPLQRAQTHVK KGRGPTPTPTPSKDGPHPLPKPKPW GRVWGKXKKKKNKGPKDKKXKKKKKKE RKIQHSRF
4484	18385	A	4514	234	362	DGDVLSKFNVPNFSFKVVEGTPILDGRL KYRLNGDFLFLRLKL
4485	18386	A	4515	190	330	CLALQSECFRRNSFALLAAGAVQWRDLS SQPLPVPVFKRFSLHFFE
4486	18387	A	4516	2	199	LCVCVCVCVCVCVCIFFFFLSKKNGFPPL CPGGPKTLGPKESPPLAPKNRNGNSGLT PPPPPTFFF
4487	18388	A	4517	94	339	SAYLGLKFFLEFFFFFFFFFFGVFPFFF FPNKKLKPQPIFPQKRPPTFFFPFP PGGKNTFFFGKFFFPNPRSGPKNKL
4488	18389	A	4518	95	3	LYLGPGAVAHACNPSTLGGRGQITRSG VQ
4489	18390	A	4519	14	121	LIFPGRNRISLCCFVNSQTGLKPSWSL SLPKCS
4490	18391	A	4520	207	2	ISREKLCVRIIPDMHVEDSILFYLYF SLAPPLPRLCNGSTMAHCSLHLPSSNPF PASASQVAGTTS
4491	18392	A	4521	169	1	ANLTQVGSYSYLSLHLLIQITFFNNIRA VRPGTVAHANPRTLGGDGMITRSGDR
4492	18393	A	4522	2	82	GFILVCVCVCVCVCVCILVITFF
4493	18394	A	4523	300	3	LPLFPSPLEQITPQSGKDLPLTFPPRVP KKFIPENFWAPLISREFWVRFLGPT QGFNYPLGPGPPPPPSLGLPKSPNPF FIKKKFSPPKKQK
4494	18395	A	4524	348	94	KVGGGKGPQNPFGGLKGNPINPGG GSPEPNFPWPPPRGAKKTRPQKKKKK KKGKESRLNYQMKRMRKEKVFLSAL N
4495	18396	A	4525	313	161	RGHPNLKSKEVNRREAPGHPRNRKK TPNLKKKKKKKKKKKQKQKQK
4496	18397	A	4526	118	3	FFFFLRRGSFALVAGAVVWRYSLSLQAL PPGFRFSCP
4497	18398	A	4527	153	2	KDAINKKQWPGVVAHANPSTLGGQGG WITRSAGQDQPSHYGETS LPK
4498	18399	A	4528	258	2	GGQKRLPGFKKPPFRKCLFLNKLGGP GKNSLSKFFFFFPETESHCLTQARVON LNTSSQKKKPPRFKQFLCLNHPSSWYR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of nucleotide sequence	M eth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end-nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /==possible nucleotide deletion, \==possible nucleotide insertion)
4519	18420	A	4549	2	340	LNPGSAGCRELRSHCTPAWTTTGRGSVS KKKKKKKKKKKKKKKKKKKTTFGGGLPW EREFLLGNFWKKGGGQANFFPLENPNGP QLKTWGNKAFPPRKGGLNPPQGFYQG A
4520	18421	A	4550	165	335	PHYLPRRSI IHRPFKSHSPPEGVAHAH NPSTLQGRGGWITSQQEFETSLINMEKS L
4521	18422	A	4551	123	3	GRVDRLSCLSLNSWDYGHLPGLHANFC IFSRRDGVLSW
4522	18423	A	4552	3	131	HPEVDIFLLPGLGISDGIAYYSIGSEF PGYVMDVSDPFI
4523	18424	A	4553	87	364	ILASQSVVRYVAKASAGGLLETSSQPS AAGTASAAVPSLEAQTAAFPPTPPGLA PSSPPAPGPPAPTGVCGRHFRLSSESA SGPLRALI
4524	18425	A	4554	114	0	LTWAPHSLIETIRNQTIIQALLITILLGL YFTLLQRESE
4525	18426	A	4555	91	3	TITTYTIAIATACVVCVCVACVPCVCVC M
4526	18427	A	4556	239	364	CIKITFSRPGAVVHACNPSLTGGQGGRI AMSRDRDHGQGGK
4527	18428	A	4557	250	1	STEHVQQLRNEFMKISVILI FLETLIYI KVHLKLCITLTDHLLGKSLKILFRPG AVAHACNPSLTGGRGGRIPRSGDRHDS
4528	18429	A	4558	2	90	QDGLDLLTWGSACLSPKCMNDYRSEPSL F
4529	18430	A	4559	65	394	DPVSKKKKKKKKIKQREKKKFPGKKKPL KKKLADLI LKPKKINFLKREWKIKREK GGDPFWKPKQVQKTKGNLNLGQNLGK GQSDLKAKNTPETKLNLVQKKFQIFF
4530	18431	A	4560	93	2	GIISAHCNCLPGSEDSPASASQVAGIT GQ
4531	18432	A	4561	125	4	GAYILYANKRSIRPGVAHACNLSYTL GGROGRITRSGD
4532	18433	A	4562	3	84	RSCHTPTAKATERETLSPKKKKKQNF
4533	18434	A	4563	145	3	GFYHVVPGGVEQSPCLSPKYNNYHCEP PPLASIGIFFFFFFTQSR
4534	18435	A	4564	125	388	IRKPOILYSPOSSENNQHLISVLMGVT GKRGKFMWLDIVTERCRFSLLKCTGTQCE DLNKWEGIPCLWIIRLNTVMKAVFSKLI CRFS
4535	18436	A	4565	59	325	VARKGNDVSLFVPIYPLPDIEEVIEPLW VLIGSFDGEGKVELEFFFFFPKKKSPF VTQAEQWPNLSSLPQPPRLQKQFFCLG LLIT
4536	18437	A	4566	326	3	PEKEFRRLVTKLIREAPERKEBAQCETIQ KSIQEVKGIKPKEDIRIKKQLKHQETL DILLVMQNALESLSNRIEQVEERNSELE DKVFDLTQSNKDAKIRIKRYEQS
4537	18438	A	4567	333	209	RQAFDPYGTLSQGISPKFHEPFHKILMA RPAVALPPOVNLK
4538	18439	A	4568	125	2	HNQSNRSITDSDPILGHCNCLPGSSD SPASASQVAGITG
4539	18440	A	4569	212	2	PICLSGKKCYGQNVVYKICIMNKINIRL GVVVHACNPSNLVQGGQPRMRSGVLBQH EQHARTPSLJKTLK
4540	18441	A	4570	142	14	GRVDRSNPGRFLSTSNSSLYRPRPEIRP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
						TSQAPSVPVNHILIST
4541	18442	A	4571	2	419	ARDSFLHDSOTSFCPSDSIPTPSNMERT QKSNLLELLRLISLLLTIESRLSPVYLR MFANNLVHDTSDSDYHLLKDLERGIQT LMGRRLDGSRRITGQLKQTYSKCDTNSH NHDALLTNYGLLYCFKRDMDKVETFLR
4542	18443	A	4572	3	194	HGRRLQSOLLRLRLQKNCLNTGGGGTSE PRSHHSFPAMVTEHGFISQISLKLPLFIS HPEPFLL
4543	18444	A	4573	2	286	CRDGLTYNDPLILPGYIDPTADHVDLTS ALTKRITLTKTFLVYSMDTIVTEAVMALA MALTGCHGFHINCTPEFHANEVRKVNK YEQGFITDPTV
4544	18445	A	4574	44	325	ROWLQREAVITKEQKYSFLHDSOTSLCF SDSIPTPSNMERTQKSNLELLHLSLLL IESRLSPVYLRITFTNNLVYDTSDDSD YHLLQDLEEG
4545	18446	A	4575	374	33	LRLARRSGASLGSRSGGPPTCANICPR YAPLIPPCRTSLLEAQLVMVVGPDPRV RLVTSRRRRFRYQPPFPFGRNFFCLSLP SNWDYRHAPPLANFNSLFFFFFLVBTG Y
4546	18447	A	4576	400	225	PIFFVVFFLEVLVLVETRLCHVVQAGLE LLGSSNLPISASQSAKITGMSHPAMPRA EF
4547	18448	A	4577	2	372	ARETIFCFSSNIPAPWNMDETRQKSNLQ LLRISLILLYRTRTLPCITQLHILQT YKVNARCSEHPSHSSSTCOPLYSCTLYVSL TGLDMKLCHSTLLKQNSALNSLLKIQVN LNQVSPVNDH
4548	18449	A	4578	349	174	GCCEFRSHHCTPAWATRAKRLKRLKLL QLKNVVKESKHQPLQNPSELHSTINTQ EN
4549	18450	A	4579	3	124	HELLNPEGEHCSEPRSCHCTLAWVTRAR LRLKKKKKKKKK
4550	18451	A	4580	181	1	MSSYYFSPCSRLLMATVYNLHLPSSNS PASASQVAGNAGARHYAKLIFVLVBTG LCS C
4551	18452	A	4581	227	3	HRKENRCVSRITALLFSLGDGVSPCLKIT IIIKVFLNLEGEVAHACSPLSGSRGRI TRSGVRDQPGQHETPSC
4552	18453	A	4582	257	2	RVRQLGAFSLPSGSGSFSLKLNGLKMG PPRAGPVGSPRYSRPLGGPGQRI PRSGD PGPPPLPRGNVPVLKNPKRSLLLIPAR A
4553	18454	A	4583	3	94	HETMAFLITERTKITGYIQLRGKPVV GP
4554	18455	A	4584	345	50	IYIYICIFLAPNRVSLHCPGWSKTPGLK QSSHLQLPKCMYDSHEPLCPAKTSHFKA QDRIPKNDPSCPTSPAQHSTNLIQWASS YLQYSYPAPVYNNH
4555	18456	A	4585	338	19	QLSHRFRFPKNGNPGSGACSEPLRQPC PSANVTKRDSVSKKKKYHTLSGLSTTG ITYFSQFWMLGVQGSAPGVNGGAVSWSI DGAVLLRPHMAEGARQLSGLGF
4556	18457	A	4586	2	224	ARGVGRAGLELQTSQDPASASRGAGIT GVSHRVQLGDRAKFSLKKKKRGIILPG EPYSPKKRPTLNTPDNP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to last amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, -possible nucleotide insertion)
4557	18458	A	4587	344	168	PPGTVVHTYNPSTLGGQGRIGSLGVQD KPGQHRQGLSLGVEDKPGQHSITP SVQS NP
4558	18459	A	4588	212	328	GLAVAQAQAGLELLSSSNPPASASQASGITT GVSHRTQPYF
4559	18460	A	4589	110	323	LSNQKQNLNPNLLTYCVVRKLKSSYDK QAEVQGSKLGSIALPHGFTPLSGINLP SSWEYTRPPRPRTNF
4560	18461	A	4590	2	127	ARGCSSEPRSRHCTPAWATBOVSKKKKKG REKTTPGQFFFWIT
4561	18462	A	4591	211	2	ARGSLAQSSTPAWATTNOSTNKKTKDT ALPWKMPSTTYARQKMPGFKSSKDR LELLGAKVSCIV
4562	18463	A	4592	3	120	HEKTKKNPDKKAKOMNRQSKEDNDN KTNQWPGAVP
4563	18464	A	4593	388	227	GHVGGDGLRLTSDAPSLASQSGATTG VSHRAQPKWLLFOHRSPCLPEAAGK
4564	18465	A	4594	1	348	PPPPPPPPPPPPPPPPPPPPPPPPPPPP PLPPPPPPPPPPPPSSSSPPNPATTSVA C
4565	18466	A	4595	2	138	ARAARGFRHVGQAGLELLTSGDPPASAS RSAGITGVSHRTQPTNF
4566	18467	A	4596	315	2	ALKNYSSTSNNTKARLPQVNNINNLIA PLYSSTSNQINIIIVILINKENNHTLFF CIWNSRLKQSSHLGLPKWDYRRELLC LACDKFFTSYSAPATQLLSC
4567	18468	A	4597	1	146	GTSVDQGSLELLTSGDPPASASQASBIT GVSHRTQPTPLTIIQLYLYC
4568	18469	A	4598	293	3	GGTFWPRKKLGQRKPPHRPPGGSQNPDP SLTFFPPFLRQSFALVAGVQWCDLGL QPPPPVWPFLLRQPGFSTSCFFLLPAS GSFGRASASC
4569	18470	A	4599	174	2	RSVAPFLKSARQPTYAKETPTDTSQFP PPPRFTRPSCLTRLSSWDYRHAPPHAS C
4570	18471	A	4600	59	252	LAPFOHELQTSSEAHQNTNRRLLEQYOK RLDASGLERASYPLAAEFKVGGRGCSQ PLILCGYP
4571	18472	A	4601	233	366	THYLPDAVAHACNPSTLGGQGRITTSR DRDYFGQHGTFPLLK
4572	18473	A	4602	182	325	LPVFCLFLRQCSKVAAGVQWHDHCSLY PQPPSLKQSSRLGLPSSWDY
4573	18474	A	4603	202	2	GGSSSGLIRPCAVLGLKQSSYLSLVRW DHNSWLKRSTHGLPKGNDYREPPHLA CILKPSINLV
4574	18475	A	4604	317	2	PRLGQVFFTFPPGAGFFFCPPVWVGQFP SRLQLLTFGAKFFPCLSLPESPGAPLR GPPSGFMAHCFVFLVILFFFFFRDSVL LCCPGWSAVIHRDPTTARA
4575	18476	A	4605	233	71	FFVLVLEEDQLNKKQEGKTRKKRKK RNKQSLQKIWDYVERPNLAGHSQSL
4576	18477	A	4606	114	1	HRPRKVSQCCPNISAWWSRLAATAS RVOATLQSLA
4577	18478	A	4607	348	3	LKPNFRGVVLRNMCPSFFQGLSGRIPE TFEVEVLVNLGPAPALPEWPPSQTLSSQ NQKNQKKQKQKREKREKREKREKREK KKKKERERKEGRKQKQKTRKRIKAKSL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
						LG
4578	18479	A	4608	174	3	TVMVQQCVFVCLLKQGLALSFRLECT GIIIAHONLKLKLGSDPPTSVKTKKLV
4579	18480	A	4609	171	334	DPHSSLNIRFSRVAQGVQWGNLNSLQ PPPPGFQRLCFSLPSSWDYRCAPP
4580	18481	A	4610	2	164	ARGSRGHTWSAPCHVQAGLELLTSREA LASQSAGITGISHRAQPLINFLYSMS
4581	18482	A	4611	2	164	AREPRGHTWSSPCHVQAGLELLTSREA LASQSAGITGISHRAQPLSTLDSMS
4582	18483	A	4612	180	334	CCANGSSYLLPRKPNTLRTAGPLQQRKS LIRPGMVVHACNPSTLGQGGWI
4583	18484	A	4613	189	1	SGPSRVVENGLKCKGQGGQSLLVLPTR VFFFFFFEMKSHSFAQARVQWGNLGLS LPPLGFK
4584	18485	A	4614	216	358	KSTPRGCTVAHTCNFSTLGGQGRKTR GCRHSCILKOTPRLSKI
4585	18486	A	4615	179	393	EKQEEEGSGWAKTEEDVALRLSEATGS CWIKAPLTDATFTTHADICTLSEKENQ IKKQTLVELVKEKP
4586	18487	A	4616	2	126	ARVQRYFLPFTLGLPLPDPMSIRGVP NQMPRITPQSGK
4587	18488	A	4617	338	181	RVGEAGLELLALSLLPASDSQSAGITDI SHHTRPQSPFLBHLHYPRYRISGK
4588	18489	A	4618	3	197	HEKRPEVNSTVEFLASSDYMLRPPLFL PFCCFLFFFKIKMGVSPCCPGSQQTSL KQSSCLNV
4589	18490	A	4619	1	339	GTRTFGSGNGPTKPDLLQLRVATERGL VIVNCTHCLQGAVTTDYAGMAMAGAGV ISGFDMTSEALAKLSYVLQGPLSLDV RKELLTKDLRGEMTPPSVEERRRPSLQON T
4590	18491	A	4620	3	306	LEPGDGGCSSELKSCHCTPAWVTERDTS KKKKKKKGZPLKGTGLGKPPNGQWQRK IPSGQGGQKPNLGLGNLNFPGEGKNW NKFLTKIKVLRKQNE
4591	18492	A	4621	397	29	NTKEKILSARKKNQVPPPHQKKNPPFK KRKNPREGIPNPPPKKSPPOKHPPO KKKPKKEKKKTARPPKKRAPPGAFFKK PPPPFFLSSLCISYSFIYFSLINLFFF FFFSHDSIV
4592	18493	A	4622	2	235	VSLCHPGGTSTHYNFCLPGSRDPTTSA SAYALLIFVFFVETGFLVAQAGPKLQ TNSIPASASQSAGITGMNHCT
4593	18494	A	4623	209	324	ILRVLWSGTVAHACNPSFLGARGQIMR SGVRDPOQY
4594	18495	A	4624	52	287	NPFSFLFSLFSLFPLFFFLFKGPRRGA RAQKGKPHPKKKKKKGCGCKKJNTQKP FSLKGPGRPPROKQQTTPKGP
4595	18496	A	4625	102	1	THSPFVSTLSLSHTHTHTHTHTHTY RVREIR
4596	18497	A	4626	125	1	DRHVPQRIANFFVVLTEGMLHVGAQL KLISGNPLVFLV
4597	18498	A	4627	3	167	ERLQQQCTNPRSEGCSEPGSPHCTFAA WATQQDSVSKKKKKKKKKKKKIVV
4598	18499	A	4628	135	3	ANSTLSRFTTQAGLCTPVSSNSPASA SRVAGITGABHTVL
4599	18500	A	4629	320	210	WPLGITPRRVENASSVMDLTYDQSFT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, =possible nucleotide insertion)
						DTGKTPSS
4600	18501	A	4630	98	326	SSPTLAFQFOYFFSCATKBAVKLSPPKSLGOTGSRVAQPGQWINDHQSLLQPPAQLRSLSSCLTLVSGWHDRCAPP
4601	18502	A	4631	275	2	RVKLLLEYMRQSCSVIQVESSTVNGSLQPQPPGPRQSSSHVSLSRWDHKGMPCLANFPLFFWRKAGLAILPVHSNLTNTESP
4602	18503	A	4632	180	1	LISIKSN
4603	18504	A	4633	234	5	KGLTLYFFFFIFKRRGLAMLADWSQTPELNQFSLGLSPKCMDFRHEPPHPVKEKPFHR
4604	18505	A	4634	171	2	KPLDRKPLRSFNSLPPKKNLFFWFFPFOKWFQFFFTFESHSCVAGVQWLDLSLQPPSPGLAQFCLISLSS
4605	18506	A	4635	324	211	GRVDILTPQGHFTTSLFSTFPAQLSVTRLKCSGVIMAYCSLDLGSNPPPTAS
4606	18507	A	4636	95	1	LRNITFMPVTMNGMYTGGCVCVCVCVCVCVCVC
4607	18508	A	4637	234	1	MROCSNLSPRIKCSGTTIPAHCNILCPGSNS
4608	18509	A	4638	2	243	KKGHDITLTKAMPVTLSSRMLINVCRCIYKVNQKSPNYSLLTBHINNIKPSFTRENTLNFILHSLPILLLSLNPDIIT
4609	18510	A	4639	118	2	WGVNVDEVGGEALGRLLVVPWTHMYFEFFGAFYISFCLEFLIFPHLEFFVSSIHIVSSFTLYLFYNFPIIFFTLFCHEFTL
4610	18511	A	4640	50	168	GRVDLQCSGATSAHCKLHLQRSRHSPASASQVGAHNT
4611	18512	A	4641	315	87	NRINKMHLITFLKKKKKKKKKKKKKKKKKKKKKKKKKKKK
4612	18513	A	4642	383	2	GIFLDRNLALLPRLECSGTLIAQCNLELISPKDSPASPSPVARTGVQPRPDTLITLSELIIYIKMIESQDQ
4613	18514	A	4643	3	205	KFKKKKFAQCKAPARLSAPPLWOPKGGOPPRAGVLSPPQPPGTPTFFLIANPKFFPHGGGRPKSPFFGGKLGENSELTREKGGPINPMLAPPAFPPKQGNPFPFKKKKKKKKNS
4614	18515	A	4644	149	1	SPAMNMDMIGTNAGK
4615	18516	A	4645	474	344	LKRFFCSLGGQCSSEPSQCIYPAWETQRDSISKKKKKKTRPGLITEPPPPFGVKPKGPLGAGI
4616	18517	A	4646	165	357	FFPIKADLVFFFFFLRRNLNDSQGAQVQHDLSLQAPPFGFMPLSLCLSL
4617	18518	A	4647	2	339	AIHEHYLPSSASGDQDQDLQACTILVNALMDHQRLAHTV
4618	18519	A	4648	313	187	LCNALSHLLPOCTPTPLISILCITDITISLLIQPITHAVRLSANITACHILMHLILLSTLSICTL
4619	18520	A	4649	236	324	ARGENDLSPOGGGCSRLRLHCHCTPTNATRVNCSQKKKKQPKPKPNQTKPNQIRK
4620	18521	A	4650	225	313	GSPGFPILNLKVISPEKSLNPNILKIPKVTFRNLWTEPLPPFWKMEKGSFDPRI
						LYSGDPPASASQSGITGVSHALPPLVQTPSHSLTPTPLFC
						QGVMPGMAHACNPSTLQGRSRWIVRSR
						QGVMPGMAHACNPSTLQGRGRWIVRSR



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion
4621	18522	A	4651	240	76	FCVHARTHTHTSPQASGSSSRHMTYTH PGSGPETHYTYHTTFLASRSAPQLP
4622	18523	A	4652	273	379	KQLAAQCVRPLSPQALASPVTCTYMPR WPEVTER
4623	18524	A	4653	369	189	GTVKQAGACRNLGSLQTPPPPGKQFS CKSLYSIMICYSKDCMTSTLGI RANNR LHL
4624	18525	A	4654	168	346	DRICRASSYTIHLMYFVFLIFLIFYWYI YFLFVFLFHTFIILFYSPILLLLILLY FYN
4625	18526	A	4655	56	354	WKRTPFFFFLETGSPASRRCILLLFL YSLGAPNRVLIRVFLPSSRCYIYFL LGLSLFLFPYMLFLIRLFFVFLVGL LLLLSSYYRPIIFFP
4626	18527	A	4656	50	186	SACLGIFKCDYERHALPAMYLITGSS YVAQAGLNLGSDPPE
4627	18528	A	4657	131	366	DHFVASSSVKRGFLPFVFPFFPTIP FFILYICFPYFKFPIILLLYIIFIFI FYFFLYLYLILIFLIFPIFIG
4628	18529	A	4658	290	155	LEYIVSRGPHQDDKASPELLTGRYLSDS ASQAGITGRHWPTKG
4629	18530	A	4659	163	372	LRLPALFAFLMFPFFFLFLLYVECFV FLFFFTFGLYFLYFLYFLYLCGLVFL FFICIFSWFFVFF
4630	18531	A	4660	227	378	FIFFSNCTALVHPFLYLSRLVLSRNR NKFIGRARWLTPVFPALNEABA
4631	18532	A	4661	3	141	RSRHCTPAWQSEILQKERRKERRKKK ERKKEKERRKERRKERRK
4632	18533	A	4662	346	3	TFKFLGGVCPFFSPKKRVFSRNSPGGF FLPPLGSEFFFPAPVNRGPPGGFFRG PFFFPFFFPFFFPFFFPFFFPFFSQ DSFNGLIIFVPIKIQDPSSSMNATS ILIKIAL
4633	18534	A	4663	302	3	GDINRRSHSPFVMSKFPAPCFMSGLDVF YKSDDFYFFFEITFHSCCPGIAYCN LCLPGSSNSPASASQVAGITGVRRHQL IFASVVFETKITYKN
4634	18535	A	4664	2	76	RLAPTQLQGHNPPTGITPLNPLEV
4635	18536	A	4665	1	210	SPTRSPKPTPPYVOTTLAKPFTKRRKKK KKKKKKKKKKKKRGGAPLKKSPGGKI NRGKKKKFFFLKGG
4636	18537	A	4666	2	356	GSRPGGKRTARRWTRPWRREGACIGTG MAPAFIHQVIYKISFLRKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKPRG GGFLKKLWGGKFFMGGKI FFFFTRGK KKMWGG
4637	18538	A	4667	1	323	RTGFIYCYDVCVSGCADIQLLLCLKK KKKKKKKKKKKKKGAPLKNPGGAQN NPGKKKKNSPKRGGPKPTPGNF EKKPF FGGPGHGAAPPQGNKPTKKEKKP
4638	18539	A	4668	167	446	ELNGLCKPKKKKKRSGRSQKPTRPK KKKKKKKKKKKKKKKKKKKKKKKK KG
4639	18540	A	4669	321	52	GVFSFSPKFFFPSPKGLNFWGSPADIF SPPKRFPSPKPPGGFYPLRGLILIN GPRNNWGP GGGLKGAFLFPFFFPFFFF FFFFWG
4640	18541	A	4670	82	359	NAYGILILKGNEDTKVIRKWSQCQANT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US55,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4656	18557	A	4687	151	2	IFFFFFDVRVQWHKLSLQLEPRFQQFS CLSLPSSWYKHAPVRFRV
4657	18558	A	4688	342	183	FFFLRWSTFALVFOAGVQACDLGSLQL SPGFKRFSWAEVGLH2PRSQRLQ
4658	18559	A	4689	126	404	NCQVNPLEFTHSIVFSVHPQWFLLEYFC ALYFIPLBMGYSYVTOAGVQWHSLSLQ PPQMSYVLTFLMHPSSWGYFVQNHILPC FDGRVPHV
4659	18560	A	4690	2	128	GESLFTYIVSPRDVVAKERDQDDHIDL LBKKYEVPLTLL
4660	18561	A	4691	407	2	YFFPFLPRMKLFFPPHQKGFPPFGCPII SPPHNBFVPSKGGGFFSPKPKRVFPH MPSGFFPPFPFNSRPPFFFFSLSF FFPFFPFFPFFPFFPFFPFFPFFPFR TILNLQKKNLSACVHLRSOCIFM
4661	18562	A	4692	1	176	SRRLNPKGRCSEPRSHHCTSTWTERD SVSKKKKKRFPALKPLGEANVKPTIGSQ KN
4662	18563	A	4693	1	403	SKABTGRRLGLRLQTVSQVNAKERFLK EVKADPTMNTMRIRKNSLIDAEKVLV VMIDQQTSKNIPLSQSLIQNKALTLNS MKAERGVEAEKKKFEASRGVWRFKERS HFHNILKQGEAASADVEAASAY
4663	18564	A	4694	343	425	HCFTSLQLNSPEQLCINTYNEKIQQLF
4664	18565	A	4695	395	2	KNKGLFFPPFLRWSTFLTVQASNVTVTA CNVTILAHONLHLPSSSNSPASASRVAG ITGSCHQG
4665	18566	A	4696	429	0	VTKWCYITKRRKKKKKKKKKKKKKKKK KKARG
4666	18567	A	4697	371	217	IPVFKQSCLSFPRSMYDKHMPCCVTQK KKIYQHTSLYKPKSKKCALFLI
4667	18568	A	4698	415	59	LQQQCFISLTKKKKKKKKKKKKKKK KRGGLKKKKKKKPPFPYF
4668	18569	A	4699	431	0	LKKIPPPQGRVLSPPPPPPPPPPPPFP P
4669	18570	A	4700	371	245	TLGDPASASQASAGITGVSHNAQLPGI FIYKFTYICRKTET
4670	18571	A	4701	410	0	KQCFTQKKKKKKKKKKKKKKKKKKKK DRG
4671	18572	A	4702	340	402	PFAGGGRVRLGAAPERESAYVA
4672	18573	A	4703	188	2	TSLPKCNRYRHPPCPAHTLLIFLFFFL VDMGSCVAVQVALELLGSSDPPTASQS AGITGM
4673	18574	A	4704	423	34	LEKKKKKKKKKKKKKKKKKKKKKKQDL KKMVGGNNYKNVGAQLLYGKLCFSFF YRVF
4674	18575	A	4705	2	297	PRVREKEREMASKEKFFTRLKALKERSE ARRKLEERKNVSLQKNDLQLOVQASQ DNLADAEBCDQLIKNKIQLEAKVKEMN ERLEDEERENRSLP
4675	18576	A	4706	2	179	QENGMNPGGRACCEPRLR YCTSSWATER DSVSKNKKKRSASLRPFILFGALTGR KRS
4676	18577	A	4707	432	578	PRIVCPRLKFPYSABICQRTSKXPPSS PLQPSSSSSSS
4677	18578	A	4708	419	35	GSFFFFFLKDDPKKGRKKGGCFPPPKK IYPPPATKMGQGGKPPPPPKGRGPPK KNRGKKKKPKKKKKKPPPPPKGRAPQK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in ISSN 09/515,1 26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						KKKKDDPPPIFFLYFFKFNIFFFFFFFF FFPFFFFKFIFNLKKF
4678	18579	A	4709	147	31	NFFFFFFFEXFIFFFFXKXKFLFFF *FFFLKIKLFF
4679	18580	A	4710	3	229	HASAHASQDPERLNAGTYFLFYTLVGS LILIALIYTHNTLGSINILILTLTAQEL SKKKKKGGAVLKNPWGAQS
4680	18581	A	4711	1	158	PTRPPTPRSCSELRSHTCPANVTERI CLKKKKKKPPNLSVGFKILGILKG
4681	18582	A	4712	163	404	KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KKGGQANRPGKRRSGVSGSEKCN
4682	18583	A	4713	3	378	FEEPVYTESQKKRKEKNPFLVSSQPM LHDFKKKKKKKKKKKKKKKKKKKKKK KKPGQAKNPGGKKNPFLGGGKKKNPW GFFKKKTFFGGGKIGAKPKKKKSLKKK KKFLRKGKKKT
4683	18584	A	4714	2	208	VSNPAVSVPHLPFVYKSSPMASMTFSK KKKKKIKKKKKKKKKKKKKKKKKKK KKKPPWGAQNKDG
4684	18585	A	4715	290	56	SAPPEIFFLFFLFLFIFFIFFFFKQI LEKKGPPPPFFLFFIFFFIFFFFYRGC DRWNFILIQGTFRKKQKPVLCV
4685	18586	A	4716	50	424	GGFKIKFLFTQLFLFLFSPSMFLISKSP AYLNQSSPKQVPMVVGKTNPLVISECK KGIYFFCIPFVPGFPHPKILCSLILFF LAFILRSALLPRLECSGAILTHCNPL PGSSNSHAWA
4686	18587	A	4717	161	2	GRGPADFRVVRPQLLRFLFIYLFERE SCSVTQGVQWNLGSLQPLPPGLQ
4687	18588	A	4718	2	115	VYTPANAEISTPEAMSGSVVLVSVLVG LAMEVGSTRP
4688	18589	A	4719	1	416	GNQGGYGGGYNDYGGNGYSSGNPSSS SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSS
4689	18590	A	4720	1	454	QPDGTSISIRSKFTLEAAQDVVYRDE IGNVTSHLILDSVEMEIRPRFLFG GWKTHYIVGYNLPSYELYNLGDQYALK MRFDVHVFDBQVINDSLTKILPISGAKN IIDSYPYISRAPDELHYTYLDTFGRPV IVAYKKNLVQ
4690	18591	A	4721	3	173	DAWGPHTVVGAGLELISSHLPASASQ SAGITDVSHTQLDVPFSSLSPLHQ
4691	18592	A	4722	2	201	LKPGGGGCSRPSCHCSTPAWRQSETPS QKIKKGKWLIRIGWGGSTNNGAKNR GKPGKKGGF
4692	18593	A	4723	2	183	LKPGGGGCSRPSCHCSTPAWRQSETPS QKIKKGKWLIRIGWGGSTNNGAKNR VBKF
4693	18594	A	4724	1	395	QNTSPILIELITFHDHALIIFLICFLP DHALIELTPSALT
4694	18595	A	4725	388	3	SESPLSENLNTIQIGRGRDFTSKTPK AMATKAD
4695	18596	A	4726	223	44	WLFFFXPLFFFFFFWGIIFFLLKKLIYF FFYMSKIFFFFFFFFIFFFIFFFIFFF FFFF
4696	18597	A	4727	41	374	KKKKKKKKKKGGGGGNNPKKKKGGRK PPGNKRGEGGKKNFLKKGGGLFRKG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
						KPPKKKNGQRKPWKKKNFKAKKKKNPFF LGPKIFKKKKKRGKKKLGFFSQSVGP
4697	18598	A	4728	323	69	FFFLROSLGASASOAGAOGHNGSLQPLP AGFQQLPIQPPPPGSKQFGRNLNLGNKDL WGLPVLRAHPQAPPLAFIL
4698	18599	A	4729	3	197	CLALLHLRSRQRYALPLGLPGCPCHTHT HSHTHAHDHTHTYTPSHAHRAHTHTHMH TLPTTTHCI
4699	18600	A	4730	309	443	VLTLSPRLCESSMNIAYSLKLLGSSDH PTSASQSGGIIGMSYIA
4700	18601	A	4731	3	172	DAWATFNGQFVSLCCTGASRTPLQKRST CLSLPKCNDWRPEPLSPAPKTLFSLYLL
4701	18602	A	4732	98	232	QVVFLLGLNGLACSLSPVQLTVKRRFLFR CLFSLVTFPICLRYN
4702	18603	A	4733	238	1	LQPFVFSPLQVPPFVLVIRGFSFKPTPL FFSPFFFPFPFPFPFPFPFPFPFPFPFP VTQAGVQNRDLGSLQLPDPGFKR
4703	18604	A	4734	121	424	LIQHRVVIYFVSQLRVGRQACDSITLL GHLPEKVRLEMPFPLSPVAGLEPTSHYR MFVDVVLVDQGHWRVYQTGHWVQCGKAG TMPGAR
4704	18605	A	4735	319	8	NPPQKKKKKIFPPPKKTPPKKIKENPP PFTIFPPPPPPPPPPPPPPPPPPPPPPPP FFYFQHWVFCFSLIHVIFFLIEVLFLAF HVGDSDADANSTKCSNRTK
4705	18606	A	4736	297	442	TQFFGGGPRKIGFFFRGLMNGGGGNFK LRFLKPGQLVGRGRTKKNQ
4706	18607	A	4737	430	0	CVLGSIDKKKKKKKKKKKKKKKKKKKK KAKKDS
4707	18608	A	4738	137	1	INYYFLKQGFPLPRLCESGAIIAHCS LSFFGSSDPRPSASQA
4708	18609	A	4739	188	3	ISPKALNPRERVGPIPPPKKVPFQNP PGQFTTPHKEKNFSLPPPUNLGGPKDP LKRPP
4709	18610	A	4740	188	2	TSLPKCDWYRIEPPCAPATLLILFLPFI VDMGSCHVAQVALELLGSSDPPPTSASQS AGIIGM
4710	18611	A	4741	410	1	RRPGGGFCPPPPPPKIFPSPPPPPPFVGV LPQTPPPPKKFFFLNPPGFFFPKPKK KIFFPSPPPFSPDPPIFFFPDPDPFPPFF FPFPFPFPFPFPFPFPFPFPFPFPFPFP GKDRVSLCCDWSRTPGPKDSLL
4711	18612	A	4742	225	444	ENLKLSFPSCSHFWLRWNLTIAGLSR SFDEAALLFPNDTYNGTVAHANCNPS LGGROGRITKSRDRNHS
4712	18613	A	4743	2	452	VSNPAVSVHLFPVYKSSRWASMTFSK KKKKTKKKKKKKKKKKKKKKKKSGGPQ KKKNR
4713	18614	A	4744	3	144	LAAVLLEGGYGIIRLITILNPLTGHIA YPILLLSLNPDITGFS
4714	18615	A	4745	206	2	IQNPQTRVNSISKLKISSKOTINRAKK QMDHSEVCKKKIPGKELISRMKELQL NNKKQIVPPTRP
4715	18616	A	4746	523	178	RHRFFMHTERQVKSQQRQKQKQIK IKDKRQSCYAAQRILRNPHRDPS QKLSSTILAQLQRTKFRZKQQRKE VIRYVRAIRAQIQKIMOLYNITLPLC
4716	18617	A	4747	3	518	ENRLNLGGGCGEIPRSRCHCTPWAT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
4717	18618	A	4748	491	145	LCHVQAGLELLTSSDLPTLASRSAGLA GVSHRTRPHSHFYFYFLYSSSFFFFFL AQQRNRPARGKKTTPFGLATLNLKNGGV FWFLFLGPGFLKREPTFALGLKDRGNGL V
4718	18619	A	4749	6	362	NKLPNGTEFLSSSLVPTNFFPSFLFFFF FFFFFWGKGGPFRGGGAKFYPLEFFFF PPPPP KGGKGGPPPTTNFLFKKEGGG PSPGGVKTGPGKGFPPSPQRGGKKKG WQKGP
4719	18620	A	4750	380	3	SLLLKFAALLCLPWLGKAGVTVPLSRL FDHANIQAHRRAHHAIDTYQFEETTYIP KDQKYSFVHSDQTSFCFSDSIPTPSNME EPQHKSNLELLRLSLLIISWLEPVRF LSMFANNLVYDPS
4720	18621	A	4751	1	345	LFYIFKKTWSLFLCLPMMKVPTFFPFL LWVFLCLGGILVSPFIPGGGKREKKR RGGEKKKKKKNVVFKKKKNPWGGGGI KKQRRGGGKKKKKGGGGSGGKKQSP LRG
4721	18622	A	4752	1	407	QEFETTYTPKDQKYSFLHSDQTSFCFSD SIPTPSNMEETOQKSNLELLRLSILLIE SWLEPVRFSLRSMFANNLVYDSDSDYH LLKDLKRGQITLNGVVRVAPGVNPGTPL ASRAGGEKYCCPLFSNKARDQEN
4722	18623	A	4753	357	1	LEFFPKRLFFFFFKKKEKAPVFFF FPFSPRGGGFFFRVGNNTQLHPFF SQNTSVFSSLTFFFTFFFTFFFTFF FFFTFFFTFFFTFFFTFFFTFFFTFF DRGLTLL
4723	18624	A	4754	1	207	LGLAGVEERVASELNAGRCQCKSPSHD WTPAWAMBQDSMSKKYKNEVORRQLIHL QSSTSGFLYVHEQ
4724	18625	A	4755	2	336	HEERERRRERERERERERERERERES RAQPRARKNSQAPHRVCTLWTEEGGS FYPLTEKDFACERAHFCVLGSHPPGN GLCKKNPECEERATHSLHGADISGLV
4725	18626	A	4756	230	446	VGFSSLSFRVCTYLYASGLTRELCEKR RSFLFCFAFWLGLPLRQSLALSFRLEYN GATSAHCNHLHPGSSD
4726	18627	A	4757	3	390	QTSFCFSDSGPTFFMEETOQKSNLELL RISILLIESWLEPVRFSLRSMFANNLVYD SDSDDDYHLKLEBQITLNGRLEDGS RSTQQLKQYKSFPTNSHNDALLRY GLLCFRKMDKVTFL
4727	18628	A	4758	234	387	LAKFLFSSAATWNTENAPQSPATGRTP VVFSPIDPPLPPPPFAVTV
4728	18629	A	4759	396	0	IYTHHTHTHTHTYIYNYVNL
4729	18630	A	4760	176	384	WVPLFNKDTQHLFLWGYVLFPPFLKR NFVFAQAGQGGRYFSLKPPPPALKPF SCLSLCTWDYRR
4730	18631	A	4761	419	208	ITPPPPPWPKGGSFLKCKKKCKCPGPG VPPFIPPLGGAGGFPNSKIQTTPAQ GKPLFPQKNONYLA
4731	18632	A	4762	158	2	GNQLNPFFSGSAPCFPLFLRSLAVT QARVQWHLGLSQSPSGPKRPS
4732	18633	A	4763	489	398	AGFELLTSSDPPASASQSVGIGVSHCT QP







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						WGGKGGPKKKNLWGAQKIKFLEIKGKSF PRGTTTNPFGPPLFPSPPKTQGPNGFLD PSFKLKN
4774	18675	A	4805	59	175	SPYFFLNMKKKKKKKKKKKKKKKKRGA LKKKTGGGPN
4775	18676	A	4806	406	300	SSGVLYSRAPTYCGQTLTPRQVDIKTS HLPQEA
4776	18677	A	4807	123	1	KSTAWGTNAHSCNPSTLGGQDQGTTRS GVRDQKKGGETP
4777	18678	A	4808	319	406	LYKSYSSNPNVVAHTCNPTLGGQGGQI I
4778	18679	A	4809	236	351	GFWPAPGVHACNPISLGGQGGRTGPKL GNLGGQGEI
4779	18680	A	4810	173	2	EVLFLQPRSLISLLQNNLLYLIKAKFA EVLQAGVQVHNLSSLLPPPRFKRPSCL R
4780	18681	A	4811	2	94	TRILKVGQRKCSVKNGPLTISHGTYSI LF
4781	18682	A	4812	358	2	PPFFPSTETSCSVAGQVQNRDLGSL
4782	18683	A	4813	362	3	YSFVCIISLQQAHCSSLVINPHLAKCVI QLPVNTRRLPGVAHSPIGSELCSFSDS SVPSHTRSPFKAARLTANHRRGCTESG WPFSLVLFERCMNPGTVAHTCNPSLIG AQGGQIT
4783	18684	A	4814	341	1	WQKRAHITKSLSQNRAGGIMLDFPK LYYKATVTKTANYWYQNRIDQWNRTEP SRIMPHIYNLIFDKPDKNKKGKDSLF NKGWENMLATCRKLELDFLTPYTKIN S
4784	18685	A	4815	2	283	VYTGERTLQKRETTTRDQEAPYLLRNL DHVAISSSTTLDCANGVPEPQITWPK NNHKIQEPELYTSTSPSSSSSPLSS SSSSSSSS
4785	18686	A	4816	266	3	ASSTLAHRAHQLAIDTQEPERTYTPK DQKYSFLHDSQSLRQPLHTSGVGTTR LAASLSSGRTAHTRTMHTQHTKRTAH TNA
4786	18687	A	4817	363	1	SPFFPSTETSCSVAGQVQNRDLGSL LRLPDSNSPASA
4787	18688	A	4818	87	372	ASYKRDYKCYMLPLRVIRKFPQTERKKNL SGLGEGNKKELLFNGCNMAVFLVGGGF ETRPSPSVTQAGQWCDLSSKPLPHRL RVSCLSLPSGW
4788	18689	A	4819	5	175	FAFLTITPLSLRFDNAMLRRRLYQLAYD TYORPREAYILKRGQDSFLQNPOTSLCF S
4789	18690	A	4820	235	351	PPKPPKPPKPPPPPPPPPPPPKPPKPP KPPKPPPPPPKPP
4790	18691	A	4821	2	155	ITPLLLIESWLRPVRFKSMFANNLVYDT SDSDYHLLKDLLEGIOQLMGL
4791	18692	A	4822	90	2	LPFFPSTETSPSVTQAGVQNRDLGSLQ P
4792	18693	A	4823	247	3	KVKGSPSHRAMVAGNLSLHRRKSPG ISNPMGNSKLLSPFNKCHQCVTAQAYN PSLGRGQWITRSGVNDQDQYSET
4793	18694	A	4824	93	407	QHPKKKKKGGGSLKIKKIKVFKHTTPN PFSROKKKKKKKKKKKKKKKKGGG GLLKKVGGPKPGPKGKKPPPPFGGKK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /-possible nucleotide deletion, -possible nucleotide insertion)
4794	18695	A	4826	2	129	NFPGVFLKGNFPWGGKKKKK TIAHCSLNLPSSDPPIKSLVAGTTHV CINAWNVFVFCRRG
4795	18696	A	4827	342	140	GGFFFFPPPPFFFKFELFLPPPPPGS CVGGVQKFTPPPPQLSRSLFLFFAP PPETDNPFFFS
4796	18697	A	4828	1	259	GGCSEPRSCHCTPANVTYDKKKKKKK RGKGKKIGKGGFQRKFKGNPHGRFLR ESHNSPKGFFKKFFGNPPPGTSKKVLP PH
4797	18698	A	4830	125	1	KGTRTFETESRSVAQAGVQMHDLGSLQ LPDGFRRRLTCLSL
4798	18699	A	4831	1	323	ARGSREREREREREREREREREPPL SRGOSSEYLKANERLLENDPLFFFG GKMGHLFPPPPPPVGGVGTGGLITGGP FNNWGCVSHTHTHTHTHTYMSV
4799	18700	A	4832	3	297	TRRERERERERERERERTLL
4800	18701	A	4833	1	150	ARERERERERERERERERERERKKKN HSRGGPGPGQPLGGGVKKPGGV
4801	18702	A	4834	1	98	ARGERERERERERERERERERERERE RRGAQGGPT
4802	18703	A	4835	2	66	HEERERERERERERERERERAR
4803	18704	A	4836	2	73	PEEREREREREREREREETAR
4804	18705	A	4837	146	2	FGLVYTSIQFLFFVRSALVITQVGQ WRNLGSLQALPGPFTAFSL
4805	18706	A	4838	354	0	PPPPPPPPPPPPPPPPPPPPPPPPSP SSSP
4806	18707	A	4839	62	358	GLVHDKHSPPHGGCGSHHVLPSLNPSPFT FSTKS PSVPPANALNPPSRWALQVGH LGLTPTTRQESAQAPRKLALLGSGTQ AQWLTPVIPALNEAS
4807	18708	A	4840	121	13	RPGRPPPEFTFPFSCSLSPGSMDCRRPP RPANLLYF
4808	18709	A	4841	3	221	LVMGFVGSSKSPFIYGGALIVSGVVG CVILLANFGGYMGLVFLYLGGMMVG GCILLSLNRYVNLNP
4809	18710	A	4842	3	84	CHCTPANATLSDIKKKKKKKKKFEN
4810	18711	A	4843	33	230	LIVTTSKAASVYLKHKKKKKKKKKKP KKKTPKKNPNPPQKSELKKIPFFWNE RTLQKKRP
4811	18712	A	4844	3	368	HELANPGRSCGPPECHCTPANATRAKV HITKKKKKKKGNLFLKGGSLNFFPKK KETPWSQNFKEKKGPRRSPRCKNPPLA LRGKGGKGLSGKIFPPFRGKTPPWA FMGTQXGEYS
4812	18713	A	4845	163	2	HGHSISKFLIVSSPKSFNQLRPAVA HACNASTLGGRGWITRSGVQDLW
4813	18714	A	4846	387	234	KGCGEPRSCHCPANATIAKLLFKKKKT KPKKNPKQKKTFFPYNINRVCY
4814	18715	A	4847	189	349	KPSRFSGQKALLKDLTGLGTAAHTCNP STLGGQGRWIMRCQVFKTSLAKNVK
4815	18716	A	4848	3	95	HENFYCPGSLGRNEGNIFNPEATFVK EM
4816	18717	A	4849	2	325	DSHTIINGDFNTPLALDRSTRQKVNED IQDINSALHQADLIDLYKILHPKSTYET FFSAPHRTYSKIDHKIYSQGRHETDCRY GKGGGKWKSRFPDVCSSKFSQ

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Yrosine, X=Unknown, *=-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
4817	18718	A	4850	241	348	SFFSQTQASEQLTKSKQGLA.LRTLPFQ FPPPPPRP
4818	18719	A	4851	2	176	LVETGFCHVGQAGLELLTSGKNDYRCE PPSPAYCFLHTIVTITYPLLCIAFFSYLC DC
4819	18720	A	4852	2	191	VGRVGLELLASSDLPTSGSPSAGITGMS HCPWPNFLIFIGYFFTVLTPCEYISGG MTVPLWL
4820	18721	A	4853	67	376	IKCTTFNKKKKKKKKKKKKKKKKKKKK ALKKKPWGQKKTKGKKKKFPSKGGKK KGGPKRVLKGGEREKIFPWNFLKNNFW GGNLCQPPFKKLALEKK
4821	18722	A	4854	278	363	TKPDVVAHCNPSLGGQGRWTRSGVR
4822	18723	A	4855	3	282	RQCSKPLRYCTPANKTQDSASKKKKK KKTKIWFEBPGGVSPFKPHFPGQGG KPGQKFKNPPQWEKPLFPFKKKETKF SPGGGGPP
4823	18724	A	4857	382	224	PVTLTGGRVQCKNPNLVGKSPNEKSP PCPPTWAKONGSLKKKKKKIKGKK
4824	18725	A	4858	392	102	FFFFFLRQGLSVQARVQWCPGCSNLGL LGSSNPPTSASLSCFLNKKKEYRWENTN KV
4825	18726	A	4859	3	111	FHRISQEGILLTLGSAHLGLPECDYR REPPRA
4826	18727	A	4860	282	83	AQTYKVNWSSGNNKICVVCVVCVVC VCIIYIYMLCSRFYKCIWGVGNIDSYV VYIPNIQCYI
4827	18728	A	4861	3	417	NHSNLGGRGCS DPRSRHCTPAMVTERDS ISKKKKKKKKKKIFPGLREKGLTLFPFLG KKNENSGFPLNPNFPFGGKGGKATLQPL GLVLRGVPPFRGGGTQNGENKPGQITLE KEKHFWGVPFPLEKTSPEHGKQTK
4828	18729	A	4862	1	88	NEENYKKAHAALLENFVYKKPKKKKK K
4829	18730	A	4863	274	369	VSLLCCAGMRAAVRSQITRALISQAAIL FPQP
4830	18731	A	4864	37	444	DPRVESEKKTPFKLLLDNAPSHPKAL MEIYEEINVI FMPANTTSILQPMHQVVI STFKSYLLENTFHKALAAMDSDVSDSGS QSKLKTFWKGFTILDATKNIRDSWEEVK LSTLTGVNKKLIFLTDIDYEGPKT
4831	18732	A	4865	341	210	VYMCVGLLYHOPVIYIRNRTEASEITP HIYNYLIFDKPSHOF
4832	18733	A	4866	206	412	QLCLSQACTTARGNARGFLKTYTHRNVS MPSVAGHTWGPQLVKGGQETCPATINF SDSPSLKITYMYPM
4833	18734	A	4867	248	78	SHFEAGLAALQTVSWFPQGTVPFVHAGP FANIAHGNSIIADRIALKLVGPEGFVG
4834	18735	A	4868	637	2	EPIDGRWPRQIVSSIGLRVYGRIDCCWG WARGSWGQCQPVCCPRCKHGEICIGPNKC KCHPGYAGKTCNQDEHLPALPDQSSBQP LQPLDHRATNIPSRDLSNCKLPPACK HCKWYTYGSKCYCLANYMLAPDQSSCS ALTCMANCQGCQDVVKQQLRCQCPSPG LQALPDQRTCVQDVDCATGRASCPRFRQ CVNTPGSIYICKCHKG
4835	18736	A	4869	276	426	VSFFLFYFFWGANFPFVFOAGGGGFLG SLNPLPGLKHFCLTPSSSGN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
4836	18737	A	4870	100	485	EERNREMTERRCSVTQAGVQWHDLOSQP SPPGFKRFSCLSPSSADYRLCDGWNIL AHGKRLRPGSSRSPASASRVAGITGMCH HAPLARLVNNTLPQVILPPLGLQQAERLL PRRQVEHNTPSLVPI
4837	18738	A	4871	718	408	EVITLQAHFPGFLGAHWNNQDAALGR ATDSKEPPELPCPDVLYRTARTALHQGET YTPRLILMDLHYDVSGLALVITAAGYRA SSCSUSVAVCTGSVLEAIA
4838	18739	A	4872	392	246	RGGCSLEKCHCLPAWATRVKGLKKKE KKKKCLPKNRILANNRAG
4839	18740	A	4873	1	156	GGGYSRSPASCHSTFAWTTREKLRLKK KKKKKGVCVCGVGLGRPRKGGF
4840	18741	A	4874	246	2	AHGTISYASMLAYSIFSRKRVSFERRAGQ VKAVTPVSVVPGFLRREHLGEHFLPFLR QSFTLVAGQGVQWCHLGSQQLPAPA
4841	18742	A	4875	72	2	CFFAJPDEPSTNTITKQKMTVE
4842	18743	A	4876	375	221	GRLRQRNRLNAGGGCEPRSHYCTPAW VTRQDSISNICIYINLFSVVHGG
4843	18744	A	4877	151	2	RAPFFFFFFFFFFVAQGVQWVRVLSGLQAP PPGFTFPCSLSLSSMIYRRP
4844	18745	A	4878	401	70	PIHREGGCVPEPPPKNFFFSGGYFFNG GGGQNPFPKGGFPFKTPPGFFFSPPQK KKIFFFPBPPBPPGFTLRDPPPPFFFP FFFTFFFTFFFTFFFTFFFTFFFTFFFP FTFFFTFFFTFFFP
4845	18746	A	4879	4	152	LPYSTPSTPFRAKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKGNFK KR
4846	18747	A	4880	267	1	TPPKKKKKKILPPPKNGPPPHIFKKTTP PLPFFFFFTFFFTFFFTFFFTFFFTFF FFFTFFFTFFFTFFFTFFFTFFFTFFFP FTFFVFFFTFFFTFFFTFFFTFFFTFFFP FTFFFTFFFTFFFPFTRGTRGTRGRT RGR
4847	18748	A	4881	2	408	LQDATSPIIBELITTFHDHALYIIFLICF LVLYALFILTITTKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKGGGPKKINRGG PKLGGGKKKIFFFFKGGKKTRGVGKK KIFLGGGNFGPPDPKKKDPGRKI
4848	18749	A	4882	413	69	LPPPPPGFKHFWALPPPGRGVPGPPPPP RVNPFVLGKGVSPFGPGGRPLTFNPG GVGAGDPLDPRGGFGHGPKFMPCPPARG TKRRPPFPKKKKKKKKKKKKRERKEKKK EI
4849	18750	A	4883	46	394	KQYQVSVKLLFVTONLSTKKKKKKKKKK KKKKGGGALKKAPGGGKKKPGGKKKNFP LKGKKKKKPGIPEKKTLPGGGENGTGP PKKKKPPGKKKKLKGKGGKKTLYPGRG KNFS
4850	18751	A	4884	399	3	FFFKKFFSPNBSHFFPPDFPLKTFPPBP RLFFPWGGLAQTSPPKKVFSKPRGRF FFPPLGLKNFFFPDGYFWDPDGFFLRA PDLFFFFFFFPPPPPPPPPSVSRNALIAI RMGIMRSRRILANGMLLRG
4851	18752	A	4885	391	47	PHFFWGGVFPDPKPKKKFFFLPQKGGG GGAPKKKKKKKFLPNFSGGFFFPSP GGPRPFFFTFFFTFFFTFFFTFFFTFFFP



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RREPPRPDAVWAGLQLLTS SDPPASDSQR AGITHLSHLTLFCHLRF
4870	18771	A	4904	384	194	HAVGRPPFNLWGQKNPPPPPJKLEYQG WGPPPPPPPPFFFKKTIPIFSQVFNPPFF FFFFFPG
4871	18772	A	4905	3	387	TIITPIYLLTLFLTLTQLKLTNTNYHLPLP AQYPLPQKKKKKKKKKKKKK
4872	18773	A	4906	1	327	PTRIETPIENPKFSVPPITPHPKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK KRWGGPKKGGGKKKIFFFLRGGKKKPRG EFLKKTTSFWGGENLATTTPKKKKARKK KNF
4873	18774	A	4907	134	2	ALYSKKVKMPGAVAHACNPNLTGGQGEN TRSGVRDQPGQHSKT
4874	18775	A	4908	59	449	ATRHYYTTLAYLTSVGTITAVLQKQAL KGARFQVRRITENYDQQLIHKGGGRPP GCHSTHTVLLPDPVWKTGNSIVANFV LILVCLSLPLLIVRCIQQLQDQNSQREG AMMNVVLSKKRGGYAGK
4875	18776	A	4909	337	3	LKTANATRONPPPLYKNTQTSQARQEP PIPLIGGGLSQKNFFTPGGENSINPDP PSPPPGAKKETPPPGKKKKKPTTKELG KDWTLRLMDSQRAQGLAEPGESSP
4876	18777	A	4910	14	162	AESGAKRRTAPPFAQQGATDRKRLNIY AAKHMKTCLPSLAIREMQIK
4877	18778	A	4911	331	2	LPLLAPKGGQKRLGYKKPPPPGLPPFF GSTPPRNGEKGPPPPRGNFWFKNGG FPLRGGGPPFPQPKPPPRPZQGGKGQ GNDAAGPFFFFFETEFSSCCPGNSA
4878	18779	A	4912	116	316	ACNAHATLFFFFFKKKPPFVLLGGKG QNLGYLKLWPLGLKKVCLTPRGTNTYGG APPHRIIFCLP
4879	18780	A	4913	93	16	SPPNQPGTVAHACHSTLGGGRIT
4880	18781	A	4914	316	2	KPKRGNPLKAKVFNPGPGETTFPPKIN PKPTRGGGRGPIYNPFGRVVPKNFLPV RGSRFHWPNISIPCPFWGTKNFFSKKK KKRKKKKKLCFSAASVPDAQ
4881	18782	A	4915	3	289	TSCNPSTLGGGRGRTRVGVGQDPDQHG ETPSLLKNYIYIYICVDVLYVCMYVGA YIYICIGYIYNWYLSLSEHTHTRAP GQYRVYFFCG
4882	18783	A	4916	1	222	ARGERERERERERERERERERERERER PTHWGEBGVLSSPQTVGREKNAPING CAAPLAPRVGRTPPGVD
4883	18784	A	4918	1	281	ARGERERERERERERERERERERERER RERERERERERERERERERERERERER SARGARALSPTISQSDPHRGPKIYRGVG VHTQRYFSVGSSLCINTHT
4884	18785	A	4919	1	259	ARGERERERERERERERERERERERER RVILPAGTYERFGGKKYTKAVRVCVR KGGRAHNRPAHDFGARGPHVKFLAQTY YE
4885	18786	A	4920	797	910	NTKPGVVTHTCNPSLTGGQGGKITGSG VQDQPGQHQH
4886	18787	A	4921	2	67	LEERERERERERERERERERERERSS
4887	18788	A	4922	1	698	TLLAKLGTTCDDPYRSCSTSEDSGLSTA FTTAEHLGHVFNPHDNNKKKKRGPGF KGNPNSPPVRASKNFFFPNPLNSHARF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US95/51,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
4888	18789	A	4923	323	2	LTPGEGKTPGVFPNPFATKAEAL LVCRGTIHKFCRCPVHLTGRFFEHGVTDCTYLFRDAYHLAGIEMDPFHRDDWNRNGQNLVLDNLEATGLYQVPLSAAQFGDVLILCCPGSSVTPNHAATYCGDGKLLHH
4889	18790	A	4924	3	225	HEBALHLFQTLMECKKKRELITVPHIGSDEHQDIDVAILTALLGKGRKRLTFLFVRPFLICWYMCVYVCICVCI
4890	18791	A	4925	371	169	HTQSISVVLVERRFHSQENFLNPGGERGQELRLCHCTPAWATRAKSELKTKTKTKDAIKCSLGN
4891	18792	A	4926	2	352	ARAARGRLIKELF FFFFFGNLKKKKGLFWPGGVKPKDLGNPFPWPPKSGEITGLTPRPGVWVIFKKKFKGKSSPPTGKSLGPREFFGLALQRGDILGLNHRGPPFFFGVLETM
4892	18793	A	4927	2	379	ARANNBETQOKSNLELVRISELLITKTLGEPVRIILRSMPFTNNLVYDTSDDYHLLKDLQBGITQLMGRLENGRRETGGILITQTYSKFDTSNDEHALLGNVRLLYCFTTOMDKVETFLRMEQCRSV
4893	18794	A	4928	175	31	ILGLDLFPFAMRPFPLFLLPLSPSLAVTEVAVQMRNLGLKQPLPPGF
4894	18795	A	4929	368	247	VDRLLFPCCPGNSPSELNQSACLSFLKICWDYRCPELCSVS
4895	18796	A	4930	2	110	ARGEPRESHCHCTPAWAMSETVSKKKKSGGLFFFLRLV
4896	18797	A	4931	150	1	KYVAPCRDLFLVLSPCRKSCFPFFPCHDCCKFPESFSEATMFFLQPAEPRA
4897	18798	A	4932	2	155	ARDDLNPGGGSELKSRCHCTPAWATERDTSKSKKKNPQINGNLKKKMLK
4898	18799	A	4933	144	249	ETLVYCPQSLNASCVCVCVCVCVCVCVCLCVCV
4899	18800	A	4934	2	153	ARESFVEKGRFHVQVGLKLLASGNPPNLATQSAGILISISCHCTOPNROGL
4900	18801	A	4935	1	355	GTSGEPFEGKRDRLASPLETNGAGAGERLAEVSTCPSGASKPLQTPRPGQGBPTGLGGRMRKHSAGSPNPAMWSIRKPSLSTALLVACSIPIHHSDFILHDVLSRCMSIKTSHR
4901	18802	A	4936	112	358	NIYKFSKAFFFSYFIFILINSVGLSTFMWGGELKFSFTSGILIIQFPFKIKGHPQRGILRTGTFTKEDPDEGNKVSLLQ
4902	18803	A	4937	1	258	GSYFVYVTCQFFSGWGRGLTSLPKLHSELRCHCTPSPWTERDSISKKKKKLFYLAGTPTFFPGGNFNLALGRLLKRGGGEKK
4903	18804	A	4938	380	1	FFFFFSETEYPSVAQAGVQMC
4904	18805	A	4940	255	1	LGNLNLGAGYKIRGLYSISLRNNRHPSPVISLQGNLFFYVIRFFDMSCSVIQAQVVLWNTGSSQALTPGATAPFSFSLPSTRQNSRP
4905	18806	A	4941	10	173	KYTEVDINKKHKHSCSGKGRITNFVMSLPPKAIYTFSPVPIKIPSVYLPVHLSIKDKTRKPTVPIHCNSSLGDDGGRVMRSGVRDQQOCHSRTPSVRV
4906	18807	A	4942	144	3	PSQRSPTRTAMTALSTPTTTSKMKFCIVAQAGLKLGLSSDLPASASQNVGTIGVS
4907	18808	A	4944	484	274	

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
						HTTWPRFTYLLS
4908	18809	A	4945	103	412	KKKKKKKKKKKKKKKKKKKKGGGPKKN PGGAKKKRGKKKIPFFKRGKKKPGGI FEKKPFFGGGKNWAPPPKKKPFGEKKK FLRGKGKKPPIPGGKKL
4909	18810	A	4946	309	81	KFFFFLKLGLIFLGGFCIPPPPKKIPFF KIPPGVFFSPPKKKINFPFPPPLIPGPP RVFFKGGPPPPPPPPPPPPPP
4910	18811	A	4947	18	264	NYTORFKVBYIANIINQGDITDIYRILY PTVEYTFPKNPHGTLCRTDMLGHTGL NPKRRTCTQSGSSDNGLKITHSP
4911	18812	A	4948	418	293	QLLRVAGRCNCPFGGGGCSFSPSPCF PFWVTCQVFSKP
4912	18813	A	4949	3	252	DSAKHLALKHVVYQGLRWKLTGKLE VPHFDSKGEVRYFWSIGIPMTSVRVA YFENFLAAMRPVKASDGYTYLTKTK
4913	18814	A	4950	434	270	KRGFFPKTPPGFKKPPPKKKKTI PPPP KIGPQKILKKPPPPPPPPPPPPPP
4914	18815	A	4951	399	1	VGFSLPFLPKPKGFSKPKRGFLPPPPK GKKKIFPPPGKIGPPQGFFKRPPPLFFF FFFFFFFFFFFFFFFFGPPSVTLLELVTL LQIQTTALGRKSWGKGRIPKPCVCPVA QQTEQGAHLLGQVVEINCA
4915	18816	A	4952	235	56	FTVVPPPKKKKKPPGGGVPPFPWGGK NKKILPFPKFGPFSGAPLPFPFGQKK KPL
4916	18817	A	4953	13	194	STLSLSQLSLITFTATELLIPYIPFET TLIPTLALITKKKKKKKKKKKKKKGG GGAF
4917	18818	A	4954	177	1	PPQKKKHLIPSPGKIGPPQFGFKGPP LEFFFFFFFFFFFFFFFFFGRCSDLDG RV
4918	18819	A	4955	450	0	LPNKADKKKKKKKKKKKKKKKKAR
4919	18820	A	4956	29	158	AMLVFLYSLGDPKKKKKKKKKKKKK KKKKKKKKKKGGGG
4920	18821	A	4957	397	0	PSGPPPPPPPPPPPPPPPPPPPPPPPS SPFPAPPPPPPPPP
4921	18822	A	4958	257	397	FFFLSFTVAQAGQGXGYSGLDPPPPG FNLPSCPSLPRIWNYTAPP
4922	18823	A	4959	419	266	RPHHDGQDGLLELTSSDLPASASQAGI IGVSHRAQSIKSLAPQVWYPPSF
4923	18824	A	4960	300	190	FFFFFFFFFIVAFFFFFLCCEFFFFF FFXIFNNIF
4924	18825	A	4961	3	179	DAWLPFTIAALAILHLFLHETGSNRP LGITSHSDKITFHPYTTIKDALGILLFL LS
4925	18826	A	4962	2	182	RVNAKDSKWLTPLRHVASCSSEAVQVL LGHSDVNRDKNNQTPLHIAAPKAVK CAKL
4926	18827	A	4963	273	440	KIHQHCWWEYKLLQSLKAAWHFLKEL KAELPFNPAIPLLDIYPEYKSVLYLKT
4927	18828	A	4964	179	3	SLPFCNLTAKKLLFFKCRKNGFFFFK MESHSVTQAGVQCNLSLQCPCHGLKQ FS
4928	18829	A	4965	268	364	TVCVIELLTSGDRPASASQASRTGLSH HAQP
4929	18830	A	4966	374	2	QNFPLKKKKKKRGVGFVPPNPPPPGQ



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /-possible nucleotide deletion, -possible nucleotide insertion)
						GGGFFRSITLGNPITKPLFTASPKISPPPL WPGFFPLPWWGNAGKNPLPGGGFFPLT KFPPLPSSSLGKKKKFRFKKKKKKKQAR WLTFAIPTPREA
4930	18831	A	4967	79	346	DKIFSNISCGIVLDLLAYNWDAYATRL GIYKHWDPLIIDKDTSSCLRSFSSYPFR LESLLDDFYILSSGLILQTNVFNKTL LKQVI
4931	18832	A	4968	3	93	FLHVGQAGLGLPTSGDPPASASQSVGLQ A
4932	18833	A	4969	158	1	SKSNFAYITFPIDKNGLTGKKTINRVTK NMANDLNRHFSKVNIMQAKRYMK VGQAGVELLSDDPPASAYEGAGIPQVS HHTWPKHFFPALFVACISSLVNCLFQLF ACISIGLSFFFFFRGDLQNLKLAGL TVLG
4933	18834	A	4970	2	266	GVKHAHLIFVFLVETGFHHVGQDGLNF L
4934	18835	A	4971	3	96	NFTPLFTYFEMESHVSAREGLQWHLCS SLQP
4935	18836	A	4972	253	348	PMRIPQHKLSLWPGFALSVSYPFERLLF SADVSYKVLNRETIVLFWIALCQRTGLS CFPTQCEKQLGLIVLRYNNRTYSIDD IDWSVKPITHFLKRGIEITTVDY
4936	18837	A	4973	326	2	DASLVFKVAETANEERVKMKMCKYKFGN KCGREGGREGKREERREGRKEGREGLR EGTDEEREEREGREGLSYPFINSI
4937	18838	A	4974	3	244	THFSLTITSLQPEDIGITYYQQYD
4938	18839	A	4975	6	79	PGEAGNCINPGGSCSEPSRSHCTPAMA TERNSVSKKKKKKKKKKIPRGRGLPPV SHPFWKAGGALWFDLGTLEPPWPTGETP VFKKKKKLTGGGAPLWAPITWGGG
4939	18840	A	4976	15	339	IEIVDPDKERGLKLLDPGSLSLNLQ
4940	18841	A	4977	204	275	RRPSHHGLVAVSVGGAGVMAVETLSPD WFDVVDGSGKLEAVQLNKGKFLKEE YTSQARRTRALDDSGAWDSNLEPMA WRRLPYEQSSVLELIKIKENKLVNRVVTG YAGL
4941	18842	A	4978	3	352	AASTMANSEFWQYRPPFFFLQPNVD TRQQLAAWCSLWLSFSLHKQSSMTLM KSRLTSLSTVMLDC
4942	18843	A	4979	219	3	FQGFFLRDLKVLCCPGWSRTEPLKRS CLGLPKCNDYRELEPRLA
4943	18844	A	4980	142	3	FFFFFSETESRSVAQAGVQRDL
4944	18845	A	4981	351	2	SFFFLEFTECCSVPGVQWCDLHLPLQ PLPPGFRFRSCLSLP
4945	18846	A	4982	133	3	LGSLHDTANTLWPRLESRTIMAHYSLD LPSSDPPITSASHVRGTIGNRSTRP
4946	18847	A	4983	3	161	GPSNKKRGSKRAHVLAAVSQGATENFL EKGDITAKESQFLKEELVAIVEDVRKQG DLMKAAGEFADPCSSVKRGNMVRAR ALLSAVTRLILADMANVYLIVQLKVV EDGILKL
4947	18848	A	4984	363	3	LQVCYGRRVMSNREYGAWQVQVESKNN PFQDA
4948	18849	A	4985	101	1	PPPHSPPDVLETSVADAAJWVDVKET LQHQRYPNVGIGDCTNIFSTKTAARVA AQSGILDRPISVIMNQTPSKYGDYTS
4949	18850	A	4986	341	1	

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, N=Methionine, Q=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
						CPLVTGYNRVILAEFDYKAEPLSTFPFDQ
4950	18851	A	4987	86	1	KCSGTTSAHCNVRLLGSSNSGPSASRAI
4951	18852	A	4988	124	3	LPWLCKSPFKTTPQFQIYYKAGKVTVMYSHKDRNIDQWN
4952	18853	A	4989	305	150	WLLNRYRSHSAEVQVCQFLTWVFTSLGSPDHFSKFFNMYFFKICFDYWK
4953	18854	A	4990	64	340	KKKKRNLKFPQGRKPLSPNPLGSLGGKNGPPGKSRDPDWPPIKPGKSKKKNPLKKKKKKKKPLSGGGGKKTPLEKKKKKPPPGP
4954	18855	A	4991	3	158	PSLVQTLRLDAGQAGLKLSTSDSPASASQSGATTTGVSHAMFQDCSLNSN
4955	18856	A	4992	116	66	FFFFFFFFFFFFFFFF
4956	18857	A	4993	3	107	QGAQLTPVLAALWEAKVGGSEFVSLRPFWTQ
4957	18858	A	4994	1	105	KLDRLARHGLYEKKKTSRKQRKRNKNKKVRGTW
4958	18859	A	4995	110	3	ERIGRYKTVPLCTQLELMARYPLPSPKPIKIKN
4959	18860	A	4996	109	3	DEVSTLCPRLECNNTTILAHNRLPSSDSPALAP
4960	18861	A	4997	1	148	ACCPFCTIYLLNFMITKAPLMGTSKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
4961	18862	A	4998	3	110	VILQGSNDVELVAEGNSRFTYTVLVGDGSKKTSTRP
4962	18863	A	4999	3	330	FIADRGAEYVSAREMWTICFELLQILKAHKKAIREATVNTFGYIAQAIGPHDVLATLLNNLKGHQRNVCTTVAJATGATCSFPFALPALMNEYRVPRLNVQGVLK
4963	18864	A	5000	3	110	VILQGSNDVELVAEGNSRFTYTVLVGDGSKKTSTRP
4964	18865	A	5001	25	329	NSRRRRNDQGSFNLQQTFFNTLPLPLPEHRSLLKRSARERTKDDIPEDKGNTKQCEIMYVKPKQSQDHLKIKSESKILKKAQKDGLHTLHLN
4965	18866	A	5002	278	345	EDEEGVNDGEVDEDEDEDEGLG
4966	18867	A	5003	101	3	VRIITSGTGKKKKKKKPKPNYDPKVTDPER
4967	18868	A	5004	18	350	VSHECLTPIHONVLTGLVLSLSCPSPVPSHTHKGTHLTHHTHTHTHTHTS
4968	18869	A	5005	26	147	KEEVNRHAFANDNIVYLVNPFVSAFVCLKISCFCKGRIG
4969	18870	A	5006	85	1	SASRVAGIIGKHHTRLIFVFLVETQS
4970	18871	A	5007	370	3	RARKPLINVLKIKNSPWLYKKTRINFQKEKKSPPSPFFFLFKGGGLPPGVFSGFLKKIPPPFFFFFETESRSVTQGVSVQVNCNGLLQRPFGSKQLLCRGLPSSWDYRCLSTRP
4971	18872	A	5008	1	85	IRILSKIKNALTHPLQGTPTPLPLILF
4972	18873	A	5009	218	93	FF
4973	18874	A	5010	3	250	RPRRRRLQENHLNLGGEGCSERSRHCTLTWATEQDSVSKKKRVFPFPHRGKFFWAGGPTFFPLKTVFPFGGGKPNF
4974	18875	A	5011	336	0	SSSSPSSSSSSPPPPPPPPPPPPPP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Yrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
4975	18876	A	5012	2	80	SNQNGTGGESLYGEEKPEDNFHYKVK
4976	18877	A	5013	53	324	FLVFFVPRNSKRTSLQHLALTSMSWV QSPSHLELMNLCKRHINLRVDPGLRBM HYTEVCGVDYIASPNARSLRGPILTAVLA AQVNES
4977	18878	A	5014	329	1	FFFFFSETESRSVAQAGVQWRYLGSILQA PPPGFM
4978	18879	A	5015	193	32	PLLTLCSERLCHCTFWAIAERDSVSKTN KTKQQQQQQQQGKTCKMPTALLGQI
4979	18880	A	5016	354	235	CGEIGMLHCWCECKLVRPLATNLPLRD GSTLTVGSSSSP
4980	18881	A	5017	348	2	RLLVKLMELHGESSSGSKATGDE
4981	18882	A	5018	76	1	YFFLSQVSPLSKEDAGSEYCHASNS
4982	18883	A	5019	68	356	YFGGVGGGFFFFFFFFFFFNGSGGVFTVG VQALIFFFFFFFFLGGFFFLVRDYYFVAVP WGGLLFFVFFVFFVPCFVFFFTFGKKK NIPQGVFLCW
4983	18884	A	5020	1	288	FFLNLKNTAKWLSYTDGIVVATARDP MQNFKNLVGYHNSITSENLPLQGANERL ESQSGNFSVVFVTFNADRKGNVLLLEN NEMTILKPRTSV
4984	18885	A	5021	133	1	VVATEINMTSTPKNMPGTGAHTCNFTSL GGQGGQITSPOKFKTS
4985	18886	A	5022	2	337	RRSDNPFKNRIERERKKQKLAKBRAGLS KLPLDKDAENAKQFFLEKILQGEKLLNQ GEYKGVDPHLLTNAIVCGQPQQLHVLVQ QTLPEPVFQMLLTKLPTISQRIVSAHSL
4986	18887	A	5023	1	325	VDGCPANLLSHRSRLVIRAEITSLGSEHF CDRGEQVTLFLFNDCLRIARKRRKRVIGT FRSPHQTRPPASLKHILHMLPSLQIKKA LDIETEDCHNAPALLVRPPTBQA
4987	18888	A	5024	135	2	ATMFLNSKVSKYSYGLLGFHECREKGM TWDGERDPSGILQLQ
4988	18889	A	5025	2	94	KTATLILGGHYDSXNKATRDGLLARR HRL
4989	18890	A	5026	2	362	QELERSWAQRCVCULALVNLMLVPPV SRSMGPRSGHQASRTPSQPSKEERVA MKRALGVPPTVVSTSPIQHEVVEVSHL FTIQGSDPSLQPYLLMAHFDVVPAPEEG WEVPPFSG
4990	18891	A	5027	222	84	AASTFCHVSQAGLELTLSDDFPASASQS AGITGMSHRTQPMVHLV
4991	18892	A	5028	366	0	SGRSKKKKKKKKKKKKKKKKKKKKKK KKKKKKRGR
4992	18893	A	5029	231	68	AGMGSRALPKPLMLSHSSLEAVELPDSF SPETLSLLEGLQRDVNRRLGCLGRG
4993	18894	A	5030	2	366	LNLAGRGCSLSRCHCTFAWVTFSTFKK KKKVPHGGYFVAQLLPPRKNRTHRRPQA QGERTPGPGWAPVITGLPERRGQAPTQP PSAPKGFPHPTNKSSSEAKKKKKKRVG RKNVNGYIL
4994	18895	A	5031	241	368	QVERNFKSQSGAEAHICDLSTLGGCGGQ ITRSGVHDQPCQHG
4995	18896	A	5032	279	396	DGGHWFTVVAHCNPGTLGGGGRWITRS GVYDQCGHSE
4996	18897	A	5033	173	398	SNRSSLRVHFFFFFLKTNFSPCPGG RQGPWSTLDP PPPKVKISFLTPPKRW

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, ^ =possible nucleotide insertion)
4997	18898	A	5034	2	143	EYRPAPPPPRRNFGFLIKIG SNPPALTSQSMGITSMTRIHALPIACFLV FVFLFFEMSGSLAQAEVQ
4998	18899	A	5035	350	2	QRISSVQTSIOLPFGMTVKARATREVM ATTYIEDIVIELIQLPSNYPLGSIIVE SGKRVGAVRLFITQKSFILFSFLT LCLCLQHFNDFLLLIIVPILIAMAFILM TERK
4999	18900	A	5036	1	100	HBOGSSSQRTLSVQBAARYLKVSNEIRI LIAIF
5000	18901	A	5037	247	334	LQIDISAVVAYTIAVKEGDELNLMKKAAS
5001	18902	A	5038	2	296	DKAPHLKVINSLKQIMINTFVPSGKNMQ VVDKELQGLCNFPQPPPERMKGLAVT DIPLGKYLHLEALKKKVIKFFYKPLRCD INTAKCTGLRYTAQ
5002	18903	A	5039	152	335	RPINSVYLLFFFLPWGLYLDVKNRIFTF ILSEKYFDMKKIQCKBGLDIYKKFLTRM TRISE
5003	18904	A	5040	336	1	GGLTISLLKEKSGSEVAKFTLEQLCLT CNIMSTASYCVAATQQLKEELKKEKVDVS LFDRINLGGMGTFSPVISSHLVLQD VDAACDPAMVAMSKMQCQNVQHVGVKSS
5004	18905	A	5041	3	204	LNLGGGSCSEPSCHCTPSWV^ARLHLK KKKKKKRGNPLKNGKENFFLQILVN PRNSLENLAV
5005	18906	A	5042	382	148	WCNHRGPRSRKKSEBGTKSRRLGATIR MVPHTTRTCARDPELTSKSKCVYIEEH THTHTHLYIHTHTHTCIYVXTH
5006	18907	A	5043	137	1	RPRERYMKGFSTSLI^IKMKIKITMKYH LSHLIPVMAITKTKD
5007	18908	A	5044	198	34	KQASRFCHVQADLELLTSSDLPASASQ SAGITVQVHSCSQPNFTYLCILVTDHFF
5008	18909	A	5045	11	357	LITVYIIMFKLLEYEKREGLTIKQISE GQKVKELQRFKEHKAQD^SALQSIRESK MLEL^NRLRESOERIQIDRKCKRKNAR GPYNKFKYSQRMKSPPGPPQMGWGPRIN FFV
5009	18910	A	5046	2	193	QLQLLTSSDPPASASQAS^IAGNSHCTQ PQVHMPSLYHFRFLQVTDKLLRASAD LIHRGIT
5010	18911	A	5047	1	196	KLCVMNNSPMKAAPRNFSCAPSLSL^PF SFRKTTITLISNTADDPAYFDLC^MEPC SMVLFPVFC
5011	18912	A	5048	386	276	AQAVLELLDSSDL^PSPASQASISGVSH CTQ^PDSIF
5012	18913	A	5049	1	324	VDAAEKLEASTGNLRRFKERSCLHNK MHGRATVADTEAAGYPEDLAKITD^RGV Y^TQQI^IANGDEI^AF^CWQIK^ICRI^FLARE QAVPGCNAS^KARL^TVLLNANAAGD
5013	18914	A	5050	1	129	PKSCHCF^ANV^TQDSVSQ^KKKKKKKKE KKKKMPV^G^ARI
5014	18915	A	5051	193	356	RSFIPASAGASTL^CLK^ES^NQ^GQ^GAVA H^CN^ST^GQ^G^SQ^I^AT^RS^Q^V^D^OS^GQY
5015	18916	A	5052	192	341	AKRVKRNHFF^FFFL^KQ^F^CV^I^NQ^GR^D DP^GS^L^K^P^L^P^G^L^K^G^F^S^C^T^P^L^N
5016	18917	A	5053	340	1	KRI^D^K^P^Q^K^L^R^L^A^T^K^L^I^R^E^A^P^E^K^G^Q^A Q^K^E^I^H^K^S^I^Q^A^K^E^I^F^K^A^D^I^K^K^S^Q^F

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
						DRQKALDILLVQNALSELSNRISQVER RNSLEDDKVFDLTRSSKAGKGRINRYS S
5017	18918	A	5054	2	383	VVKVATQPADNPLDVISRKLLHGLPNVGR DVPRLSLPGKLVFPSSGTSHFFMLGLGD IVMPGLLLCFVLRYDNYKKQASGDSOGA PGPANISGRMQKVSFYHCTILIGYVGLL TATVASRIHRAQPC
5018	18919	A	5055	2	383	GSVLSKKGDYLYKHYNASLLDGTLLDST WNLGKTYNI VLSSGQVVLGMDGKMKMC VGEKRVLLIPRLHYGEAGVDSEVPQSA VLMFDILLLEIAVAGLPESGYMFWNGEVS PNLFFRIDKDGNGEV
5019	18920	A	5056	2	383	AVIDEVRITGYRQLFHPQLITGKEDAA NNYARGHYTTIGKENIDLVDLRIRKLADQ CTGLQGFLVPHFSFGGTGSGFTSLMER LSVDYGGKSKLEFSIYPAPQVFTAVVEP YNFILTTHTTLEHSD
5020	18921	A	5057	26	452	KLMSLRQRQAMHEAALDEFRTGYRQLF HPEQLITGQEDANNYARGHYTTIGKENI DLGVDRIRKLADQSTGLQFLVPHFSRGG GTGGGFTSLMERLSVDYGGKSKLEFFI YPAPHIVFTAVVEPYNFILTTHTTLEHSD CA
5021	18922	A	5058	2	385	AVIDEVRITGYRQLFHPQLITGKEDAA NNYARGHYTTIGKENIDLVDLRIRKLADQ CTGLQGFLVPHFSFGGTGSGFTSLMER LSVDYGGKSKLEFSIYPAPQVFTAVVEP YNFILTTHTTLEHSDC
5022	18923	A	5059	3	390	GDAANNYARGHYTTIGKENIDLVDLRIR KLADQCTGLQGFLVPHFSFGGTGSGFTSL LMERLSVDYGGKSKLEFSIYPAPQVSTA VVEPYNSILTTHTTLEHSDCAFMVDNEA IYDICRRNLDIERPTT
5023	18924	A	5060	103	3	KIFFFLRNSFALITQAGVQNRGLSLQP LPRA*
5024	18925	A	5061	262	412	KASPRTGTAFONGKRTSYLLGNFOYT FGGITGCLKNGLETSYNWFTH
5025	18926	A	5062	293	406	VIIGSIFEVIWVIRKGTSGISVLRL ELLRIKFVTK
5026	18927	A	5063	419	15	WEEEGPLPKKKRGGPSNRKGNITMGPF KRPEKKKPPPPPRKINPFFFFPKRKGPP PVRVKGKGAIGSRNPLFGSRDFFSPA PQKSGAPGGPPPPPVNKGQFFFFFLVE TGPHIVTQAGPELLSSSSPTI
5027	18928	A	5064	2	216	GLWHLFIKDRKILLCCQWNSQTPSLKO SSHLSPKPDWVLEPLCLIFLYPWFLC SLSLSPSLHYTYFQ
5028	18929	A	5065	259	36	SQPHWDYRASRARELATPLEVMLQAPV CCLFLQSPFLAQAGVQNHLYLSLQPPP PGLKQSCFCSLLVPLA
5029	18930	A	5066	2	404	GKGAPTTSLISVAVTKIAVLNLDLP GACISLTCGGANIGTAMAKDERVNLSP TGSTQVGKQVGLNVQERPGRSLLLAGN NATIAFREDADLSIVPSALFAVAGTAGO RCTTARRLFIESIHDEVNRL
5030	18931	A	5067	1	400	GENMITGTSQADCAVNVAGVGEFEG ISKNGRTREHALLATYTLGKQLIDGVNK

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SEQ ID NO. of nucleotide sequence	SEQ ID NO. of peptide sequence	Method	SEQ ID NO. in US 59/051,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						MDSTPEPPYSQKRYEIVKEVSTYIKKIGYDPTIAFVPISGWNGDNLEPRANIPLVITGWKATP IDC DAS GTT ILDA
5031	18932	A	5068	41	392	GSPHHPCAHIERKKRPYNSNIGPTTKRNALRVABVMDDYKSHVYIAWNLPLENPGIDIGDVSERRALRKRKKCKNPFQWYLDHYPMKRYNNVTAYGELRNNAKADVCLDQGPLEN
5032	18933	A	5069	3	395	GTPTRPHILLQALFIRANLPCEPYDITDKKGLQALKICQMLDPAHQGVLTVTLNNTNLIQMAIQGRWFDKSSLLITLPYIENHHLHLFKKKRPIMKGPBASKSTSI ECLPELIHACGGKDHVFRSLVQQ
5033	18934	A	5070	3	405	PRASEVCGFSCHITCNVYAPTTCVPVPEOTKGPLGIDPQKGIQTAYBOHVRIPKPAQVKKQWRALAVCDPFLFLYDIAEGKASQPSVVISQVIDMRDEFSVSVLASDVITHASRKDIPICIFRVTASQLSAS
5034	18935	A	5071	3	393	ITRQEPIDGILASNFPPTTITMTVIGADIFDRBGDGYIDYEFGAALHPNKDAYRPTSDAFKTFHOGTROVAQCI CAKRFLVRHEIGENKYRFPFLCNHFGDSSHQRLVRLILLSTMVVLDDGGWALDQFLIT
5035	18936	A	5072	3	394	ITRHEPFDGILASKFPPTTKIKMTVIGADIFDRBGDGYIDYEFVAALHPNKDAYRPTSDAYKISDEVTROVAQCKAKRLLAHSHIGENKYRFPFLGNFPGDSSHQRLVRLILLSTMVVPVGGWALDDEFLND
5036	18937	A	5073	1	393	GEDAAANNYSRGHYTTIGKIFIDLGLDRICKLADQCTGLQGLFLVFRPGQGTGSGVTSILMEHLSPDYGPQSKLEPSIYAPQVPTAVHEPYNMMLTTHITLHSDCAFGMDNEAIYDICTNLDIERTTYTN
5037	18938	A	5074	39	482	IGLHSAWRDDKTYGYNPDTVSPVPSGNNGDNMLPFSANMPWFKGWKVTNDQNASGTTLEALDCILFPTRATDKPLRLPLQDVKYKIGIGITVPVGRVETGVLPKGMVATFAFVNIDTTEVKSVMEHLSALPFGDNVGFNVKIVSV
5038	18939	A	5075	1	390	GVSMASVLVIIYQYVVRNMPDHNLPITVAGWKYPLFRGTAVFAFGIRVVLPLENOMKESKRFPQALNIGMGHTTLYVTLATLGYHCHEIDIRGSTTLALPDQVWVYQSVKILYSGRIFVYISQIV
5039	18940	A	5076	330	462	VNFFFRKGTTFESFTAQARVPACSLNSLQPLPPGFKRPSCLSLP
5040	18941	A	5077	1	403	GGWGVSAEDFEYADVDURBLEPTLSNITTEQSLNVIPLGGKGGVKTTCSCSLAVQLSKGRESVIITFTDPAHNSHADQKVSUKVPTKVGYNLNFAMEIDPSLGAELPDKFFEDNMLSMGKMMQAMSAF
5041	18942	A	5078	348	1	RPGQNNITERWQSGEVLITQLLRTAKSVKNVOLLNWKTFILKHLILFYDPRIPFVSNYPKKKKTYVHKKTQAIFISLPRTFLLRQSLNMLPQDLSS
5042	18943	A	5079	248	3	PGQVLERERTCRPWAVNVNVCICLAGPAKPNREDVSSQESLQNSIPPTPTLTS TAVKSRQPLMGLKMEEDCGSLCF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, - = possible nucleotide deletion, - = possible nucleotide insertion)
5043	18944	A	5080	3	192	GDGSELRSCHCTPAMLTREDTSSQKKKK KEKKTNWPAPELFFPFLLEKKGQNGKP NMKKVL
5044	18945	A	5081	10	171	CPCLGPGVGVCRSLLLKPLGCPGLGPPNLQD ARQKFRSVLVEATVKCLDELVTIRSTRP
5045	18946	A	5082	94	1	DFNPGHVAHACNFSTLGGRGGWITRSQV QDT
5046	18947	A	5083	142	3	AASTGSHSVAQAGVQWHDLSLQPLPFG FKRPSFLSLPSSWGKRIA
5047	18948	A	5084	257	177	ISLGEVAHACNPSSTLGGRGQGITRPG
5048	18949	A	5085	143	1	GGESHSDTQAGVQWCYLGSTQPPFLTIF KQPSCLNLPSSMNYRCVPP
5049	18950	A	5086	3	87	IFVGQGLVLLASCDPPFSLASCSGDTITV
5050	18951	A	5087	375	220	LSLSLGHVLAATSKKPAFLMFAFPTLSFV STNWVQFNFSPEGLMLLIFPFFF
5051	18952	A	5088	40	203	IFLFLLLVSFTFLTWQTFPFWGLTLY NDLAWFFNSGIFSPFSWFSRAGELG
5052	18953	A	5089	1	145	WNRVVAQGLGLLLSLKSRACEIQMTQ SPSSLASVGHREDGDVDA
5053	18954	A	5090	146	328	FMFPFLLESLETPSSKLTNPNLPPFP TESCSVAQDGVQWYDLGLQPPSPGPKR LSCLS
5054	18955	A	5091	338	1	PNLPSVOLPPTTSCPTPLGLDILVARAHF AGWKHQINSFSLPMAPEGMEADPNPF HPHIFLCLLHGPHLAVSKLYSLFYFYYY YFSRWSPTFLVAQAGVWNRDGLSLQPLFP
5055	18956	A	5092	2	327	FPLTFPIFPSSPKGNPPPHYNPPPPP FRTPPPPPPYPLSPPKSPPPPPRVDPEL PYSIFPRPNLISPPPYSPFYLLQLQAF P
5056	18957	A	5093	133	3	AQTCTPSTQINSKWTIDLNVKGKTIKLL KDNIREKLDDLGCGE
5057	18958	A	5094	170	350	AGGQQGNFYSLQPNPFWIRESSHSLTPK FNRIRATYTPGNPGFFFLMGFGLVAQ TLFN
5058	18959	A	5095	133	274	RDTITPLESGIKGYLFPFSKITSSELVS KIGDKWKIRKGBLDEVAQ
5059	18960	A	5096	2	188	REMQIKTTVRYLITARIVLLKSEKRN CWIGCEKQTLHLHCWBECKLLQLPLWKIG WRVDA
5060	18961	A	5097	235	81	FPKKKQAIKKFOAQSINLSLSLYIYA FTYTHIRHRTHTHTHTYIHIS
5061	18962	A	5098	355	169	KILLITDSQAHISCPSECKKYPNFFF HPHSVYVTDKIRLLEKQLPHVFSNME PFEVCN
5062	18963	A	5099	160	1	FSASYFNSKKKLTFLMLKLWNPPVCF GMESHVSVAQGVQWCHLGLQLPLPS
5063	18964	A	5100	364	151	QMGFSHIGQADLELLTSSDPSASASQSA GITGVSHYAGQFELKCFSAHLPLQGG TCVQKTAQPSREAL
5064	18965	A	5101	205	3	AASEGVOWPDSRLQPRPFQVQKFFPLS FPSSWGYRGAAPPFGHFFFFFPSSRDEIS VCLGWSPTER
5065	18966	A	5102	349	207	DGASLCCPDWGLELLSSGLPALALQNP EITGVGHITQPWTLISLLIY
5066	18967	A	5103	425	0	CEFFENKDFCLPSKKKKKKKKKKKKKK KKKQSSQTSYS





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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y-Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RDHPGQHGETPYDL
5110	19011	A	5147	3	413	SFYRGFIPVLQIVIVLITGDPSLHGDAW SWNEFFLTVLFI TALNMLPLIGLTVVNA INFQDIADLAFVSWTKPHFPFSVSQII ADMILFPLLLQALFLIQGIAYSLFFIHLV GQLDSLAINLTLVLSLYCSEYRLVIN
5111	19012	A	5148	409	247	QTRFRVDAQGPHFLGSSDYPTASASQV GITNMSLHAGHGHFTASMGRAFEN
5112	19013	A	5149	284	1	AEASRAHMEAHARTQGTGSKABGVSPV BEYRINRRPGPDRAHADSRESGEPGPGP PPTHANFVFLVETGPFPRVQAGLEFPPTS GDPAASASPV
5113	19014	A	5150	439	120	FSGPILKSGVISAICNRLRLGSSDSFA SASHVAGITARNPARIILKAFAPSTCTV VNEKHEQOTCIQRSDLPAGRQKKTGPKN RPGVNAFPNAPSLGGPGGRIA
5114	19015	A	5151	415	0	FFFFFFFFFFFLPFGVSPFYIYIMYI
5115	19016	A	5152	67	179	TCISLPIATVHVCCVCCVCCVCCVCCM VFGVSLPCN
5116	19017	A	5153	280	2	KTPFFLLNLKERTRAPFFLKRTPFFKKKDF KIFPSKIRNTPFFPPGKRPPTLFKKKFF FFFFQKQNFPSPKKGGKKKKKKGRS RSKTSRV
5117	19018	A	5154	296	406	DRVLLCHSSCSEVAESRLTAASTNAQA ILLPQPPPW
5118	19019	A	5155	114	402	VNRIFASVEKKKKKKKKKKKKKKKKK
5119	19020	A	5156	110	1	QRFLTLKSLILRLGAVAHACNPSTLGG QGGRLWS
5120	19021	A	5157	382	95	SSSSPHVLTGSQLRFPFFFLKIFFFP KATNPGGVFFLTPSPKKKFFQNSQVG FNGPPQKQKNSFPFPVKPGPKGPKFR DDPFFFFFFFFFF
5121	19022	A	5158	2	350	TLQDGRQSETPPQKKKKKKKKKKKKKK KKKKKKRGGGFLNKGGGPKINGVEKFF FFFFGGGKKDLGFFLEKIFFLGGGIWA DPPPKKISFWGKKKFWGGGGKTLFFC GGKK
5122	19023	A	5159	1	208	PTRLTYLVKGLNGPAETFLSSFOETRL IDYKIMVDHGRVVRVAFQNAVAGAKYA RAYITHFLNVLGE
5123	19024	A	5160	1	208	PTRLTYLLKSLNGPVEIFLSSFOETRL IDYKIMVDHGRVVRVAFQNAVAGAKYA RAYITHFLNVLGE
5124	19025	A	5161	419	25	AQKKKKKKKKKKKKGGGPKKNFGGKK NKGKKKKKFFLRGGGKKKTGGILBKKN FGGGKKRHKPKQKKKALAKKKFLRGK GSKLAWGKKKN
5125	19026	A	5162	475	150	KSFSTGDAKVPDPPRCCLDDKLPSP VLPVLAETCDKVGQDGLQLATSGHP HLTFPNCNYRREPPRPTS SGQPHDIET LHYRKGADRFKAHLPK
5126	19027	A	5163	237	409	PHNQKTYLDSALCTLYTVVFLVLDGLP LLPLQLCSGTVMWACHNIGLGSRSPPAL A
5127	19028	A	5164	373	476	LGFLLSFLSTRSHVAQAEVQCDRGL LQOPTP
5128	19029	A	5165	374	132	IFYSFFLYHMLGRYHKTINKLXIMNL DAVAHACNPSTLGGGRGRI TRLDGRDHP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
5149	19050	A	5187	346	3	RFLPLQGQGVIELTPSTCLQPPKQWMDY KGEPLRPAQKCKPFFKKKKRRKKVQNSVA VYMVYHSMCGENKLENKRWAGLFTTHTHH THTHTQKKNILSRTHKKLVITTSBEG TL
5150	19051	A	5188	11	109	GETPSELKLVQNIKWAKWKNPVPAMPWEA EARES
5151	19052	A	5189	3	151	QLLRKPRQENHLNPFQSKCSEPRLEHCT PAMATVQDSISNTNNDNNKCP
5152	19053	A	5190	2	373	AVAAKGVFLVRIITANLAGNFDLILPVP APSVINGQSGHAGNKLAMQGFMLPVGAS SFKEAMRIGASVYHHLRGVIKAKYCKDA TNGVDEGGFGPIILDNDALDELVKTAIQ AAGVPDEGAIGR
5153	19054	A	5191	55	421	ARVADVCSMKELHVLIVERAKYIGFC ELPLDDQGALVTAGHGLLIGATKRSN VFKDVLGLGNDYIVPSHCPELAZNSRVS IRIIDELVLFPQELHIDDNEYALKAII FFDPPKETEAA
5154	19055	A	5192	163	466	TCFLGSGSAGITSVSHCSREVFFLKLI HWRQGGQVALLINATPHSPCCPQYRLAPI PRARHDFACASLIPACILLVHVLMPRV SAGRGVPRAGIQGR
5155	19056	A	5193	470	0	ECLAFQVVAHNSPWTGGRGRDKK
5156	19057	A	5194	491	281	RGLALLPWQGSQSHLAGSLDLDGSD PPASASQSVGDMVSHIANPSLVNLSPV CLIHSEPKTKPEGR
5157	19058	A	5195	3	222	LSFHSILHRCILVGLTTSNENVSPPSLLEL LSRLLATLIGDYCGSLSEGTISRNVLYV ELLDEVLRLESRCVAQA
5158	19059	A	5196	20	191	STWNNSSRGQCSFPSEHCTPAMVTER DSVSKTKKKKNNKALAPAVHPTSHPG S
5159	19060	A	5197	460	350	RRLRKNHNLNPGGGGCSLESSHCTPAW VTERGPSD
5160	19061	A	5198	174	41	SLGELLTECLFETKSHSVTAQGVQNRHP GSLQPPPPQPKRIIPP
5161	19062	A	5199	131	454	FEYFKNRKKFFFFFGKGVSPCAPGGK AGDPFKLREPPPPRVKGFPGPPPPSGGN NGPPPPPRVTFWFFKKGSGSPFWGQVLT TPGGGPPPPAPQRGGINGLDPPAR
5162	19063	A	5200	168	51	TVKTPIRPGAVAHACNLSTLGGRGWMIT RSGARAPNR
5163	19064	A	5201	414	497	LFXXXXXNDSIYNFVELDITEETLSR
5164	19065	A	5202	381	614	VGPQAPFENVALSTCFSAAPEGSQQFYI PPTCFPFVKNLLSVTHMLFIYFLSWI SVAGQGVQNCNHSGLQPRPSLL
5165	19066	A	5203	377	485	PKEPGQPCAPQKQPHADQPPRAPQFP PCAQPPQ
5166	19067	A	5204	54	434	MRTDENLRNLNPFQFGSSNAAVECPDIL DPRDMCVLNPRLREPPFAKCECILLSEVF EICHVPVVDVWYFVSNCLDTCGCSQGGD CECFCASVSAZAHQCCQGHVAVDWRTPR LCRECPQSPPEGTE
5167	19068	A	5205	201	418	GDAGAHAVILRLPGHFGTSHLFFSSLT TSPILGKRVVGGPNKRNCRDARTCYLLP TFAFAHKURDVQDRTY
5168	19069	A	5206	27	177	NSFHHAGQSGLLRLTSSQPPASASQSG

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5169	19070	A	5207	6	1175	ITGVSHRAQPHAGTFLSPFHR DLGPHTPAWTRPKREDLVYQSTVRLPEV RISDNGPYECIVGIYDRATREKVVVLASG NIFLNVMADPTSEIVVAADTPAPFSRYQ AQNFLLVCIVSGGKPAIMVYFKRDGEPI DAVPLSEPPAASSGPLQDSRPFRSLILHR DLDDTQWQSLSLIDAFNKGKPIETRP SRGLTDPDNIILLOPTTENIPEPTVSRFP PRWVHASPTTYFLRHSRTPESSDGTVEVR ALLTWTINLPQIDNEALFSCVKKIPALSM PMQAEVTLVAPKGPVKIMVTPSRARVGD VRILVHGFPQNEVFPEPMETNTRVGSRLD DGSAEFDGKELVLRVPAELNGSMYRCT AQNPAGSTDTHTRLVFPENPIPRGTED SNGSIGPTGARLTLLVLAITYILELT
5170	19071	A	5208	401	3	FFFFFSETESHSAQAQGVQNHHLGSLQG PPPGF
5171	19072	A	5209	402	229	GFKKKGPPPPPPPPPPPPPPPPPPPPPP RLSGSKGVWVWSGSKLYNTPGCCGRSW FT
5172	19073	A	5210	198	2	PFQAKILSSSSPPRIPPPKGGFFFPNPQ VGFPYAPHKKFTFLPAPVKGPCKDPL KRFPF
5173	19074	A	5211	516	222	GSTLRITQRSMFASSTWAPSSKRLLLP RPRSVPAAGTGAHHEASRNCGRGAG ADRGPAIKGDSHPKPGYCRAPSAAPV PPGPEINPMRVG
5174	19075	A	5212	103	203	DKVSLRCGPNPQTPLQSSCLSLPKCW DYKCE
5175	19076	A	5213	409	249	RRNQVGGPRLNPGKRIKSDGIDPYIYG QLIPDKAVRAIWNREKGSFLQKALE
5176	19077	A	5214	2	170	ERKILGYIQLRKGPNVGPYGLLOPPAD AIKLFTEPLKPATSPYPLQSPAPFPKPF
5177	19078	A	5215	270	454	GQLNRNVWGDGPKVTFPRGDSVLYCHW NAVAIIGHRRHSPVQPTGPKGSLRLP SSNDYMPLY
5178	19079	A	5216	156	248	PDKSYITICVCVCVCVCVCLCVVWVME CP
5179	19080	A	5217	412	2	PPFQIFFFSPPHFFSPPPKGGFFFFPPPP KIFFPPPPPLFFFWGFFPPFPSPPKKFFP PKSGPPFFFPFKKKKFFFPPLFFFPF PGFFLTFFPPFFFPFFFPFFFPFFFPF FRMGCDRWHGFWLLRQDF
5180	19081	A	5218	165	1	QVYHKKCTNFIKIGHSBQTFHEKDT QMAKVMKSSPFLSLKGLQCTIVY
5181	19082	A	5219	408	88	PSSSPFFWSPPILGKVPFFPFFKLEFFP PLGLFFWGVVPLFSPPPKRVFPMSPG FFFPPLGKKKFFFSPPFPWPPKGFLLS DDPLFFFPFFFPFFFPFFFP
5182	19083	A	5220	3	259	NIILLIVPILIANAFIMTEKTIIGYIQ LKKKKKKKKKKKKKKKRGAGAFKKK PRGGQTFPGKKKKFFFLREVKKKPGRN F
5183	19084	A	5221	10	479	KIMPASDGRHREHREHREHREHREHRE ESSARARCVSLDQYKRVYMKVARE LCBRLIAYISQAPTMFLLRLINIIH AHTLTQNDMCLHTTLITLARGRERV PLYLRLQRMHKKKIPQVLNNSHNV

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RLWQQLYLHRRDRSDIC
5184	19085	A	5222	142	56	KFQPGVAHTCNPSALGGWGGQIKRSGV
5185	19086	A	5223	14	471	LEMRSSEIDSONYCNCDAGRNEWTSDDTIV LSQKEHLPTQIVMTDAGRPHSEAAVTL GPLLCRGDQSPWNASFNTETSYLHFPFA FHGELTADVCFFFKTTVSSGVPHENLG I TDFIRIELRGKGLATLDKSGQTRYLAIKL LTQKKKKKKTRG
5186	19087	A	5224	480	0	FFFFFFFFFFPLLVAGFYPL
5187	19088	A	5225	16	422	VSRKAKIRHEEKLYEACACGKAFNRSAA LTHQRTKHTEGKPYVCKCKCKTFSRSTH LTHHLKHSVCKPYQCNCEQKLPYCYRTS LIRHQRTHTEGKPYQCNCEGKFSLSA LTKIKRIRHTRERPYQCKKKKKK
5188	19089	A	5226	99	436	GHPSPFELPATMTAAPGPFPOVPMEDVR YLDEIMYGGHITDDGDKLCRVYLEEF MNP SLAALSGTHACGEPRLPANSHVS RPSKWKILQPOSSLOMTALANILTATS
5189	19090	A	5227	473	9	FQITATPHLAVDPTVQPEFWFSKQYLA DIRQVRASTRYGTALYMLAASINIKPG HDYVPYIRSNTVVGSAFVAVGRASDD ABGYLDFFPKGLIASHLGLLEKVELT EDIASRLREEFSKEWKDASDKNWAMNAVK I RQTVGSRDVTSG
5190	19091	A	5228	1	473	PPFIDRLPHCTACRNSARVMTDAGPHS RADYTLGFLLCGGDKSPWNASFNTETS YLHFAFAGBELTADVCFFFKTTVSSGV MNLGITDFIRIELRGRLATLDKSGOOTH YLAIKALTQKKKKTRGAGPPFPLIGS RITIHGPPFNNAAMREK
5191	19092	A	5229	170	25	KTFLLPGTVAHACNLSLTDGDSGCIMR SGVRDQLRQHDFTPSLLKRI
5192	19093	A	5230	465	0	VVLVPPQRAQKKKKKKKKKKKKKKTRK ARG
5193	19094	A	5231	419	56	CVLLRSTKKKKKKKKKKKKKK
5194	19095	A	5232	79	451	AGSNLQEBHRLPESTFNPGGGGCREPR RRHCPANAKRAKRLKKGKGRNQVEA QQRHGPFFFGLGPEGFLPRRPGSRKRKR GRNVPGPELKGPAVLFSRHRRGADLIR PFRKGRPGGGG
5195	19096	A	5233	39	467	VQQQQRAGEQQQQHPVLHLPQQIMQLQ QQQQQRI SQQPYPQQPPHPSQQQQQQQ QAHPHQSQQQQLQFPQQQLHPQQQLHRP QQQLQFPQQQHAIQQQFHQLQGHQLQQQ QLAQIQQQHSLQQQQQQQIQQQQLQRM HQ
5196	19097	A	5234	194	45	KLLKPPFNPKLHPFFFLQSLALVAQAG VKWCVNQGSGQPPPPQVKNST
5197	19098	A	5235	204	475	ASITVHLHNVKCYSGSEKTVTPMPSSS WFGQPDAQLHGLRPGAVHACNPSTM GGRGRIITSSGDEAHP
5198	19099	A	5236	59	357	NHWKRIYCKVYRKKIKNTNTNTTQVQ NFQRNRTKSSPTIFRQSHYNKHKH I QRKRQSIETDLEMTOMLELVWIFKVIV ILTKIKTPKYLKING
5199	19100	A	5237	447	166	ELLAPWOTVYNNMVA/VLFFFWIKAPGI PTPSFASRTHSPFFSFLFLFPLGLGX GFPLCQGGPKSLNLKTPPLIGPPGGKK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
5222	19123	A	5261	1	175	IKGNQIGKKBKVKLPLPTDDNLIYLNENPK DSAKHYKQSKTFCPLPVLGSRCKRTCP LA
5223	19124	A	5262	2	145	QVSLKLLGSSDDPALTSQSGIMGVSHR TRPRNTDFKNNYQKSNITQ
5224	19125	A	5263	182	3	STTSFLNFFLTENVSHYVSQAGLKVLS SDPSSASHSAGITGMSHTRFQQPLLN LKV
5225	19126	A	5264	183	369	WNSLDPPFFPFPSFPRGYSSMGKVQDAPI FYRRFIDKSKPRANTWGSIGGLYQQQIH PMDALR
5226	19127	A	5265	329	207	RGCSERLSRHCTPVNVTBQDSVSQKRKK KSPCHLQGTSG
5227	19128	A	5266	177	13	TLTILLNFFFLRQSYSAQAGVQMINLN SLKPPPPGFKRFSCLSPFQOGHNR
5228	19129	A	5267	474	122	FYCSFPHFGGLTLGPKLNLTLGFSQPLFP LRGSKKQGIPIFYSYKIKGPPGAGPGS ARYSNPFGGYGRVLPPEFDPDPEHK PRPFLKKKKKHQVPTSKYLPBYLFAYY NASLE
5229	19130	A	5268	55	311	GIOTFGKNVVAGRSKNGVPMIAMLHT DGEHERPGGDATVTIAHRYTPKEQLKIH TQLADIIIVAGSLISIHAGVQWRNHS L
5230	19131	A	5269	238	133	NRNIWQKKKCVFYIYPLPICVCVCVCVC VCVCVCV
5231	19132	A	5270	336	517	PVLYLLEHSPYNASTYQLAKKYQSRPG AVAHACDPTLGGRRGRTTRSGDRDHPG QRGE
5232	19133	A	5271	262	467	VLSMEPRIHGSAAREDEHSPYEMALTAE TKKVVLVDGKTGTPTPTGRTNSKGIF KUCDEPWKGKMS
5233	19134	A	5272	213	2	MKIYINVTYILLPSLKKRQPTLSPLLEC SGMIIVHRSLLKLVGSSDDPALTSRIAWL IGARHTPDCSVCKF
5234	19135	A	5273	284	105	YSCSYSYFDEPVELRNS3FRWNHSSDS YWKKSSKDTPEVLKPPGYARYECKTV GSS
5235	19136	A	5274	290	449	IFYPSGRVRAKLSAPLACNANAZDSRG RRTTENVVSQORMYCLSLALLYSLC
5236	19137	A	5275	248	423	NKVNITLMTKLEKDTYKENTYRIFSLIN IDMKILSKILQNIQQYIQSTIHHDQVK LL
5237	19138	A	5276	425	30	TRRGMPHRQGSPPKAPVSVRRQRVRBEC GREPILWFLQSQLLGRLRQETHLWGGGR GCSSEPSCHCIPAWATTRANSICPNFQAS SVWVRSAARKLPSDLAGINTITWVRVS GLLLVDSYFGLRLATPVRQ
5238	19139	A	5277	25	185	SLFSVARPATNAYKVTKEKEKEKESRSX YKEAKESQRFLENHEKMTSTRYK
5239	19140	A	5278	263	483	VFTVVFPQLFCVYKLI FSPFLTECRSAQ AAHAGARMNHLGSLQPLSGFKQFSCLSL LPEFFRMYSVLSPSP
5240	19141	A	5279	25	252	LETTGLMHTVQCQGGIPGCHVQGGKLL LTSGDLPASAGQAGIAGMSHHTRPILL HPIYPILLYHPPCLAYFIIF
5241	19142	A	5280	326	203	IETESCYVAQDGLLELGGSNPPTASQSS AGITGVSHHTWT



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						FCLPMVKNGVFFFFRMBGRSVVQAEVQ WHDNSLPQPKPPGLK
5262	19163	A	5301	368	3	IFFPPQKRGGGGLFYIFFPPKIKGGFFPK KKIFFFFPPPKKKKKIIRAAEKRGPPLP FLKKTIRNPPPPPPPPPPPPPPPPPPPP VFMSITSTQ
5263	19164	A	5302	389	2	ANAGSSGCLCSRLITUDGFI PWGVRYF IVEAGSCYVDGGTALLASSYPTTIVSQ SAOMTQLSHRAARPLNPPPLTPSLSM VPKANVPSLLEKPTGLTQALRITLANVS NAPQTRSGLEGWGCF
5264	19165	A	5303	84	333	PHDCRPFERSRLRNPLSSAGTQSTAD AYRLALPQGLLYGTNFAPINAVARFA AAHAHQGTASVRVVGSGSGSGNQLP
5265	19166	A	5304	485	93	PPLFRFRSPPPPPKFFPPFPKAFPPGGGF PSFFSPPKKSEFFFNPPGFFPPPLKXK KIFPLPPLFLAPPKDSFLAPPFPFFPPFF PPFFPPPPPPPPPPPPPPPPPPPPPPPI I I I P I Y L P R D R L P C C L G
5266	19167	A	5305	157	2	PPPPPPPPPPPPPPPPPPPPPPPPPPPP SPNTESQIGPERAMERIQENRYE
5267	19168	A	5306	1	133	TOESTMDLENDKQDERLEKKKKKGPFAV LKQPWGGQSLPGHARE
5268	19169	A	5307	239	2	PERNWGFFSLPLKSSSPKAPNFWGG VOPNPPKRRFSSNPPGFPLPLKE KNIPLSLFNNLGPFRVFTGPP
5269	19170	A	5308	454	116	PRLLSSSNGDADSWAGISGPRCUGRA GLQLLTASDPPASQAGTADGVSTPQ CSMVPRLECSGMSIACYNHLPAACLP PKCRDCSLCLAATPSGK
5270	19171	A	5309	123	1	CSVSKWYPIAPLKNITMLWEARAGSRSK QEIKTILANTVKP
5271	19172	A	5310	153	33	WFGVVHTCNPPFLGGRSGLITRSQVOP QPQHSSESPSI
5272	19173	A	5311	350	3	NSRNLITQHSPEEKNEFLPSLPLOSV SMNTTSSPLLSNLSLPHFTIISPLTRPLV GPSITRSFPAGSPDRISFSSRLCSGT ITAHRLSNLPGSSDPLISVSQVAGTTCM CHI
5273	19174	A	5312	1	392	ETRGRTRIGCKSITIIHHNRNTRKNNH MIISVDARSAPLQHSKALKK
5274	19175	A	5313	1	239	LKTSFHHVGGAVLEFLASSDLFALASQS AGITCMSHCOPYISINFLPAESTQSS PELVPLPAGQKTPSPSTPLPSLP
5275	19176	A	5314	345	237	LFVHTPLKSACTVILSLTLCVVCVCVC VCVCLM
5276	19177	A	5315	268	412	GMYSSNSSSDPGNCNPGCKCCPEGS YHYPPAMATUTPSKKKKKL
5277	19178	A	5316	112	224	PWMLENELGLIARYLAVSTPLSPVETEC ASKKIFTFC
5278	19179	A	5317	377	139	KPPDRIFVLGPKKKKLFYPPDFKRCFF IGVPPDPDIFMIFPPPPPPPPPPPPPP PQWVMFLFPLLSASNONSPSWSP
5279	19180	A	5318	216	385	RGVLLCCPANSOTGLKSSCLSLPKCN DYKHLELRPATSCNSILFFNLQAFMYH
5280	19181	A	5319	376	3	RIDFGPKKKKILLPPPAVKIVSLKGP LFFFFLNSFPADAGGQWVQLISSGDP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						PPPAPESVRIKGVFCAGVPQGFPPFFFLNSSVAQAGVQWRDLGSLQPLPPRSKRVSCLSHPSMSWDYSH
5281	19182	A	5320	377	287	ELLTSSDLPALASQSGAGITSMSHHTQGSF
5282	19183	A	5321	381	65	SSSPSSRTSGPPFFFPSPKKKKINPQKKKNFLYPFFFPFFPPFYKNPKKKKLGGPKKKKXLSFPKKKKKLSLKNPPPPFFFPFFFPFFFP
5283	19184	A	5322	132	396	EGGFVLKIREGIGPFFPLGLEEEGSGKPEHIFNEKHRESFPKQGPVPHFMTGTWGLSKNPYFVRVQKQVEHIGPKNPFNEKKDFLKE
5284	19185	A	5323	366	1	GFLKKGVPFFFPFGKGGQNTPTPKPFVLGGKQPPPPPLKGNPKGGPPQQKKIFFFLTRGGVSLGPPGGGFPFFFPKPKPPGGFPFFFLKCPPPPLFFFPFFFPFFFPFETGFCSCRPGRTRG
5285	19186	A	5324	131	1	DGALSPRLEWCSGTTLLACSLRIPGSSASCVSASRVAGITGVC
5286	19187	A	5325	112	1	DGILLPLPRLSNLGAISAHNHLPESTSESTASAFLS
5287	19188	A	5326	404	18	PVSPHIGNIEKHTVTCVGSTSGAFILHGEHCHGNTLHPFPSPNPQTACQSQANRIRHNSFPKHLWRSMAWMTVPVSAIQDAEMGRPLSPRLSLAWATQDPSLQKQKQKXPTHLSWYILGHQLP
5288	19189	A	5327	109	3	KCVLTPIRALWEASTGSGQDITETLLSDTVKFR
5289	19190	A	5328	1	117	ETGFCCVAGSLQLLDDSNLLALVVSQSAVGTGMSHRSEF
5290	19191	A	5329	3	120	DAWVAEAEAGQNTIEERNKQKRRGIENDVPAGQAH
5291	19192	A	5330	105	2	ESGVVAHCNPSTLGGQGRMITSGVQDQSVQDG
5292	19193	A	5331	204	411	SKKKQKKKKKKKKKKKKKKKKQDKG
5293	19194	A	5332	185	2	FFFETESHSLTQAGVQWRDLSSLQPLPFGFKSLPSSWDYRCLPPCANFCIFSRDRVSLCW
5294	19195	A	5333	561	325	WSTLISFPIMLLNTGYFKELTGFFFLTVALSPLRECSDTILAHYSRLGLGSRDPTLVFQSTKITSVSHCTQPSVRP
5295	19196	A	5334	3	96	EGKAAPSQKSRVRKENPEIAVSASTIPES
5296	19197	A	5335	375	228	LSPWLECSGTTIAHCNIRPLGSSNSPGVFGFYFFLTLLIGSGVHVQLC
5297	19198	A	5336	403	0	NISVPASRHSFPFKKKKKKKKKKKKKKKKQKQKSRG
5298	19199	A	5337	397	80	IIITSKKKKKKKKKKKKKKKKK
5299	19200	A	5338	406	34	KRTLLDSKKKKKKKKKKKKKKKKKKRERKKKKKKKKKKKKKKKKKKKKKKKNPAGGKAYFFFLGGTKKKKKGGGDTKPLGRKNSPAQTKLGGNNPPFVERGKKKKTKGI
5300	19201	A	5339	410	0	KKQKKKKKEDAPQGGGGKKKKGGGPKKKKGSILKTPKKRGTGGA
5301	19202	A	5340	306	392	IQYKTIIPQKRNWDKTKQSLATPVSSIN F

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=possible nucleotide insertion)
5302	19203	A	5341	3	173	TPTATELLIIFYIFSETTLLIPTLAIITRG GNQPERLNAQTYFLFYTLVGEGLSARS R
5303	19204	A	5342	247	426	GRANWFTFVITPLWEAENGQVQRDLSSL QPLDLPFKRFSCLRLPHNWDYRHRVPRP ANFL
5304	19205	A	5343	3	149	SNFLHRSAGLELLTSGDPPALALPKCN DYRLVSNWPEVTLQPOPPK
5305	19206	A	5344	464	147	LRLLRWENRLEPGQGCSEPRSHRCLLA RYTESLRVQCQORDPRLAQTSRRPAGS SEFPFAGPASFVSNSTYORALFPAGGAPW TPRLPLGPHGTISTSSVLPV
5306	19207	A	5345	228	1	VIRLEETYPILLFFVLPLFLFPROTRSGS FAQAGVQSSHLSPSSMDHRYTPHLANF CIFLQKSLAMLPRVSNK
5307	19208	A	5346	2	106	FVLELLGNSNPSASSASEAGITGVSHCG QPLNF
5308	19209	A	5347	140	436	FLCDNRVLYVITFFFGKQVSFFPGNRA GGEGILNENPPGPNFFFLNLPPKGGEL RAPPPAPLFFFFFEKRGFRLTQGLN FWIWEPPPLILPRGG
5309	19210	A	5348	1	465	LESRRFEDGTVPFGSTISWDPPEZAVCP FSDLQLRAGRTTTLFKAQRQSSLSQRI LLFPVWQCPAPRGGVIRURQASLSCSGL HVRPASWLLCFPSKAKAMSGTPPPASLP PCMLISDCCASBQGVSGIGPSEFGEVY NLLLRHLKPEEKRS
5310	19211	A	5349	183	58	ERDYBDFGAVACACIPSTLGGRGWIT RSGORDHPDEIVDP
5311	19212	A	5350	288	404	IEYNMILAHNCFQLPOSSNSPASAPV AVITGMHYAR
5312	19213	A	5351	413	305	AEAGLKPLSLSTYLKASASQAGITGVSH HTQPLLF
5313	19214	A	5352	91	356	TVPKENTFSPHVAITTAQTVSTSVLAL QNRRESALPTIGWALCCFIWGGGRHVR PLCHPGMSTVARSRLTATSTSQVQAILL PQPP
5314	19215	A	5353	2	410	FVWQPLKTGSDRSHKAVESLGYEKVER AMTVNYSFRSLNTXGKLELLGKISVNLV AKWKHREKGRRTNTLGPATAAFYST EKTEFLPVVQTCXKPFIDSFNKYLPGA ADHACHPSTLGGRGKIKTRSGDRD
5315	19216	A	5354	3	288	SLDDLLKLLLPMLAQYDEFVQSAYS RLIAYFCARLISLLSDSNLLAASPH MGIOPNNSLGAPSPGPGGHSVQLGA FSDPLSCQH
5316	19217	A	5355	187	3	KKILKQTVGNLFSFKGAPLFFFFFLARV LLCCPQWSAVAKSPLTATSASRVQAILL PQPPK
5317	19218	A	5356	383	261	GYKINGQKSQAFLYTINQTESRLWTCY DSQRLTHLSIK
5318	19219	A	5357	367	241	FFFRHVAQGLQLGNNHPASPSQSVR VTGVSHCTOPLCFV
5319	19220	A	5358	217	1	SCDRENTGLKLLSTLLHHCETDTRSL LCISLSIKREINLGAVARACNPSTLGG GGRTSREDRDPGETP
5320	19221	A	5359	255	412	TQLCKRRIAFFFLATHNSQKQSRWQTV AHACNPSLGGRGGRITRSGDGH

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
5321	19222	A	5360	391	271	RSCHIAQAGLKLASSNFPASASQNAEITGVSHILTPICC
5322	19223	A	5361	232	397	BGLKBPAGLPTMEYTTARKRNKIMPPFVVTWMLQLEAILGESSTQEQKTKPQMFSPV
5323	19224	A	5362	213	392	LFIVKVGKFFLRSINILNLSLLFLSSNGPGLLKKLGVPWPGVVAHACNFSITLRGQGGRIA
5324	19225	A	5363	306	418	SGITVGTLPPLASQESAVVEDLLYVLGVVDGRVYSAQP
5325	19226	A	5364	347	48	KKRNKLPFGGKKNPPKKGKKGKGTTPFPFKKGFPPPPFFFLKRDLS PQAGKGRKKKPPDPWKABGKKNPWGNPQQRGGYKGNPTRPPDQGGFFFFFL
5326	19227	A	5365	412	172	PDSNLSFGAHYQASILGSGSIMPLLLYSKCSQNDVARSACCTSKSSQNKERKKERKKERKKERKKERKQKNPLT
5327	19228	A	5366	400	256	LVBGGPHHVGRAGLELPTSDPPTPSASQNLGIDA
5328	19229	A	5367	162	1	APSLDETPTILKRTTFGPGDLVAGICNPSITLRGRGGRITRSVGRDQPDQHGFT
5329	19230	A	5368	152	403	TTVLCKLQVPLNKTIVRFLKELEVDLPFNPAPVLLGIYPTBKKSYSKGTCTHVFIAAQFQIARIWNQSKCPIINQKCKKKGAPV
5330	19231	A	5369	170	367	IVFETLVISYFSSFPQKTSWNTFFPHFKVFNWNPSTVAHACNPSITLGGRGQITRSGDRDHPAR
5331	19232	A	5370	396	1	QMCVRAHTFAGGRARITHHITHHITHHSVVAITPVSNNCCVCCVCCVCC
5332	19233	A	5371	139	3	FKLEGGASTIAHCSLELGSIDPPPSAFQVAETTCAPPCIAFFP
5333	19234	A	5372	1	341	PLINTLSHLILCRNFTSFVKFCIRFMSLLYVVISLFHVLCCVVSFLDTRRAINASTYTGVLVPTVFKNSPLPGVAHACNPSITLGGRGQIMRSQVQDQPGQARSSRPALPT
5334	19235	A	5373	280	449	ICHNLQCPSKETIERVQRQPIEWKIFANHISHKGLSS
5335	19236	A	5374	170	1	QKRGFSMGTWNSIFRPQDLTPLGFPAWDRPVNPNWPCPLFFKGNPOLQAPG
5336	19237	A	5375	462	165	FPTRFLHVQTLGLPTSGDLPASAQGAGITGVSHHAQPRGHVFDVLLYSQQGVFTLLSLFGSVFFPELFC
5337	19238	A	5376	3	451	PRAKLTGRRGLRNLDTTGVAVDLILFLRLRVQBSLLTAPPGQLFLRNIAHRHDSQSIGWVHAPPPVPWPCLSLPPPHGSSSITLPPPLPHRPHPPHSHPPMAYLRSPPFPHPHPLPPLSPPLSPSPPPPPPPPPPL
5338	19239	A	5377	460	300	KVLLCCPRLECRGATMAHLSLELGSNPPTSASQAGVTVGSHCRSPVVEFL
5339	19240	A	5378	452	191	DSRFHHVQVQDLHPHSSDLHNASQSAVITGVSHRTPDIAFAPSISSTVSCVAEISLHLSESFPKQFL
5340	19241	A	5379	240	395	LATSSVAHLRNTFTVLLKSSVLGVRAHSCNPSTLGGQGVRTKSGVGRDQPGQ
5341	19242	A	5380	210	411	TSVNSAPNSQKASVEECFGQVTVTKVKNVFLGNAQWLTPVLPALNEAGAGGSDRQEDTILANTVR

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5342	19243	A	5381	406	300	PHYVGQGLLELLPLGSGTCLGLSKCWDYR REPPHOA
5343	19244	A	5382	364	479	INDGLSKISLPLSHLKDOAQGVWMLTPV IPALWEARAG
5344	19245	A	5383	182	395	HHLRGSAASFLKSAQEPDTPRHITQPKRF SCLSLPSSWDYRCPPPRGGGVCLPCGW RTVVQSWLTTISLSQ
5345	19246	A	5384	37	478	GGHSTVPYLCFLILGSSVSLPFSSVAC LMLLLPSFLPSLLPSFLPSFLPSLGR APL
5346	19247	A	5385	201	458	WRPPPTSPDKMAARADTPNGVQKTAQEP GLSSRLQAYEERQRMOREREALEDCA AYAQCAQRAOQLLOLVQLQOEKRLQ DD
5347	19248	A	5386	206	407	FFSPQCRAGEKFCFNEPPFPQPKLWAL NPPGKWKQRAAPPPIPVYFLFEKKGKGP NMVQVGLNRP
5348	19249	A	5387	468	0	NFFFPFPAPPPFFFFFPAQAGVQVRVL GSLQAPPPGFTFPSCLSLPSSSWDYREA RVSPHC
5349	19250	A	5388	136	2	LFFFFFLFETGFCPSVPRLECSGTITAHCS LKLPGSCNSPISVSQV
5350	19251	A	5389	397	0	ILYPSQKKKKKKKKKKKKKKKKKKKKQ
5351	19252	A	5390	299	3	AQPLAPPPGSGFTILYFNNLLPLGIPILLY MEVIMGQMLVDNIRVHQLVPMCLCMS YAHSLVNEGSPSPRPSISLCLGLQVSAHR VHPQVCASVSLYNS
5352	19253	A	5391	264	202	FFFFFFFFFFFFFFFFSNNKI
5353	19254	A	5392	2	150	PRVRFLETREPCWQVQGLLKLTLSDVDP TSASASAGITVCHLVPEKS
5354	19255	A	5393	382	0	NSRAQWMLNPVVISPHWEAEVGGSLPT S
5355	19256	A	5394	395	239	SLESSWDYRHAFQCKNPIFLVETGFS VILCSFRLGGPLSLNLCSLSL
5356	19257	A	5395	24	265	LLPHEKSRNRYRTPHSLRQYQGNLGG GACSESRSHHCTPVMATERDSVSKKLF TIELVTVFLKXNSKGEPLKVLGL
5357	19258	A	5396	174	118	FFFFFFFFFFFFFFFFRSS
5358	19259	A	5397	406	134	PSATSPSPPPPLILWGPKGFPFPLFYNP PPKFFFGAPKKKLYLPPPRALNVLKGG PPPPFFFFFFFFFSF
5359	19260	A	5398	294	64	IFFFFFFFFFFFFFFFFFFELHLMGALF LLKSRIPPGKKNTCKPLCTPLTGYIP LLKCFQKQNKKSQSONTELS
5360	19261	A	5399	1	211	LLLLPTPIHINQSSNKYHETKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KKKGGGGGYKKR
5361	19262	A	5400	305	1	SPRRPPPLPLPLFLPSFFFKAPHTINH FFSPPLPFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFELKLYIFKMRINYTSNI LKLINIVSSPSQGR
5362	19263	A	5401	416	3	ENHSHDRGRQRERDRSRAETQETNRAQ QESTPPQKQKNTYIPSSSSSSPTQK GKKGPPGKPPPAGEKGGPKKKKRPQ KKKIRPPPPGKKKPPPKTPPLPFFFFF FFFFHKKPQTFVGVNTYILLRSVS
5363	19264	A	5402	154	416	KKKKKKKKKKKKKKKKKKKKKKKKKK

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SEQ ID NO. of nucleotide sequence	SEQ ID NO. of peptide sequence	Method	SEQ ID NO. in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Yrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
5364	19265	A	5403	327	2	KKKKKKKKKSGGGA PPQKFFFLGGVFFFPFFFYNNPPPPPPPP SPKKKKYFSPGRKLFPPPPPPPPPPPP FFFFFFFFFFFFFFFFFFFFFFFFFFFF LRWLSALVAQAGVWMLNHSLSL
5365	19266	A	5404	372	181	YKGLAHTRCSTRNPLNPLITITMGSRFV AQAQLGPLGSSDPPPTASQSDIGITGVSR RTPLINIC
5366	19267	A	5405	110	1	PVPVSTEVKKLVLPPTVVHACNPKTS GGGGGRT
5367	19268	A	5406	2	401	GFHLITTYGNRQKQKRVREKASARPLQKT PPGHALEWTLNVLALAPPRKQVLF AIVASETSSMDREKLTWLSLEAKCKGIT LFVLAIGPGVGTHELAEALVSAPEQ HLLRLQGVSKPEVNYAQTFR
5368	19269	A	5407	3	181	QLILFHDKLSPKLLSGNVDLLINFLS HCSPEKARKLQAKMNTNLWMAKURLQL GIN
5369	19270	A	5408	371	222	SVRMGFHRAVQPSLEPLGSSDPPFASAQ SARITGVCHCARPNHDSYRS
5370	19271	A	5409	204	416	NQGVGVVTRKGLDGLDMSMTPLFPLVVR SKDEKNTKIMPGVAHTCNSTLGRGG QITRSGVRDQGRHG
5371	19272	A	5410	236	308	AGRGTVTHTCNFTLGGQGRIT
5372	19273	A	5411	375	216	GCSEPRWCHCTTPAMVTQDSFPKKEK RKEKKKLLTTENSCKALKRNGYL
5373	19274	A	5412	1	381	RFEHVAQAGLNLGSSNDLSASASQSGI TGMSPTQP
5374	19275	A	5413	144	3	RPPPIFFFLAKIKALALFFPHSVIQAQV QWRNLGSLQLPDPGKQ
5375	19276	A	5414	412	32	LNNSFVFFSKPFFPLKTVGAPFFSEIYN PIPIFLYIYFPHKQGVYIPTHWYGGD IWGYMTPTPPPLPIYFFPPPPFYIEKK KKTVECFPAQGVRLCLKKKKNDRGWG DITMTHGGRLMVAQVWGLRYV
5377	19278	A	5416	1	240	GGGCGSEPRSCHCTPAMATERDSTSKKK KKKGPPKRTHTSSPLGSPFFFFFFGAPK FNSRARFLTEREGKNFGLPFFFYFA
5378	19279	A	5417	2	63	LCLNNNNNNNNNNNNNNND
5379	19280	A	5418	322	1	WPLCFRCSKRGSPGLGFFSFPGLQSK KTVRFACKTSPAFKPPSLSFFQRWAGP PPFLQGLGELPKGLFFQCFPPFFFLRW SITLVAQAGVQWHDPSLQFPPL
5380	19281	A	5419	1	392	FRMGSPFEGAFAILADKQQRGRSFLS DPAKVFNHNDVFNSEEQAAAEKRV QENSTRQVCQEQVDYEINAHKYNDFY KTHNGFFPKDRHWLFTFELAPSQNQ HLKDWFLNKSAPSKK
5381	19282	A	5420	273	91	RNYIVDNLIFTLNCTCETSLKTYLGP GVVARACNLSTLGGGGQITRSGVRDQ GGHGE
5382	19283	A	5421	1	149	GGGCGSEPRIRCTPAMATERDVSCKK NLKKFPCDGLGYQKNTWTL
5383	19284	A	5422	381	179	SSCLGLPKSDYRCFLCPARTANLKT IKKSKNNRWRWCGEKENLHWCWBCDM VNLVCPVTQISC

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
5407	19308	A	5446	198	86	PWPLGQAAILLPQSSCLNPKCWDYRRR PPHTALLNS
5408	19309	A	5447	143	3	TMIVYFFVFFLLQSLALLPSLEGNGTIS AHCNLRPLPGSSDSADAW
5409	19310	A	5448	324	1	KKNSATSPFVSVEPSTGVLANKGALTQ EKILPCFKIKKIRKRGAVAPARNHFLF FSPPFFKEGLQGVIVYFFFFFELESRSVT QAGVQWRNLCSPPLPPGFKRTRG
5410	19311	A	5449	403	0	LPFFFFFFFPPFKKSN
5411	19312	A	5450	114	409	LNMTLKLILSKHLLIVCLPDTLSSLC LKYIGLQGVLLFFFKPSATDKLQGN IAVVGKGFAMHSLTKKWLPGNITQBS QNMIVTGGLSWWD
5412	19313	A	5451	192	406	RNFPLGHLKYVRPEQYQWGRDPMETP KARATKNNMDKGLIKLKSFCPAKETTF RGTGHPYKGEKIFAT
5413	19314	A	5452	254	48	NAPGWLCHYALQFIDKSVKNSVCWGLA VAHACNPSTLQGGGHIITRSGVRHQPGQ YGETLRTASTR
5414	19315	A	5453	1	288	PLLFILIPSPFSPFPPFGQPIKPIPRE KKKKKKKKKKKKKKKKKKGGPPKKKKI FPRGGKKIIFFWAQKKIRGGVILKTGG RKCPGGKKNKSG
5415	19316	A	5454	285	415	TSGCCFVFLVLLKLSIFCKRGVNLAEEN GLKNSFTYFTSDHG
5416	19317	A	5455	372	125	ITPAFSFSPMGKGVFPFPKFFGFPFGF PPPPFKPPPGIILFLGPKKKKFSPPPPR VIFFFKRPDPFFFFFFFFFF
5417	19318	A	5456	3	159	NBSAIAITITDIALGLLELSLMLTL LPSDOLLGDQKKKKKKKGGGP
5418	19319	A	5457	109	392	NITIKRSTSLPLRFPFPHLFFPTIYL FISRLTLFFFFFKRSCFLPQVGGQGP FLNGLKPLPRGLNQFSCITILRSQNYGP PPPPPINFFF
5419	19320	A	5458	243	402	FLKIGFIHLYLKEFVWGILNIVFNPNBS HERAPHAIVFNGTTIEGHVKKCYW
5420	19321	A	5459	394	105	IPPPSPRGGGGAAPFPGGGGSTTTPPK KKPPFPKKNQPGGGGAPPPPPRGL GPKIPLTPGTIVFKETKPPPPPRGAP PKFLSKKKKKT
5421	19322	A	5460	56	379	VCFSPSITGAUVLNKSLRSHSSSSSTG WGGLSPSPFAQRLPLASQVQRHNGHVEA SYQVSIPQSCBQCLSYIWMIDKALLCSG EWLPHQAPKPSMSPTTPHCSRGLQ
5422	19323	A	5461	184	420	FFFFFFLNNLFFFFFFFPPPPFFFLG RN
5423	19324	A	5462	295	384	LGAAVAQARNPITLGRGGWITRSQVQDQ RG
5424	19325	A	5463	413	257	PLNPGRGCSBPKSHKQTLAWYTRDLI SKKKKKKWIPOBPRGQWSPD
5425	19326	A	5464	2	181	SLKSGWQTFGLKQSSCLSPKCHYR CKLPRPVVLLKYSFPKRVVFGHLCLF MSQ
5426	19327	A	5465	1	229	TGSCYVAQANLRLSSSDASTVSQNAQ TTGVSHVQPYTSSFSQVPLRAQSAAT ETTSILWOKLRLOVVRCSV
5427	19328	A	5466	1	368	ERKERTKKRRRRRRRRRRKKRGRK ERKRRERKRRKKRRKNNLQGSAGIT

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						GMSHHTRPKSHNVLSKFPNLCWAAFKRAI LGHMNGRLDKLNVEQCSTLSALFSLII ATSHMLAVI
5428	19329	A	5467	183	3	VSLCYGSEKFS PQMNSQLFPRPGVAHAHA CNPSTLGGGRGQITRSQDRNHPQGGET GRV
5429	19330	A	5468	1	128	GGAGYSELNLCCHTRAMATRAKIHLLKKK KKGGPLMAKKKIGG
5430	19331	A	5469	1	155	NKFPVLNSVNIIGMCHCTPAMATEGRD SVSKKKKKKKKKSLKRLARSLV
5431	19332	A	5470	113	1	FFFFFQKTSRRIGTVAHACNPSTLGGGR GGRTTRSGD
5432	19333	A	5471	407	281	NGMTFGGTACSELRSRCHTPAMATEGGRS ISKKNKSKNPKNLG
5433	19334	A	5472	1	177	GGGCSSEPRSRHCPAMATEGRDYLHKKK QSKTKGERMEVACVCIILFPLTDALEVL LNA
5434	19335	A	5473	76	267	KERREBKKEKTRKSEERKGRKKSGRDR EKEKEKRRKERRRGEGERGEKKEKKEKD IKRRGVVP
5435	19336	A	5474	133	2	LCRMVVLFCFBAAGSHSVTAQGVCMGGLN SLQLPLPGFKQFCSCL
5436	19337	A	5475	5	394	YGVGTGRFAGVKEFQALFLIATVHSQIL CHIBOTRHHSRHLIVVDFINQINGTFF FPLVLSNGCINLLIVYLEWNIPTREQGQ FFYGLSKSHYSVFVFCFLRRSPALAQAGV RWCDLGSLSQLPLPGFKKF
5437	19338	A	5476	163	2	SEKFWVVALTLMTFSHYFFLYFYTYIFI FQMKKCSITAGVQWRDLASLSQLPL
5438	19339	A	5477	111	2	FLFLKQDLPGAVAHACNPSTLGGGRGQIT TRSGDRDH
5439	19340	A	5478	232	0	HLVWRRESGSVAHAAYQWCDISLQPPP PRFKPFPS
5440	19341	A	5479	388	225	ALFSSKKKKKKKKKKKKKKKKKKKKKK QRKGGLPRVCCGASMSVPGHKLGL
5441	19342	A	5480	150	2	HRVAVIYEVFFCLFPFLPLRQSTLTIV TPGVQMRNLSKLQPPHGGFK
5442	19343	A	5481	156	395	DSVCTCVLHTCHISGSLSGRSCLHCSLIG LPNSNCPVCVCVCVCVCVCVCVCVFC PLHQGVVCVCVCVCVCVCVFLSAHPTKGC VCVCVCVCVCVCVCSPPPI
5443	19344	A	5482	391	115	RACPDRCVRPRHTSPCLPGCPRAEPQPP GPALRELVLQPLPGQLQPPFGMPSPGLGA AFSPAPPACAWTRPPHLPSSPSSSVQ ISSLFLCF
5444	19345	A	5483	392	2	FFFFFSETQFRSCCPRLCNGAISVHCN LRLPGSNNSP
5445	19346	A	5484	381	282	PVPVGGQATFLPPPPPYIIGPPPPPPGL FLFP
5446	19347	A	5485	407	3	FFFFFLRLSLTVAQAGVRWCDLGSITQA PPGGIT
5447	19348	A	5486	2	417	QENHLNPGGVGCSEPRSCHCTPAMVTEY DKKKKK
5448	19349	A	5487	3	413	VYLHPSLQPLSSLSLVPDQALSHDITLKK KKKKKKKKKKKKKKGGISPPSPVGGVGP RWGVGPGANLPORGGGVRLSLSQKKKK EKGQNPDKPKPHKRGPGGPKKFIFF KKKKKKGGKPGKKTKPPPRPVNPGG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
5449	19350	A	5488	229	411	THGPGFNGCGKRTLGLPNLMALKKIFF SPGGYKPKNP
5450	19351	A	5489	190	50	YHHHHHCHHHHHHQCHRRHHHDHHYHGD NDYSSHHKSTCHVAVT
5451	19352	A	5490	615	402	RWCLTSLSPRLCSGHTSAHNLHLPGSK QLSCLSLFSSWDRCFFPGKTTFSRGIR DAIKPRKPRNLIT
5452	19353	A	5491	338	53	KGPPPPFFCKKQGLPCSNPLTPGGKMF SPPTPRSGGKRVPPGCGKQSLFFV EGSGCHIAQAGLXLLGSSDLVTSASQSA GIMGKSPHAWP
5453	19354	A	5492	266	412	NPNPFPERKSCSVSQGVHRELNLKRAA PSGYTPASCVSLPSSWDYKRP
5454	19355	A	5493	285	412	RDGVLSALSPGLECGMHTAKCNLLLS SDPSALASQSTWNY
5455	19356	A	5494	1	1350	NGFMWIGTCTEDNVGSPSPSGVLTGCG VRIQMIDRCHTAHCFVLPGLLRGQLWTE NLAEKNSHRRPFPPTVCSHFADLMWE QSTKDSYQKVLLRKPFCKCGHNLHPKKG CBSVDCKLHGRGYNLNQCLTTQSKY FQCGKYVKVPHQPSNKRKRKRHTEKPK LKYIEGDKAPNQSSTHTTHKKIDTGEKP YKCECGKAPNRSSTHTTHKIDTTHREKP YKCECGKFKYFSSTTHKIDTHLHGEKP YKCECGKAPNRYTTLTKIDTTHTEGP YKCECDKAPNHDATLSHKKIDTGEKP YTCDCKGKAFSSSILSSEKIDTTHREKP YKCECGKAPTRSSHLTHKIDTTHREKP YKCECGKAPTWASGLHGRHTHTEGP YKCECGKAYTTSSNLTEHKTHTHTEGP YKCECGKAPNSSDLNTHGRHTHTEGP RT
5456	19357	A	5495	4	146	PPTRPTCYILSFYVSYPGYKEDTRVNV KMKKRCSTSLVYLLMINFY
5457	19358	A	5496	5	388	CGCFFFSPPPKKKVPPPPPPFARGFPP PPLFTTTPPPQFFFWADPKCKNSPPPPGK KIFFLKGPFPF
5458	19359	A	5497	231	163	FFFFFFFFFFFFFFFFFXXTNKF
5459	19360	A	5498	163	2	SVKPTLGRVSQLKHTFAGWAHTVIPA LWEARAGGSRGQIEITLITNVKPH
5460	19361	A	5499	229	388	RTHLQASSDLFCLYSLKTS CCVAYAGV QRHDLSSLQPPPPFRKSSCLRPPE
5461	19362	A	5500	405	289	HVAGLGLLASSDPTPASQSAVTSV SKTHPKCLV
5462	19363	A	5501	286	375	QDFVRFSPWPGGAHSCPNTLGGRGQ VT
5463	19364	A	5502	20	374	TLQFONFVTLVFNYPHFGKELYTLNWN PSGLFWYVFSRLSCFSLSSKINTLNLLS GILNVFVPSISGVKKIPLIKRYCMLGT THACEPSTLGGGGRQITRSGDRDHPQR VVKIQN
5464	19365	A	5503	1	185	FHITGQAGLTLTSSNLPASASOKAGIT GMSHCTQPIIFLYLSFLQLSFSWODFV MRKKF
5465	19366	A	5504	202	402	NSFSSTAKLREKYQFLYPTIPTGTQPL PLITFCRTPRDTVAHCNHSILGGGQGI TRSGACNPGQ
5466	19367	A	5505	118	7	IKKNNWPGAVAHACNPSILGGRGGRIT

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						RSGRDRHPG
5467	19368	A	5506	205	422	ANHFTSIRMAIINNRRQTRNNKQWQGG EVGTLVHCWCEKQVWMLRQIVNSPLKK LNIQLSRDPATLLAI
5468	19369	A	5507	3	425	RSCHCTPAWATERDSVSQKKKKKKKK
5469	19370	A	5508	3	86	EKKLVLLNCWTEIYYQFKDKKAERSK
5470	19371	A	5509	395	108	GVLECNDDTITAHCSLDLVGSSDPPTAS QVVTGTGTCHIAQLGLPKWMDREHPRL PAWNKTLLRRQWHLPLPVVTAIQELEVG GSLPRRLRL
5471	19372	A	5510	421	59	FFFFFLRRSLAVSQAGVQWDLGLSLQA LGA
5472	19373	A	5511	168	3	ETCRNCFPVPPGVFFLNLIVPVVPVFL RNRMRSLVSQAGVQCNLSLQPP
5473	19374	A	5512	446	149	FFFFFFFFFFPRTSCSVARLESSGMISA HSHNLCI
5474	19375	A	5513	74	398	DRIDAGPKGVARFWMHCQCNCFCK WSVNGDTRVGLFALSDIKAGKHFRLIQ LTSFQGCPCPLQTASSDINFKHFFMYRS LELSSTPLCNHHHSPPELSSS
5475	19376	A	5514	73	335	EGGSLFCPOKSAAGALFWLAPASRSGWG GAPGVVPVGVGVQGNWNPGGGCGNELG LHHCI PPWGTGRTLSPKPKKKKGATDMG GAS
5476	19377	A	5515	416	0	WLGPGAHAHTCNPTTLGGRGWITRSRD
5477	19378	A	5516	242	423	AGSPLTHOQGCAIILTONPTPGWGTMPV QPVLRPVGLYNANHVTSPPVASQPIIF .TTAG
5478	19379	A	5517	2	151	GRVGFVGMGSHCAVQAQGLELLSGGPP SASQSAIAGVSHRAWPFP
5479	19380	A	5518	312	405	GVVRPGAHAHACSPTLGGGRITRSRV PDQ
5480	19381	A	5519	3	387	ACSQPRSCHCTPAMATRODSVSKKKRRK KREKPLLEKKRGPTLTWGEPKKGLPLG ERNQPPSHFKKGPPLAKCPDGNLHPEI AQGPSPSTDNKKGDLNPTPVYFKKTP EQAINNAAPFPPEK
5481	19382	A	5520	292	140	EKGPPRARPGGSGSPPLFFFFFFFFFFF FFFFFWNSTLKKRLHRSGLCV
5482	19383	A	5521	1	399	KRWLFLSAGITPTKLRRRRNRFTWPK RSKINLHKPLIKKQRELPDKEFKIALI KMLYELKVTHEDQENINKEKENTKKKK KKKENPPLFGTGKNSPPPEKFGQGGQP PPPPQKKKPPPNRPFVSP
5483	19384	A	5523	316	399	MLLYWPGTVAACNPSTLGRGURITRL
5484	19385	A	5524	400	0	FFFFFFFFFFCFPPFLFFS
5485	19386	A	5525	3	429	TTNIGRAMJATTSIVGSDTSQAERPGGT TVVSGASSTSQSSRGTSVTPDSSASE SETVITKEFGGTTAISRTSHGTTPASG QATGSLTATTGVAPGTTPAGSSNTHA TTSVGEKKKQKKKASSP
5486	19387	A	5526	135	3	GAKICITLKSIVQSWPGTVAHACNTS TLQSGSGNIMSGDR
5487	19388	A	5527	105	5	KKKKKKSGRWPGAVDACNPILGGQGG QQITI
5488	19389	A	5528	411	31	GQRVPLSRGVAKKKKPLNPGGAGKNG GKNFLKKKPGAPPPSGPKKGPDPDP

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						KKPLILVSPPPKGGAHNMHFRQKSGSGN KGGEGSTRGKKEI FLGKPVQKNFPPFF DPEFHSCCLGWSAMP
5489	19390	A	5529	411	142	PRFSFLFSPPPKKEVFPFPPKILGGPRFF PPPRFLKPPHFFFWGPKKKKPPPPPG EKFFFFKGAVPPFFPPFFPPFFPPFF
5490	19391	A	5530	174	401	QVQPOQKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK EKGQGGERNITWVPLLEPP
5491	19392	A	5531	410	0	OPOSKKKKKKKKKKKKKKKKKKKKKKAS QKKKKKKKKKKKKKKKKKKKKKKKKV
5492	19393	A	5532	383	145	GGFFPNPPAKKGGFPQPHNLGGPPVPS PPVPKTPPRNIFPGA PKKKKTFPPPGAK KYFFKAPPPFFPPFFPPFFPPFF
5493	19394	A	5533	418	328	KTPRHRVQAGLKLASSDGLPALASQA GL
5494	19395	A	5534	169	3	YILTIHPCSHVPRRETILGLKACTPKNMF WPGMVAHACNPSTSGGERRITRSGDR
5495	19396	A	5535	1	254	PTRPCPKPQTSNPGSLSPSSNGCMNTL HISSTNTVGEVTEALKKFLVLTESPAKF ALYKRCHREDOVYACKLSDREHPYIHD
5496	19397	A	5536	43	404	OGGLTVLPRVLNWSWDRKSSRLGLPEC WDYRYEPHQAN
5497	19398	A	5538	2	212	KENHLNPGGGGSELRSCTPAWATER NSVSKKKKINFRGGGLKGGGPGFYPLEK KFGVGVPFKTNLV
5498	19399	A	5539	2	387	IFQEHKNGEMSETEAKRVYKVLKRS LR TGVYSFFLVKRMKGRKIKLVPRLLGTTK DSVMRVDEKIKVLQEWPLTIVKRRAS PKSFTLDPOEYQESYYSQVTTGGBQISQ LIAQYIDILKKKKKKKD
5499	19400	A	5540	317	407	GLSHRVFFSEGKLLKPRKQKDKRVPEP DN
5500	19401	A	5541	120	3	NFFFFFLRRSFALSPRLCSGTISAHN LHLPGSSDSP
5501	19402	A	5542	430	0	QKAQSNPRKQKRGVIGNPKRTLSKKK
5502	19403	A	5543	172	2	FI FNFLHISFNFITKFGCFIVLFLRQS LALLPRPGVQWRDLGSLQPPPPRVPRV
5503	19404	A	5544	149	2	EKDIQELNSALHQADITDIYTLIRKST FFSAPHRTYSKIDHI VGSKAL
5504	19405	A	5545	84	276	TLKKRPKEIRNGQSGPQRKRAQLGLQQ KYPVLNFKAPPPQERGDYYSFFTKCLD NLPRGGK
5505	19406	A	5546	2	914	RPAMHREQSKNEPETDEKQCGQMDRE PSAVKKKPKPTNPVEIKELKSTSPAS KADPGAVDKASPEPEKDFSEKAKPSPH PIKDKLKGKDETDSTPTVHGLSDSSE LVIDLGDHSGRGRNKKSPKEPS PKQ DYVQKTPSTVYGSISGPPVPLTRSA QTSAGATATTSSTSTVTVTAPATG SPVKKRPILLPKETAPAVQRVVWISSK PQTSQKQWYMQDSSSSSSSSSQVQQQQ QSSQCTRYHTRQAVKAVQKQKITQSPS TSTITLVTSQSSPIAVTSQSSMT
5506	19407	A	5547	2	244	TRLIFVFLVNTGFRFVGGAGLKLITSGY VQTSASQRMTHLCLPRCWDYRCQHLHP AQRFKKRLSVAVDAAALLHTSGM
5507	19408	A	5548	406	1	FFFFFSETSCSISQARVQCNLSSLKP

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5508	19409	A	5549	417	43	IRPARKKCSSGLPGAPLAGGGAPPPPP RQTS PPPPHITGGGGGPHKPPPKKKRPP PKKKGGGKINPPKKKKKQNTPPPPKSAPP PAAKTDPPPLTVPPPLFPYITKKIIF LKSYFFFFY
5509	19410	A	5550	3	136	QPRFFLTITNINENNPTLLNPIKRLDGS LFGFLITNINISYHSP
5510	19411	A	5551	75	194	NKELSRNKKKKKKKKKKKKKKGGG LKKKKGGGAKT
5511	19412	A	5552	343	493	ITFSYFFFFFLTGGSVFAPQGGHGNF GPLKPPPLCLAKKFCSTLLSSW
5512	19413	A	5553	148	3	DVSLFCPGSLHESDTITATYSFDLLGS SGLGASTSRVAGITIGCHA
5513	19414	A	5554	407	252	KKKFLKKLGGGGHRLQSLLRRLRQED HSSSGVQCSLWGGHLYSKNR
5514	19415	A	5555	3	231	HEFVFLVETRFHVRGALGELLLSYPL ASAFREAKARRELLSPGVKDXPGQYRD TLTLKKKKKSFYLYGECW
5515	19416	A	5556	3	131	SVVVSWEESKIDAKELGVGYIRASVAGS KWEPCKNNPVKGSR
5516	19417	A	5557	3	131	SVVVSWEESKIDAKELGVGYIRASVAGS KWEPCKNNPVKGSR
5517	19418	A	5558	462	255	RSHLSAQGLGLQSSDPPALTSQSAGV TNVSLRAQPIIACSVSVSSRQVCLHV RRGKCPRAESYR
5518	19419	A	5559	445	29	KSSNLLILQKVENGDLSNKKILRTDFGL AREKWRITKMSAGTYAMAPSVIRASM FSKSGDVSVGLVLLWELLTGVPFPGID GIAVAYGVAMNKAIPISYCEPFAKL MEDCMNPDPHSRPSFTNILLASQAWR
5519	19420	A	5560	225	475	GAVRSSCTSEHMTPEKAVBESLTPFTE SRSAIAGVQMINVSSLQPPPGPRRFS CLSLPSSMDYTSAGEGRASYSKVLK
5520	19421	A	5561	248	142	NRNINWQKKCVFYITLFFTCVQVCVCV VCVCVCV
5521	19422	A	5562	262	456	NFFLKITTYFLFKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKASSPPFLIKROPKN
5522	19423	A	5563	314	444	LKSMFCFLFCFFETESRSVAQAGVQNC HLSPLQPPPPGFKRS
5523	19424	A	5564	220	486	LNSSHFESPLPLFLGLVLFPFYFSNPRSF NKKNLRIEMLTVDGRPNHDSLFFVHS NVDTVFLPQGGPSFLQLPGQGITAFEH NQAYV
5524	19425	A	5565	176	492	CTKAVASKARYIQAALLYALASVTIAT ATRIASISGASPIFRSPYLPQTPAGLV LPSLLILLVDGLKEKGPPIVVAHACGPG TLQGRCKRITRSGVDRFDH
5525	19426	A	5567	24	470	PHDXEPKKKSTPLNGGGSNODDMFAK LKKKLENSINKPLPWPALIAIAGVAK LLLTCCPCICKCKCKKKKKKKKKKK KNAMMMMDMGQGLPQDDAKTGHTRG EGEGEKKKPPENLGLKQFSLDYDFQANQ LTVGVLAQA
5526	19427	A	5568	45	485	GXDGRLLRGHNQYAYDGLDYIALNEOLS CWTAADTVAQITORKWEAREABOLTAY LEGLCVENLRTILHENGKLTQRADPPKT HVTHHPVSDHEATLRCAWLOFYPAETTL



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						ISRLPEFEKSSLSQSLVLTSGYFAVY RVKLTAKKLGIIHGAQITTYDILITI PVKARNALC
5547	19448	A	5590	208	91	KGHFWVIGKKKVPCCPPPPPPFFFLDGI SLCYPGWSAVV
5548	19449	A	5591	325	467	ADLCSPCDLQDLDFRHKRTVDTLLALG EKAPPTSAIRSRDITSPCF
5549	19450	A	5592	332	403	LSLVCYXHHHTHTHTHTRETFY
5550	19451	A	5593	292	26	FLIDNMGARAGARLGLYHCLCAWETPS KLAVLQHLRTPAHRDAQQRRLQLLQNG PTTEGLAALQSILSFHQQLRTPGEEE GTGE
5551	19452	A	5594	387	51	LKKIFLGRGQVSLFFSPPLGQPGGRPL GLEIGALPOLPGKTPPFKIKNYPLGLN GGALFPLPLGLGGGMAFPRKGGAPFSQ KNPPPPPLGGKTKPPPLKKKKKKKVL
5552	19453	A	5595	88	362	AETSPGGQSYDGLRRPGFAEGPPAGRN PRRKKQTDRRGSGAGSQACAGVRL CTRLOCSGATSAHNCNLPGSSDCPASA SRVAGIT
5553	19454	A	5596	92	366	DQPFQQLQFQSRSPAGIRGGSTRKKFQ EENSDRSPGRQRIIPASGVRCALY QAAVQWCHLGLSLQLPLPPGFKRLSLSLP SSWDYSH
5554	19455	A	5597	3	138	TRPKTNGVQAELELLSSDPPTLASQS AGITGVSHRARPQSS
5555	19456	A	5598	150	3	SCVLYSHKPFPSLRNSFTLVTAQGVQW COLSSLQPPPPRFKLPSCPQ
5556	19457	A	5599	148	3	TQHNLAKKSGITTPGVVHNSVAHAGRW CDLGSFKPLPPGLNRSCLP
5557	19458	A	5600	195	1	MVYFKKPGFFLVEKSDCSVAQVGHQ WCNHSLOPRTPLKQSSHSFPSPRWNN RHMQPCPGA
5558	19459	A	5601	228	415	VNVSIPEVDVILITITLFFGPAQAGG RGCNINSLPLWPPGLKQFSCLTLPKSN YGLPPP
5559	19460	A	5602	405	2	MTGVDRHARQTQGLPLKTPQPCPNF TSKAGTSPAQHPSCTRQHQASNPQR RRRRPQAEHSIRTDAHGGLPASGHVAG ERPTKQASRINVLQRILALLPRLCT SAI SARCSQNLTSQGNPVSCL
5560	19461	A	5603	3	236	ROENGMPGGGACSEPRSRHCTPAWATE RNSVSKKKGIKIKGHCSSAMHQLSPF GWRQVCHVCPEPVLVRGH
5561	19462	A	5604	184	2	RPFLEQGKIRMPGSGSRFINFLILETW SISVQARVQWCHRSSLOPKPLVFKSS YLLP
5562	19463	A	5605	261	2	GNFLKGPPLPLQPKGLPQPKKVL QKKNPPPLGIPPKLKKTPLEFFFLRR SLALSPLRECSGTISARCNLRIPRTNS PA
5563	19464	A	5606	134	2	GSFPKNLVFFIQAQSLTSPRLCSGITS AHCKLRILPGPHOSPAS
5564	19465	A	5607	3	269	RQESHNSPGGGCGEPESRHCPTAWLAT ERDSVSKKKKRNFLNPIGKKKPCLP KPKLTKKKKWGITALVLKLYGRLAPK TGGY
5565	19466	A	5608	36	380	PPFXXPQGETTGGTREGPPPKFKSPR



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						KRGGGGKKPPRGAGPPPKHLLGGKRRGG GTPPPPRKTPPLNPKKKGKGGKRGVFP PKGGIFQKRGFFFSRGGGGGAPPPHPP GGG
5566	19467	A	5609	3	411	SSRSRAAALFYFFFFSRKQKBEFFLG GKTPPVVVFPPGGVGRKNGRFPFPAG KGPFSGGGRGCTPIMSPPPPRGRGK PKPPTTNFNFLGRVGLAKNPSGPGVC PPPKTPIFFGTRPPPGGFTWGGG
5567	19468	A	5610	364	483	ISWLVLEFLFKNSFVLVAGAGGMRGLG SLQPLPPOLKGP
5568	19469	A	5611	399	285	GGCSEPKSRFCTPAWTERDPVSKKNK NNYLKKSN
5569	19470	A	5612	408	3	KEVFSFFPGLRGVFFYSLPLPFPKVG FSPPPPPGGGGPRGPPPPGYTLFPK GGFPPLPGGSSPQIWPFRPPQKGVFPG GAPRPGNFFFFFRFPFLARGFPK KKCTNNVTLSHSASVSSLL
5570	19471	A	5613	1	112	LAQHVVFTLNTSLASPADSSLLMSVHG NGKRPSPIR
5571	19472	A	5614	2	389	FVRBGERKKERKKERKKEGTLEKGE BGRKERKKEVRKKTVDRRRPQVTFQA VNLESEGAPNGCVIAPPGGHILWKQVE VQTHLENCRHLKATVTTTTTRPGAREP PFLITCGEIMNVFSKM
5572	19473	A	5615	385	3	KEFGDPSKTPFFLSKQITGGGGAPL FPPPOKVKAKKRVVDRGQGFYCARLGF PDSRGKKKAGFKTNPPPKTKQOTKEM KAKTSKLLQENRSGPGTVAHACNPSTLG GQGGWIMRSGDRDTK
5573	19474	A	5616	218	402	RSYSFSQIVGTIVKARKPSSSWLZAPN RKNAFMPGAVAHTCNPTLGGRGGRIDR SGDGD
5574	19475	A	5617	2	235	KSFGCASRLQMHGRTHYGEKPYKRCQG KAFGCPSNLNRHGRTHYGEKPYKNCQG KVFRCSQLQVHGRACIDTP
5575	19476	A	5618	347	421	TVLXKKKKKKKKKKKKKKKKKKKK
5576	19477	A	5619	92	1	ENLALLERLECNGLTLAGCNLPLGSSD SP
5577	19478	A	5620	3	402	ADPPSFFPKRGLIMATISPTLGAIKLNF LFFPKGKKKKKKPLERKKKKKKKKGA PLAKKKFSPGGGRKIFFKGAPKISRA RVKKQRRGEKTRGNPKKRGKKKRPFPN TVSR
5578	19479	A	5621	420	3	HPPQGSANFFPPFRKIGINGPPPPAGI IVFLACRGPPVOGGKIRFPKPPPP PPPKNGLQKSPSPPPPIFFFLRWG LMTLPRLVSNVLRQSSHLGLAKWDM SEAPHLAKNPLKEYEVVSLSFVREGS
5579	19480	A	5622	246	132	EVAPHLGLCSIPTMCVCLVCVVCVVCV CVCVCLCSW
5580	19481	A	5623	219	424	ITNVNVLIGITGFRLLGLEGRALNTGK ALIRDMGPGAVAHTCNPTLGGREGWI MRSGDGDHFGQIH
5581	19482	A	5624	32	454	GLEKVSMTXDRNSRLSVQLRDWDGGB LLQFSVHLGDGTAYSLQIAPVAGQLG ATTVPSPGLSVDPSTWDQDHLDRDKNC AKSLSGWNPOTCSHNTNGQYFRSPQ

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QROKLKKGIFWKTWRGRYYPLQATIMLO
5582	19483	A	5625	166	2	LFGLVKLTALKGLRMILPSQVWMLTFVI PTLWEAKAGGSGQSEFETSLANTVKP
5583	19484	A	5626	120	406	GEAATQENLAELRPEPELLSTPTVLSRE FELPSPTVLSREPELPSPSTVLSRKPD LSPSTVLSRKPDLLSPSTVLSRKPDLL SPSTVLSRKPDLLSPSTVLSRKPDLLSP STVLSRKPD
5584	19485	A	5627	324	16	LSFPEPLFKTAPRQKKNPPPKKKKAP PKKKNLFFPPFFPLVFPFWNCWSRLAE WNETLGCMDRMOQAVGTGTRELAPGG SRSPRLRAGKELGPHCAP
5585	19486	A	5628	378	72	GRGGRPPFPQSRQAKKKGVNLFFPQR GKRSGFPGPFPPFKLPSQEAAPGPFSSFF WGRSLALFSSWARGGFLVPANLGFAPG APKGNFPSKKKKEKIED
5586	19487	A	5629	3	204	QRSCLANNGRGCSPEPRSCHCTPAMATRK DSVSKKKKKKKGFFTEVIGNPLPLHFPK WSYPPSPRIF
5587	19488	A	5630	177	1	SPHENRFPWKLFIIRIYVIFERRSPVPP QSRVQMHDLGSLQLPLGPKRPSCLGLL SNW
5588	19489	A	5631	154	3	KWFWQMSRSVIQAGARQDSSLRDPTP QLKRSCLSPFGGWDTXRVPPFC
5589	19490	A	5632	239	17	EGVRNYLLTLQPSRLCRNCSFFPNREKE LCHSSPSSPLAAKSSQGEKGRLLSQD EGLLLVSVFVEDVEINS
5590	19491	A	5633	2	110	QCSREPSHICTPAWVTECDVSQKQPPP QKKKCIAG
5591	19492	A	5634	433	0	FFFFFFFFFFFFLAKKIPPPGGGGF
5592	19493	A	5635	306	433	FSLSIERSSSGRAQLLTPVMPALWEAEA GRSRSQEIKTILAN
5593	19494	A	5636	2	285	QSRTSVIFNSEKAERGSETTEKPEASR GWLKFKRSCILHNKQVSEASADVEA AASDPEDLAKIIDEDGYTKQHIFQGLALC LMSNPTTLGG
5594	19495	A	5637	160	1	LYCGKIYVVRFIRLNFFLSQGLTSPKL ECTGTITAHCSLKLSPSNPPARAA
5595	19496	A	5638	3	261	KIQLNPGSQGCSGLSCHCSFAMATETL SQKKKKNPFPFGPKLGRLEPLRPFQTK KKKGFLKKFPFPLGFFLEPFTWGGFW N
5596	19497	A	5639	2	121	SELRSCHTFAWRQSKRTISHKKKKNKK KNKFFLPFRFN
5597	19498	A	5640	370	180	VMERFCHVDQSGLELLISGDTPTPSASHN AGITVVSHTRWQSPSPFFKERRNLKSV TSLANSP
5598	19499	A	5641	254	1	PYLLEKVPFLFAVSQKQCTYPAYDAS YSADITYSKPDSNGRKHMYVVRVLTGVF TKGRAGLVLPDPPKINPHNPIDLPDSVTIN
5599	19500	A	5642	292	106	NFVILPYLQKQSHYVAGAGLKLPLSSSD PLATASQKAGITSVSHRAQTKQASTYVV PFSLET
5600	19501	A	5643	3	100	DTTFEVREVMRKEVCEDLACTSPDRREG FLII
5601	19502	A	5644	1	282	EKVPRAKRLYGRKGDFFTEAOENHNLIG VANVFLBCLPCDVKLQYAVPIISQOGEV

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						STGQFWRTMVVQVFCPLFWPSFYLSYV LEVQDQTKAN
5602	19503	A	5645	142	67	NKNRPGLTVAHACYPTNLGGQSQIT
5603	19504	A	5646	350	213	GLEILTSSDDPPASASQAGITSMSHRPW PPLASRIOLCCGTYLYLI
5604	19505	A	5647	3	180	EBNAERAFIAQAHIQGPACTPGPFSFI PTQFPFRSSGLPNIPWQTISRAAAEKL FG
5605	19506	A	5648	366	1	RSWFTTYKERSLLHLIKVQREASADIE TAASYSDLAKITHEBSYVQQLFNVDRE TAFYWMKIPSLTCLAREHSLSQFQAK DRLTLMLGANAIGDIKLPMTIVYHPTK RALKNYASSL
5606	19507	A	5649	1	355	QIQSSQSGKGLLLTSFDEBETKLPFRGN KVMFCIDPGGGKLCCKKKIKPLGYDPG GGFWGPQTPPLAFTPPGFPDPGPNFS PRGFPFKMGPALRGPGKKKPKPEKTKPA EGGTGP
5607	19508	A	5650	348	124	RAPPVFFWVFLGQFFKKKSTNSPRGGGP PRSPQPSLSLPPFRNVFKKKPPPPFFEG GRGPPAPPFKNPFFFFSRL
5608	19509	A	5651	194	43	KKKFFFFFFYMESHPTQAQVQWHLGS LQPTTPTTFRPSCLTSLIALP
5609	19510	A	5652	27	244	KKQQTSLFLFPLSLFLFFFLVKTGSHY AAQAGLELRASSNPNTSVLPSKMDYGH EHTVPSPTWFLAAKTP
5610	19511	A	5653	38	429	GLFLSCLFFFFLKERGVPLTPPGATGENP APEKKGTGKLLKNRPFLLKAMPGRQK QKKFFPATITSDQRAPEVKGPGAQGE PPAQKKKERGGGKTRAAPNKKKKPGAP FSLKKTPLWAGGGPPDPF
5611	19512	A	5654	391	68	NLYPHGVGVGVSPGKGLKADNPLGFI PPSGRPPPLPPQGFPPCLXPKRGLGAP GPFFFFFLAILLWGFQISNTDSVCVQFI IQTIWIIFTTIIKGCHLFTFLF
5612	19513	A	5655	139	34	GARFLFPSPVLSPLIEHCVCVCVCVCVC VCVCVCVCVLCACMCT
5613	19514	A	5656	88	388	STFCFTYVFLRQSFITLVAQGVQWRDL GFLQSPPKKKKGKBTSPFLGENRYLPK NFTFLTQVCFPERKIPPNGLINGRPKW LPGCEFLKTLVVGWV
5614	19515	A	5657	176	371	HFYFCSDDINLAARPKVNRGAGVKRSA ARMYGSVTEHPSPSPILARSGTLLITL CPSVGIPTF
5615	19516	A	5658	3	113	CSEPSRHCPTAMATERDSVSKKQTKN LSYKKTHW
5616	19517	A	5659	409	67	SSSKNPTTPVFLPPFGHGVPRLPGRK KPGPPPPPPPPQVPRGGFALNL PPRQKNQMLYSPVLEQK
5617	19518	A	5660	2	377	GRISCSRNTPLARHSLMLVLCGLARPLS GFLPWVQVFLALIPVNPQPSISLQVRTI NDMLRCCDRDIYGGQWQFARLWAGCS QQYTEFFRKLIPTISSLFPNVLVLEVAR AIRQEKELNGLQ
5618	19519	A	5661	256	381	NPNFGQAWMLMPVILATWRAEAGESRGQ EIETILANTVLPKHL
5619	19520	A	5662	19	313	LYSSIALGLPLPLINFTIIITIFFFFER DGGQONQNVSLKKRETPPPPSLGVFG

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						FENNNEICMIKSTGSIYVLRHKKHLKVYS SNIWQKNLILRGGAVAHACNPSTLLGGR GRRITRSRDRDHP
5639	19540	A	5682	189	3	NNNRKASWKKKIDRVLLYCPGNCNCDLGS LQPLPPGFKRPSCLKLPKCDWYKHEPLH PAPHV
5640	19541	A	5683	2	227	THVCVCVRVCCLLRDSAQPARCVCVC VCVCVCVCCLDRRLRSTSTQLSSSCH PLYVPSGGSRINRPPYQOC
5641	19542	A	5684	318	421	DVPCFVPAFCDCCKPPEASPMANLCSM KPLSFI
5642	19543	A	5685	213	398	SLCCCLPCCCVFTETSRVWCAGVQNHED HSPQPPQPRPLKSSSHLSLRHDSHPQ PPPPRL
5643	19544	A	5686	398	1	SFFTSTSTSTSSSSVGGGGAHYSKCTAP TAQPHDRPLTASSSLAPQCRVQNLHAYQ SGRLSYDQQQQQQQQQQQQQALQSRH AQETLHYQNLAKYQYKGGQGGYCPQDA AVRTPEQYQTFSTSPSSSRE
5644	19545	A	5687	2	288	SDRPSFSTSPSTSPFAOVGRASSIFPIL SATLLLLGGVCVAASRVYKSKGNITLGA GILFVANGEREREGATGAHLGAHVVCV VCVCVRARARA
5645	19546	A	5688	314	2	CRPGSOLQELRDSGGGSEFVGGHQQHP GAPQSRRYLQPLMCGASPHASPROPLA ILAGVKFRLRLRHAGRLRLMLQINFL PYSRVVHTYRLRPSQCLTICI
5646	19547	A	5689	122	3	WGGQEPSKKMNTNGQGVAHACNPSTLG GRGQITRSQV
5647	19548	A	5690	144	1	EAVKKYTCFTWAGAVAHACNPSTLGRG GMITRSRGRDNDKHKKEIPR
5648	19549	A	5691	377	65	LGVFFPFFFLRGEGLSPFPGLVKNQF FFPQQGPPPGTTERGQGLGPKFFFP LPQQGPKGIFFLKKKKKKKIPICALAVL TYQHFCYRTQGERVDGLREL
5649	19550	A	5692	12	147	YERRFCHIGQAGLELISGNFPASASRG AEITGVSYHAIIMNLS
5650	19551	A	5693	183	395	GHRPGPLHPPPPGPGGPRP PPFKTRBK RAPPPPPRFFFLGGGGSGGGPRGVLF LRHENPPPGAPKQVG
5651	19552	A	5694	177	283	THPLNRTDGRNLSLASLSSSGYGNTPS STVSVA
5652	19553	A	5695	266	460	LSQRKYAFFFFFPPFKKIF PPSPPGGEI RAQFLITEPSFFWVKGPSPLPLPTMDY IGRDPPLG
5653	19554	A	5696	1	412	WQPLKYNLLEQKNGLEFVAPFTWIMCP SYNSLAYNVYPSQTSFINVFTCMFITVH IPKKKKKKKKKKKKKKKKSSSPGSP GYAPKKAIPNKKKK
5654	19555	A	5697	379	0	FFPSPQKKKKKKKKKKKK
5655	19556	A	5698	1	187	PIRPPTRFRFENGYNLGGGCGEPLCH CTPANVTERDSVSKKKKKKAVGGPWF FQKKKV
5656	19557	A	5699	374	0	DFLLQKKKKKKKKKKKKKKKKKKGGG
5657	19558	A	5700	219	413	PFCPGGGGGGPNFVLGPPPPGLKEIPP PPPRGGKKKPPPPPGGFFFPFKKQVS PGGPGGSP
5658	19559	A	5701	381	249	FHRAGQGLDLGLAPGAPLGLPKCNDYR

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						RRPPKPAFFFFF
5659	19560	A	5702	382	197	LANFCIPSRDGLPCCPGNSGTPGKQS AHLCLPKCNDYTHKPPCAPQVIKPS IN ILLVN
5660	19561	A	5703	1	381	ERGSICHPPRGLKHIRGRTCFVLKGMCIQ LCVVPPQQKKKKKEGGGKKKKDKRREE GREKKKNGQGERVKKKKKSRKKKKRSS SS
5661	19562	A	5704	291	167	NGPPPPPPFLVKGPGCHVQAGLEFLTP GQPPALASRLLLG
5662	19563	A	5705	367	23	KNFCPPFPFPFPFLAKKKKGPFPKKKTKF VFPPLFLIKGPPPKNGKPPPGGFPPLF CPLGKRGGVLS PRVCKPRKGQNPFLF PKKKKKKKRRRRKKKGKORKERQVYH TV
5663	19564	A	5706	411	116	FLKRWGSHYAQAQGLLELLSSDLPSAS QSAGITGTHCSRLSYSLAQCQLCQPVW RIPWRGRGVGRETSFRGMRRYGRANSS SGGGARSLPGLSPG
5664	19565	A	5707	162	2	SYCFPNSDDPFPQPLPMTHFLMRRPFF IFKTAHGMARWLTPIPALMEASAG
5665	19566	A	5708	1	416	LPPLLRLFPFPAFLFLPKDSPPPPPPPP PPPPPPPPPP
5666	19567	A	5709	403	142	LSKRRKMGWPRGSPRLPEKPPPPPKIFF APPKKKIFPPPPGGEKKFFFKGAPPPPPF FFFSFFFFFDCYNSSTYMSAMHRCISI SIC
5667	19568	A	5710	339	461	PSTFILFLRRSFALVAQGVVRNRHGS PQPPPPQKRVPA
5668	19569	A	5711	408	42	TGARITPSGTFPKKTPSPFPRAFLILGFK RAAPQLIYFVLNLFAYKLVKLTVTHMR RRPTFFLLFKTFLVVEGPGCHVQAGL QFLGSSTCGSLPQCWDYRCPQLAKRS TFIKSESAN
5669	19570	A	5712	277	9	GUCVCVGVVVVPMGLQTPSAPMGLSLA PPLGTLCSVQWLAESIHLICQALVEPL RRQLYQVVRKLLASSIVSGPGDSINN GSYLR
5670	19571	A	5713	411	0	FLQILLFLIDIAFFLVFFPPFFWK
5671	19572	A	5714	205	400	HYLTQSSSSNAGESVQDVVMKPIPLTNP GAVAHTCSPSTLGGRGGRITRSGUGDHP QOHDRAPSL
5672	19573	A	5715	1	89	FFFFKTSRSVAQAGVQVCTLGSLLQPLP
5673	19574	A	5716	176	392	GVHLVLEWKLMSVCARDERLFLPLCSWKK FFFLFLRQSKSVTQAGVQGNFGLSLQPL LPGLKKRISCLTRPSS
5674	19575	A	5717	1	89	FFFFKTSRSVAQAGVQVCTLGSLLQPLP
5675	19576	A	5718	306	42	GGRLRCALNSVKCLATLECLLGLTYLR QIKICVYTCTCKFIVTLFIIAKKYY PSVHQLINKMWHIQTPLVIKRNBOCGG SCL
5676	19577	A	5719	1	263	PIRPGRFPLIGDRGCSRLKSCVCTPAN VTEGDSISKQNKQVRLSPAAHLGLGL VPMRQASTRIGDPTCKLLELSKPSK AAA
5677	19578	A	5720	3	278	NQEILKNVRSSTVQPHLEFLSLGWS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						QGMVRVFPNLPFPIKPETVARRTVEAVQ LTQALLLPWTMIALVILKSLPQAA
5694	19595	A	5738	335	152	GVEMGFHHVQAGLEFLSSSDPPASASQ SAGITGVSHQASPFFLPPLSGITLPLSY SSGSD
5695	19596	A	5739	35	462	IDASDFGCSQAANDNVVIVYELLEEM VDNGFPPLATESNLIKELIKPPTILRSVV NSITGSSNAGDITPLTQLSNIPWRRAGV KTYNDAEYFDAEELDALIDKSRSTVFA ETQGVINACKLISGMFDLSIFMNPILL DD
5696	19597	A	5740	429	325	NPGGRGCSSELRSHPCTPAWVTEQDALIG GRSGRIT
5697	19598	A	5741	344	423	FWDGVAHAHGNSTLGGRRGRTTFSR
5698	19599	A	5742	431	103	RGPFPPRPQKKGSGPGGPPQNKKGSP PLHTGAKGSGFFKKKKKKVPKKGPGPL FFPGQGRKGPVGAEPVILPNRLGPPR IPGWEPEGRGIFFLAPVFFPSKKPK
5699	19600	A	5743	31	224	IEWGFYHAEQDFELSSNDPAALAQG AGLASMSHCSWPGKGNFMCCIMKRL AIHNECIA
5700	19601	A	5744	217	400	HSVMGSGSPFFFFFFFGEKGLFFFCP GGPNLKGNNPPPGKRGFPFPPPKKGN NGAPP
5701	19602	A	5745	4	455	DGLEFGRRFRGQRCSSPPRRGRGQVEA LITSQTGRRRGGAAPHVSDGGRGRDAPH FLDGLVAGKGRSSLPINDGGRATLITF QTGGPGRGAAPHVDDGRGREAHPFFDG VAAQQLQSRHFGGGRRLLGGGGCTEPR SRHCTPAMAP
5702	19603	A	5746	381	212	PRGGGGRYSPFPFGGGRGNSFPYGGGG LNKPHGCPCPPPGGPKMKPPQKKKSL RHITC
5703	19604	A	5747	334	432	MFCENYKELAWPGAVHSCNPNTLGRG RHITC
5704	19605	A	5748	190	1	IPPKKGGLNFFSPPTFKGVKSKPPQGG VFFFLRRSFTLVTHQGVQMDLGSQPP APGSKHE
5705	19606	A	5749	425	297	ESAPHVVAQAGLELLGSCDLPVSASQV GVTCMSHHTRLYS
5706	19607	A	5750	425	0	KKKQKKKKKKKKKKKKKKKKKKKKRT KSDE
5707	19608	A	5751	136	3	AQSSRFAMLIFLVLVETGFHNVGQAGLE LLASGDLPTSQVPRRP
5708	19609	A	5752	3	237	GCSEPRSRHCTPAWVTEGDSVSKINKQ TQRLKSIALFPAIHSLLFPVVIKLAMP LAMDIPHPDIVEFSYHWEQN
5709	19610	A	5753	1	358	GDGCSBLKSCICTPAWVTEQDLPSKKK KKKKKKKKTRNGPQTGGDLPPPPPLGG KNFPGSTFWHSGKKKRPFLSGKKGK FFTPAPKGPCKTLGGPNRGGAKKKL RPPGPVY
5710	19611	A	5754	2	191	QGCSELCSYHCTPAWVTRAPRSKKKRD KTKNQTKKRLGKKPNLIFPPQKKK WVQIPGK
5711	19612	A	5755	42	408	KHAAPPASLSLELLHNGKACFPAP CRDQFLEGSAMLPVQPAKLTPRSTPP HPCSELDNSAHFN
5712	19613	A	5756	179	410	LQAPLRSPPPVPLFLYADLSQNLWPGM



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5713	19614	A	5757	166	2	VARACNPITLGGGRGRIT GRPGPADFRVRPOLLORFLPIYLFTME SCSVTAQGVOMCNLSIQPLPPGLEF
5714	19615	A	5758	334	3	BEKVFGPLSPILLKGGGAASGPFCPI SPRAMGPQKGMETHVFTTKAPSPSPGV LVKQSPGIGFVPMNFFYLKSLALSFR AGVWRDLGSMQAPPGSTPPFSCNLS
5715	19616	A	5759	373	470	SSCSLRNNSPGAVARACNPITLGGGRGG RITR
5716	19619	A	5760	210	384	EALDTTITFFFFPETTKFCVPAQAGQQQ NLGSLGAPPTGLTPFSCLTLRKTWDCGP PP
5717	19618	A	5761	257	400	SLGSEYTVVCPVETESRSGVGGVQW CNLSLQPPPPGFKRPSCLR
5718	19619	A	5762	400	2	ARAVSGVGEDPGLTGPSPATETMNAV VCRACRGSLLMGKFLIRHWDLRKVL RNGTGEDCLKQLMSQCGAGNGKGPQGL KGPVGCICSRKRVFYLFLYFRDEVSL CHPGNNAVKOTRLTAASAO
5719	19620	A	5763	34	440	RVRAPLGWEENYFVIRAKPKSGKRSCL PFLRQGHQEPILMGLISTASPLRLHVGAS QICGVFLFCQVSLKDPAGSKVVIQNDG ERKAQRLLCPRLATRVBGFICFRFVPLRW SFTLVAAQGVOMRDLGSLQPPPL
5720	19621	A	5764	297	468	LVGAGVPTGCGQENGUVSRKSVQAQWL MPVTPALMEABAGGSRQETETLLANMV T
5721	19622	A	5765	1	205	GPKLTDSPASGAKALLRSOLLGRLBEN RNNLCGGCGMGLKWHNCPPAAIEGNLL FKKKKKGGGT
5722	19623	A	5766	307	1	KERDPFPTPGRTFFFTFFKNTCFPPF KEGQGGILGPRHPFFSRSLFLRGVPPRG FPPGPRNFFFWFVILVQGVPHVQADFK LLTSGDLNKATASQAGIK
5723	19624	A	5767	2	319	LLNGEELSRFFPORSQAMVFESSAGI FOGKAGATGLEKLTGSFQQLTQHPDPT PEELGDPKSSASEKTRGLQEVGPTEI LKAVTYTQAMPKEAKVDPIPT
5724	19625	A	5768	787	1118	EAAWRELEAERAGLSQLOREQEELLAR RRAEKQOLSEIAALQOEHEDEGLLAES EKQOVREPWRLCCSLSCSSGAGPCSA TWOLGALGOATALLGASVSLPAGED
5725	19626	A	5769	2	452	NGAGTMSVSEADENFFAQGALKSEDCF ILDHIGDKGIPVWKGQARTEERGAALK TSDFTKMDYFKQTQVSLFEGERTPL PQKFKWNRDPAQDGLGLTYLSSEIAN VERVPPDGGRLDTPTMAAQHGDDDTGT CQKQWIRIEG
5726	19627	A	5770	2	130	GTQGIKIVDLVKELDRFTVFLVNYIFPK GKWERPPEVKDWKS
5727	19628	A	5771	422	8	HIARWGARAPGGGALLKAEICLNAPAP PIGARTAPLNPGCCFLRPVFLLLFPFF SLFTQSFRILYPOPWPLCGRES TTLSRM GTTDHIIVLASTNRADILDGALMRPGRL DRHVFTDNP TLQERRKMRHIGASN
5728	19629	A	5772	432	3	YSLNKKRWVPLTTHNSVHYYSSEKSL KLGTVVINSICSVVPDEKIFKETEYNN VAVYGRKHCVRLNVLKLSASRMSSAIO

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
						NVTDTKAPIDTPTQQLQDLKNCMTSH VVEQI YKRKKILRYTHHPCIAAAVEDHD ND
5729	19630	A	5773	20	432	SKMAALLSAVITSLFPYYEVAEKIWSNKA NRQCADCSSSRPDMAAVNLGVVICKQCA GQHRALGSGISKVPQSLKIDTSVMSNHEV OLFIVLGNDRANKPFACTLPPEGGLHFD ATPQPRGEISRKCYRLGLPKRPHPO
5730	19631	A	5774	433	2	RGAFOTLLOKRDLOAFVLSVQLQVLIGS CFKLRTVINI PVPSNKVDDRCPLVYGL HVIVHFPAKGVQSATLS CALEVDSFGYF VSKAKTRVFRDTAEPKNDERFEIELEGS PSILRTLWYEEYNKSKVNNLYSAAVGS AWQ
5731	19632	A	5775	133	436	MLISLPHPSITLSTLSPFCDFGTQRTTG AASHVLTLSAHSSVSCPPLMGEATTSR AQDLPADEHITAFAHIELEAPALSKGGLS ILRLTGHLLPGQEVNL
5732	19633	A	5776	397	58	KOTFISGKLEELKRONANQALADATIEF QLLPASLCTIEDTPTGMQVVKRSLGSRCH RSKQDSVAGERAKVGFGRGTSNNYIKT TYSQLSVSLSGHHPGATLAAVNGSCSP T
5733	19634	A	5777	1	324	MRCVSAAGVELEETYPALDMMVRSKLE GSDIDPTQYEDTLREMTPTTHAYVGTNDK LVQNIARQVSRAGVGPALRTAEMLPSF HSPILGRGPPVSTANLSCFFLLETK
5734	19635	A	5778	1	398	RLGSRPSLEHQSPLRESEIQELKGDVK KTVKLPQTEPLCAIQDABGALHEVKAC RERIQSNAVRSARKNLFETRSLDVINQDP SQVRLIRGISLEEGAREDSATRWIFDT QSLDAIREILVDEKDFPSP
5735	19636	A	5779	281	12	VACNLGWRVRTPTPASYPFCVPOLSVRG KNRKEILGGFLRNIVKSADRALITGMSG LKEVDFFFEHRTNLLHYHTLYCGRSED HATSR
5736	19637	A	5780	406	23	DSQATGPGISRRGRISSPSSLCRTFSTS IVKCS PLEHLKYLDPPPPPTRCSRPAS LRSSPKHCVQOQFPPIACRPGAAAPFPFP AQCPHGPAPASAGHEPKNGSRTEGGPA RDRRSGGTGRKKR
5737	19638	A	5781	415	18	TSQAGDILLHGSLLRRGPNGLPGVDP DPTLATPPAGQTLAVPSLPRATERGTGP LTTAVTPNGVRGMGPSAPELLTPPGTGT APPPPSPASGPPPLGPRGGRKRPPTILI TTTTIVNTVTSIPMYGKRSBG
5738	19639	A	5782	168	432	GMRQTYGLDQSGRGVGNVDFFFPSS LSFFFFFGKESYFVLKFGIHGLKPGYL EPLSPGLKEFSRLSPPKGHLKCRPPSP LFFF
5739	19640	A	5783	1	423	TDDDLNWLDSHRTFREQVDRNETILLR RKFFYSQDNVDSRD PVQINLLYVQARD D ILNGSHPVSEKACEFGGQQAQIQFGPH VEHKIKPGFLDLKEFLPKYIKORGAEK RIFORHONCEKISERSAXV
5740	19641	A	5784	273	400	DSVLLMLSPGVCPH/VWPIISCTLGAT FGYYAGLVISPLW I
5741	19642	A	5785	445	28	DTNRAPIHMEIKGSGGTAKVNGADSID

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
						KEAGDETMKARTMKAEATGAKPTGVFA TGAKVTETKPTGAEVREMERSTEEENMS SKPTGAQATDTTETTOVERAMOVATIKKA ERAEWQAYGVGAQQAAPPVVTGTVLRPL
5742	19643	A	5786	380	2	QRQESPEASSLHILERSVQELQLLIVE SQEEKESLGRVESLQSRISLLENERGN TSYDVTTLQESGELPDLPGAZVLLSRQ LSPSAQEHLSLQEQVAVLIRQNGELME KVOINENFENDECT
5743	19644	A	5787	663	2	FGVERRATRTIRLTTRTVLDLYSFLAGVS ENLRHATQDDASRTRAPGLSSCHP KPDT TVSGDTEYKSGPGVFNTERSGMKDIKSE LAEVKTDLKNSDKLEELDGVKVGVEGQ LRQLQEAQGGPTVMTINELYCAVVDK IDALREELMBGMDRKLADIKNSCEYKLT GLQQQCDYGYSSYLGVIELIGEKETSLR KEINNLRLRLQEPSAQAQNCDSVY
5744	19645	A	5788	398	1	TRCYTHSALRYGGSFALGPRIQRLOQQAQ LWNFTYGSQHRARVLPPLBQVNNLLHL EYKRNYYAKRGOPPVKRAAEPVTVQVPE PAALSGPSGEEGLSPGKERKRGENSEQT GLPGLPLPPPPPLPPPPPPV
5745	19646	A	5789	116	371	RHPKIWLRGPPGLTLEKRGKGEPLDP RSGFKAEATPPAPPTFRGKGTPLRLKK PKERKTRERGKKGKGGKKGKNEGTNP I
5746	19647	A	5790	406	284	RKGFHVYQAQLELPTSDDPTLASQSK PGPLCPALHPT
5747	19648	A	5791	200	3	GDALTYNEPEKQVMSRSSDECVVALCDQ MLVSYSKKIPLVNLLITFLKKHISICPL PGTNIMEMY
5748	19649	A	5792	372	278	LQIQSPAGQSRCSGFLVREDFVLDAAHC WOR
5749	19650	A	5793	1	167	VAPPKLDPHSORVRAQAGLEMLTLCDFP ASSSQTAATGASHHTRQVLGYSKALS
5750	19651	A	5795	112	3	SSWGVVAGHGHYGAENLRPLFSFTT KTYFFHC I
5751	19652	A	5797	356	238	FLFCNNGVYSIERPCLAEAGDDAFVR DVTVLQNTDGR
5752	19653	A	5798	379	60	VKIRHCHTMVMSLLKMTLRLILEEQVE GNYSPCVLDNQNLQQLWMDHRSILTKA GIMYFAFNPRLCVSEIYRMBEVTGTGR QSKGDINTSRNGERASCB
5753	19654	A	5799	377	3	KVAPFGRRGQGSWSAFQGHTRVVSCLK NAVTPDLAVTYSVGTIYIMDLIDTRK LTVALEVVAQASQVKNKKANCLATSH DDVRLWDKRSSTAVEYLAHLKSKING LDWHDPSENHLY
5754	19655	A	5800	143	316	CPTSPPRILPYTFEFGVSGITVVEPRKI NGFPNAPFWNGGRDDDLNRYLCSRSPGV F
5755	19656	A	5801	390	2	LEFFFFFLLRQSLTNPQAGVWRWDLSS LQPPPPGFKRFSCLCV
5756	19657	A	5802	342	455	VIFFFKLKQGLTSPRLKCSGTTITICG LDLIGSESEPTFT
5757	19658	A	5803	1	378	VYSSRFENIKKRYRGRGPPTICYFEKGR FLIQYDNTYGSTAEIDVENLKNPQPPQPQ VPETPNADRGSGVGHITDFTDQVTEKH

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						SSVLVMPHAPWGHCKRMNPFERKASEA LHGRADSSGVLAIV
5758	19639	A	5804	152	1	KPEIFFFZSRVVTQTGVQNCNFGSLQPP PSGFKLFSCLSLPSSNDYTAIV
5759	19660	A	5805	207	31	LYLQLQQTASSGNLNTLSSLPMPGKGC FTAAEEQQHGGQQTQLTTVLGVWHRFCE NIF
5760	19661	A	5806	199	2	GSBCSCLLSRGGMHVLSLSFKVTFSCD ATIHFSFLFWRQEFPSVQAGVQRDLFG SLQPPPPGV
5761	19662	A	5807	385	239	QQPSTQMKVGVGVGVGVGVGVGVGVGV KSCIRLSYMKMPINFGIKNL
5762	19663	A	5808	39	184	GRITIKFPGRKSRHAAQTGLLGGSD PPTWASQAATIGVSLRIRP
5763	19664	A	5809	376	2	NAPTSFPHVCTISYVTFPRGLIAPTRVR WKCLVIDEMQVRKGMTERHWEAVFTLQS QQRLLLIDSPHNTFLELWIMVHVLFPVG ISRPYLSPLRAPSEESQDYTHKVVIRL HRVTQPFILRSV
5764	19665	A	5810	271	120	FLCFIKTSESGSFSLYSRDTGLPGQV SLMIKKSNMVFHINKGSINR
5765	19666	A	5811	367	3	DKSFKWEKMLEDANAPTERDERIAGL YEEIRDLMLLQASAVEDKLGQGVISTV TSLSLANIKIWLTDGQETAINIGYAC NMLTDDMDVFIAGNNAVSREELRKA KQNLFGRCI
5766	19667	A	5812	294	37	FRGENPDDSVRGSPPEYRLRQVASSLF RGEHHSRGGTGRLASLFSLEPQIQPVY VEVPKVSMAFFPNSSLEPLTYKAILFLP TA
5767	19668	A	5813	184	3	YISVLNNYLLFSPQGRQNFVLLPRLCS GTITAHCHLLKLVSGDPPAPASQVART GMRH
5768	19669	A	5814	468	1	DDMEYEGSVSVTFQVPRKSNKGLDYTL MVAGEFGLGKSTLVNLSFVSDLYRDRKL LGAEERIMQTVREISKHVDIESEKGVRLR LTIVDTPGGDVAISTEGKRRAMY
5769	19670	A	5815	24	314	QAPFGPKCFNMLCFSLSSKGEPEFHY IAGAHGNEVLGRELLELLLVQFVQGYLA RHRARIVHLVEETRIVLPSLNPDGYEKA YEGVMALAHLTQ
5770	19671	A	5816	474	3	YTLRKGYSRHHGLIHSIRQEVQATPLEG IIVSGQMSTMMNLSTLWPSPRVRRLCI GRTLRLSLRIRPCKRTPLQTRMPQMORA LYGPGSDPPLSRAPASSPGSTGSGFR ARPPHPLPPIILLRGEPPPLLPVLPQR RQDPLPLISQSRITV
5771	19672	A	5817	511	389	GNYCTEGREVVTFPRHETEDSDHGRV SASILTHCSNR
5772	19673	A	5818	510	2	PLSCFVNPFLPVVPGVVMQHIEACMQ VRGMQRIVLIGVYQDEPLAQFIEAAQQ EFILPVRYLQEFAPLGTGGGLYHFRDQI IAGSPRAFFVYNADVCSGFPLSAMLEAH RRQRHPFLLLGTANTQTSLNYGCIVEN PQTHEVLHYVEKPSCIAAATEDQASSRQ R
5773	19674	A	5819	282	152	FSLFLPLQSERHPIMQVVCBATQCPDT RVSVRLYEKSVLHLS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5774	19675	A	5820	347	1	EPHPVTPPAVGTSTRYNPLIMMDNRSAVTPFSPHPQQPSSMQTGMNPSAMQGPSPPPPPSYMHIPRYSNTPIPTVTSQNLPSGQTVPRALQILPQIPSNLIGSPGSYIRQTKV
5775	19676	A	5821	482	13	TYEKLITGCTNLANHADPSNGDSELLSECLQYLEKQLESQARKMEFFPSDSGELVQIMMATANENLSAKPCNRVLKFFTKLFQLTEKSPNPSSLHLQGSQAQLACVEPVRLOANLTRMTTS
5776	19677	A	5822	608	7	FRFAKVVVEGNFTIVNSITTKIHSKAFHASFELANQLQGYSVNPNWQSDRLRTRITDPCRGVITFKKETTQOTLRLEADATDNGDQDPVTTPLRLITNQGRQIQLKRRTKDCHVSSKLMFLDLDLWVITDSQLKAMMYAESLSEMEKSAHQKSLAPFVQITPPAPSAQSQWAQAFGGSQGNSNSSSPVLRPL
5777	19678	A	5823	328	3	AEVASRDCSLPCFLAVNRITIEPVAAHRKEADMRLRFPPEYLKGRKELFGLTVHAVLRIABSLGVBESCONLFRYGRHPLMELPLMINDSGCARSEIKLLTHKRSLL
5778	19679	A	5824	69	308	TSVPSVCKRYLLRRTSALNTLQTHSSSFPHASSALHSCCFPPFSNLQTLTDINVKAPALMTKAVVPMEKGRYRE
5779	19680	A	5825	424	2	LQRAFSESRIRKLGYYQADRQTYHRRCSFANHVSVRPSADRKCSNFPFQRHGGSHQSKKTPVPGAPSTSSQSKRSSGLQSGHSSQRTSAGSSSGTNSGQRHDSYNNSSGSSRKKGQHGSEHSKRSSSPGKPQTV
5780	19681	A	5826	107	2	SSLTAGVRMGVPAQSTQGTNGSSPQMSGTAALTS
5781	19682	A	5827	2	437	FPTDSRTSKESMS EADRAQKNDGESEEQESVDTGEEEGGDESLSSESSIKKFLKRGKMTDSPWIKPARQRRESRKPSGALGESDSSAGSAEHGFCDS TGDMEVBSGLPGRRRPENPVFLCIVAVRAICPGFLMS
5782	19683	A	5828	487	22	MEBVPVPLSHFQPTTAARKLQFOARLSRCVFDVPSLAARNDTLRLNQLCLRVIEHGQNRMSVQSVAVFVGPFLRPEVRETSMPMTNVFQNRVVELLQQCADI FPPH
5783	19684	A	5829	2	871	BGICQNRNREGSSQSRGGLVITSPSGSLVTTASSAQTFFISAPMVISALPPGQALQVVPDLSKKVASTLREGGGGGGGGSSVADPKPGRKKRMLSLGLPEMNDPVLSPEDDDDHQKDGKTYRCMCSLTFYKSGEMQIHSKSHSTETKPHKCPHCSKTANSSYLAQHRIHSGAKPYSCHFCESFRQLSHLQQRTHIRSKMHTETIKPHKCPHCSKTANSSYLAQHLRIHSGAKPYNCSYQCKAFRLSHLQQRTHIRHTGDRPYKCAHPGCEKAPTQLSHLQ
5784	19685	A	5830	463	1	LPESRLPSPHKREBGSRRVIMTSYPIEPHRRKGSADVAVATLKQKLEBMTREQSDSCNCKLLSKDWKRMERLNTSLLGELIKTTPSLAKKRLATHTITQLISLRBQLLAHDEBQKLLAAGIEKQRQMDLA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
						ROOQEQIARHQZLY
5785	19686	A	5831	462	2	MILPDSLLYFLCGWLSNLLGTGYGVRK PWYFPPTASVYKSGVPLVEKRPPLSSG LFFNFENFDPNQSLLQNRSGELEGGAPG VTLVSVIKKEYEGHKAIVQDLSLFFYRQD ITALLGTNGAGKTTIISMLTGLHPPTSG TIIINGKNLQTVY
5786	19687	A	5832	396	2	VFSTPASKRKGIVPCCRDIIFYDEGGALP KDIEVAGILFASAMGNVPLLSAIZPHS AWAMGMGVNFFVASTHIVSLMSGSGRY APNGKRKYHYUMKTEWGEILLSEVDSPH LSSIAYPPTADNWNATLY
5787	19688	A	5833	384	137	EEICIANPGAGCSEPRIMHCTFANATER DSSKKKERNCLSKKKEKEMFACVVCV CVLFSIYAFPSRAQELSNCKEYGNF
5788	19689	A	5834	171	2	FVEGINISGNFYKSLKYAPLKKKEMNT NPSRGPHEFRASPLFWRVKGMLPHMY
5789	19690	A	5835	278	404	SVLIFKFKTKYKATWFGVAFRCNFS TLQGRSGITTSQSG
5790	19691	A	5836	417	3	SKGEGKRCWGYDLPSTGTHVQPPPLKQ QGRVPGLTQAVQVAMSLIDLAGSERAS STHAKGERLREGQNTINSLALINVLMA LADAKGRKTHVPPRDSKLTRLLKCSLGG NCRVTMLAIAISPSMNTEDTYSTHV
5791	19692	A	5837	409	230	AGRAYCYNGMCLTYQEGCQQLKSGAL LGSTALPSFPLPSQPLALRVNMLGFK WHL
5792	19693	A	5838	3	409	LRSVFCKDYLQMHVITSPLSSTEEQAFP LAYVMVIRKDFU- FERLFRALYNQPNVY CVHVDEKAPAEYKESVRQLSCFQNAFI ASEKTESVVYAGISRLQALNCLCLIVAS EVPKRYVINTCGQDFPLTTTREV
5793	19694	A	5839	385	174	GLAVEIGSKRIADGELLEASSDPPTSA SQSAGSTGVSHAMPDTVSSVYVCFLLCC TKGVVVGALSIVSL
5794	19695	A	5840	260	2	PLPRYTLACSKLLVQYDAARQVQSSSEI SSIDRCKRKFLLDCLAMERKEEDRPIT IKDDKQMLNRCIADVVSFIITVNDKRLQ CI
5795	19696	A	5842	299	3	FSQIKYICITPLPVCVPLVILGICSPVV AQAGLTLTGSSDPPPSAQSPQIIQVSH YVQPLHTVAQLSPSSIFRTFSFQTETV PIKHTSHSPSPSLY
5796	19697	A	5843	391	2	APHAPAPFLRARGEPQDPLSHRPVPAVSA NCRMWKLVPVHSPPTPTPLWKLQARW LLPQLVYLQGWGSYLLRPPALISVLL AREFLYPKMSVSEVCSGLSFFLLBQH KTNLIFYASGDICSAW
5797	19698	A	5844	479	59	FVCMGPQVGRASLAKRLHRSIGRTKL RKRKCTLFNFTQEKSAKRKHGELGENIY LLLFAIALRLNCLIVQTSFVPDEYQGS LEVSHEMVFNPGYLPNEMTERLSYAYP LICASIYKVLHLIGKGSVQMLVSGNKS SVQTKPFETESHPTQAGVQWNLCSL QPLPCRSKQLCLRLSSW
5799	19700	A	5846	2	394	TLCHRAKDPVHHESGRKINYLNCLPLM GPALQTRLSSRQSC
5800	19701	A	5847	472	201	LSITLSDTSLCTGRFFTYENGCAFFHEE

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 59/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						REGLARLCRLSHSYEDFVVDGFNVLY NKKPVYTRSAFARGLQSLCNQVMWYQ VATLKK
5801	19702	A	5848	127	3	SSNVKAAMKQVGAHAGEYGAERALEMPL SFPTTKTYVPRCI
5802	19703	A	5849	238	1	MAETHPNPTGLFLAFLPCLAGSATHFC LFSPEISLDVDADRDGVKEKNPKVPS FQGRHUVFPRASEDTAPDAGMY
5803	19704	A	5850	423	2	LSPLGNSSANQKVVDTSVKFSKCLRA VDYQVGVTPVSLTAGHQFGDGKGRAGE QATQAGDWSNNMGSDGILSHSAPLTV PQPLLTGPQGFCLCRPLPNQQTSPFALL PFSTQLCSMCPGPASARPPPLLLKPTMY
5804	19705	A	5851	326	682	PSYSLSLTLQVKNSEVKLPRQKRESMK QKMEHTQKQLLVSPWPLGSAGAGAR PGMVTRPPLCLCPTPAQIPRSEYLNLA SSFMAPLSPPPPCSLHRLSLHLEVRNSI SGYPNCI
5805	19706	A	5852	263	30	HEKTDDERGPGQSAASGAITKPPGPPLP IEPHETTEHPAFSOTTEPFLPVELHE TTPQRPVPGTILFEPILLQ
5806	19707	A	5853	389	2	GLPTQREKRLSHMTPTTQSLAVVTSF VCLVGBGNVQGFRAESRCHRYDPRNR WFQTSGLQGERADLSVCVVGRIYAVAG RGYHNDLNAVVERYDPATNSWAYVAPLKR RCHPTKAKRWGRCLSP
5807	19708	A	5854	379	2	GRSLRYSGSCSGEENSTNNSAQGSRAVI AAJARRRGNSHNEYEBAEHERVRKR RARLVVAVERAFTHLKRQEESQKNPRE VMDPREAQAIFASMARAMQKYLRAAKQ QNYNTMESILQHC
5808	19709	A	5855	374	2	SDAGAPVNIYEFRRHRPQCLDTPKPAVK ADHADEVRFVPGAFLKGDIVMPEGATE EKKLSRRQMKYWAIFARAGNPNGDLS LWPAYNLTQYLQLDLARMSLQQRKCEPR VEIWNSTIPPCI
5809	19710	A	5856	516	18	PYECKECKAFNGSGSLVCHERLHTGCK PYECKECKAFPSGCHRTQKHLRGEBT PIKCKECKAFNGSSSLVCHERHTNEK SYECKECKAFPSGQSLSVHQRFTHTGCK LYQRKRFKGTPTHGSKLVHERTHSNOKP YKNEKCEAFMTWTSNEKCIASAK
5810	19711	A	5857	392	3	CERGWGSGPRALGRWISFLKRLRNLCSV PGDSTFYFDVLQALTGPVNLHGSGALFG VFTTQTNISIPGSAVCAFYLDIERGFEG KFKQRSLDGAWTPVEDRVPSPRPGSC AGVGGAAKFTSSRDLLY
5811	19712	A	5858	391	3	ARKTTGMVPRAGGCKRRGSAVFSTYIRE IEELRSKLVSRAMNBSLRSLSRASDR SPYSLGASPRAPAFGSGPASSMEDASEV IRRAKQDLERLKKKEVRORRKSPPKEAF KKRAKLQQENSBEITNGE
5812	19713	A	5859	409	3	SLPGEBDFWAGQBEILLVQEGKLSLFP ASRVLRLACRYDPRNSWSAETAPMKNK REHVLGAMERYLYAVGGBSLRQLVPT VERVCPKKNWTFQSPFRSLSCHGTYV ADGLLISGGVINTAQYQNRQCI
5813	19714	A	5860	405	135	NLSRLSLCRQPMTLVTVWLLFYDSREKA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion
						FWLLVALAKRMLPDYYNTRVVGECPRVL PRLGLQVPAGSMRVAALPRPPSSRLHVGS IAGVRG
5814	19715	A	5861	389	2	YVSELSEBQLTDFPNALANVPLKRLDLI FVTFQDSRMVAKVRKDYKVGQGVQVQ SSVTTIVKSYWVTVMAHPKDIIWHL SVRRFPWMAFIAINTFLFLFFFLITP AIIIMTIDMYNVTBPCI
5815	19716	A	5862	525	0	SHLPESERIHHTVQKEQVLMDTSKTRP NNDVPEPMPPIADQVSNDRPEGSGVED EKKESSLPKSFKKKISVSVTKGVPA DTEGGQPKGRKRWGASTATTQKKPSIS TTSELKSLIPDILKPLAGQEAVIDLHAD SRISEDETESKGGDGTICKGLTIC
5816	19717	A	5863	399	2	ATRRNRNRVPSGNTTRTVRRHTAAVGP PSPYPLPPPEGTSSIEYSNQNTCQGH GNFDFPHNPGGTSMNDRHGGPPQLSHP PDMPNMAALEKPISSHPOETMPHAGSS DQPHPSMQQDKARNTPQWY
5817	19718	A	5864	3	714	RRPFIALCLSNVAFILPWQFAQFILFTQ IASLFPWIVVGVYIEPSKFKLIYMMIS VTLDFLAFQSWHLASQVSGSLMLTWA IILKRNELQKLGSKLNCWILQGSAMWC GTIILKFLTKSLGVSDHICLSDLLIAG ILRYTDFDTLKVTCSPEDFMEKATLLI YTKTLLPVVMVITCFIFKKTGVDISRV LATNVYLRKQLHSELAFTILQLLAFT ALAILRLKLVL
5818	19719	A	5865	423	1	APPVSTAQAQNSSEBAREVGSQAQEF KYQSLPFRFORQQQQQQQLYKMQHW QVYVPPSPHPORTFYPHHPQLGDFPRN MMPSYMDPRIPTRTPTVDYFYSALHPS GLMKPMQDSESLNGTGRSEDQNVPPC I
5819	19720	A	5866	497	2	AVGAGQGRGGRGGGRELMPFKIRGGGA FNNHNVGPLKIMPRILIRTMLEETHE KVVQGLPFCVPELSIDINTKLSQLLER RQALCPGSTRFVIRLGLLISQFSG HSAEQCKTYSFCSRHGKALKLYLY ARDKRPOQFIRKVCYCRCHGSGOQR
5820	19721	A	5867	382	74	LALSRLKSCGQITAKCSFDLLGSSDFP PSASRVAOTTGARHARIYSLRIYHIV LRLFNPSKIKSLKHFHILIRNPKGVGS YSFQMSDLLQSRRAQQS
5821	19722	A	5869	378	3	SFSRSANLISHQRIHTGKFPQCECGK SFSRSANLISHQRIHTGKFPQCECGK SFGNRSNLTHQRIHTGKFPQCECGE SFSYNSNLIRHQRIHTGKFPQCECGQ RFSQSSALITPV
5822	19723	A	5870	375	3	IIHIVFNOATGHVMAKRVFDTYSYPHE AMVLFNLMVAPGRVLICTVKDGGFHLK DTAKALLRSLSQAGPALGWRDTWAFVG RKGEACHWADTEINRRRRRRCFCSKVEY GSCVCKDKPTV
5823	19724	A	5871	373	1	QREVSAGLSPPPSASATVKVLVLGLINC VSLACRAIISLMLVKSEALHSPYVFL DLCTADGIRSAVCFFVFLASVHGSWT FSAISCKIVAFMAVLCFZHAAMFLCIS



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5824	19725	A	5872	382	2	VTRNNALAHLY KSFQKSLTILHLRTHTGEPFPCBCG KAFREKSTVILHYRTHTGEKPYECNCG KAFQKSNLIVSQKTHTGKTYBCAKCG ESFIQKLDLIIHSHSTHTKKPFCNCG KTFSDKSLTIIPIV
5825	19726	A	5873	370	3	NGRVEAQNTSGVMSGPGKRLMQSQFPTQ GQQGFCEGKPEYQAMQNMNTQDMFSP DQSSMTMSNVGATRLSHMPLFPASNPPG TVHSAPNRLGLRRSDLTISLNQMSPG IGHLNTTICI
5826	19727	A	5874	362	2	GGKFINLGNLPSKLEESMVQYYRLVTAA SLVRGQISEYNISIRASDGGSPPISTET HITLHVIGINDNPTTFFHLSYACIPEN NPRGASIPVTAQDPDSNNNARITYALT EDTLQGVY
5827	19728	A	5875	369	1	RIRPRPTARLASARTLHEVSLQESIRYA PGDAVEKNLNDLCLCLNLIARIVSVCP LPEACDLGYVNRDTLFWCHKASEVFLR LMALYVASEFENSNDLQMSDAPARHL LAKLCLCPV
5828	19729	A	5876	119	39	VTDYTFPPNELLGRLDLKLPYR
5829	19730	A	5877	461	2	RKGWTSRKKPKEDPSGNAVPEPKKSGK IAGETPKGGKLSAKKEPAPSHSGIPLK PGMKMPGKSPAPAPSKBEGERSRSGKL SSGLPQQKQLQDGRSSSSSLASSEK GPGGTTLNHSLSSQTVSGSVGTQTGTGS NANSVQLPOLCI
5830	19731	A	5878	503	3	PSQVPGCEPSPKRLGARAFTTPDPAP LS PQSRVASSGSEQTESQGSSRNSFOED GSGMKDPSNLKSLRLHLKALFQMSY ERMVTLTEQHLESQNVTKGARKHKLISI OKLPERQSVLESLKEDVLEGGNLRNALQ ETLQIIITPIHAYSVLQATVAATLY
5831	19732	A	5879	421	34	LVHKLVSASNVLDAGTVKTDYSISK PLADICKEDVFQTRVRFSVNAMHYRTG NRGDVNRLLGLMLLSLQQQCEAEYPVAI PGLPGGPDPLKCKVCDDKKSMRSPA VVFQKNSPANIPL
5832	19733	A	5880	379	3	AQQLLWNPALNQHPCSCSHLSFTFI QHWKSGLSLKTAPAGQGSVLSSDLPR AVLTGTFAVMSVGVSTESLAPQALNG SMINETARDARVQVASTLSVLVGLFQV WNSQEVVPPTICI
5833	19734	A	5881	429	1	SLVSYMDTESTAEKLGKLGKLAQKLSA VHSSHHEIGVNDNSNLSLEMRPLESSN TKSFHSAVRINKRSQHELCFQHHGIDT PTSLQKRSACPPSLRLBETASSQDG DPQTDWDLPFSSSLNKPLTVLPSEIATV QCI
5834	19735	A	5882	436	3	WSLVSYMDKSKTAETKLEKLGKLAQKLS AVHSSHHEIGVNDNSNLSLEMRPLESSN NAKSFHSAVRINKRSQHELCFQHHGIDT TPTSLQKRSACPPSLRLBETASSQDG GDPQMDLDPFSSSLKFKTVLSESEIATV TQCI
5835	19736	A	5883	195	353	DSYSYVSTAPAVAYDSKQTYQPTATA ANVAAAPQPSVAETTYQGGFS

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5836	19737	A	5884	432	1	LSARVVPVAVSDQAAAMHTSQCPKNIAT SLABLRITASQKAHLQCPMBIDSAINTV QTAJNHLQDAINAAVBSQLKPLPGSTLE KCAQDLGSTSKAVGSSMAQLLTCAAQEN EHYTGVAARETAQALKTLAQAARGVAAS TTDP
5837	19738	A	5885	313	1	GKSPHLLILQTSPLSKAPQLILLLLYW SKVGVSIVTASARETEAGIQVSSSEPP RNVSIMSRQLQETNIRISAEINLAAYRQ VREVOGRDRBRKOLMATLY
5838	19739	A	5886	432	3	GGFCSFSLICLWVVEAVGIRLHMLIR ELGCMHSSPLPGTYSLSPLSTCTQVLPY SMGGLLFPASGNLYSLYLVPSSRAZTDSRG SQPLVARGHVGACKCKPQTRPGLSPQ VCVEKLMPSSFCSAFQNTTNKQFMSR PV
5839	19740	A	5887	417	2	ASLMVADPYARTSLAMDASSGVCTP IMSTSSSEAMSTPLMLAPDSGELSPLIM ODMNPVGMSTQVPVPAPEAMSPLOITD EDTEAMSKVMTALASGESSLLMSGTD SEATSSLSMAVASGGTSPQPTSTLY
5840	19741	A	5888	420	3	KFDLTKGLGLKIMSSYDLDEASDGGGL SGKCSVSVKVLDMNPNFELSLSLITSP LPESSPEVETVALPRIRRDSSGNGNMC SLQDVLKLPSPVESIRLVTEGALDR ETRAEYNHTTTTDMGTPLKTEQSV
5841	19742	A	5889	321	414	FNMTWPGQAHAKCNFSLGGRGRYTR SAD
5842	19743	A	5890	415	1	PGLPOTSVKGTIPASKQSDHESPTTLHLK TSPIIQGLGLYSHTAIRYHPQRTLKRF VQLVCPDAGQQAQGVFLNPNMGSSCDKV HNFFLPITPMLPPPPPPPPMARPVLPVFD TKPPTTSTEGGADYPTSPYSTPSLY
5843	19744	A	5891	193	3	KPSSKVNRRDPFLSSVEQFVKDAVIT VPVFFNQARRAVLQARMAGLKKMQLI NDNTACT
5844	19745	A	5892	412	2	KHQSVDNRDSFYVSLYDPDSSLRSRATLD VVQFFPKNTVTVVYDSDAGLIRLQELIK APSRYNLRLLKIRQLPVDTKDAKPLKEM KRKKEPHIVPDCSHMAAGILKQALAMG MMTEYYHYITFTLDLFDLVEPSV
5845	19746	A	5893	413	3	ELLCSNTSCRCFCVCELEVLVGITGTA AAKALQSPMCTCLKPCRGVLRKRD WNRRLQAFPTSDVGLVFAKVLPA ARRRPVRLSLPDGIATGYLVKSLGIK VGKVVASVCEKESLANGTVKHEWR
5846	19747	A	5894	424	3	CSGRREPSVRGVQCKGDGHHGARMAPS RAPGTBSCTPSHGQNTAARATPAQKTPA KVVYVSTEMANKAKAVLKGQVETMVS PHICNTSSSKTERSTAPLNTQISALRND PKPLPQQPPAPASQDQNSQNTLRQPCI
5847	19748	A	5895	400	1	ASVQNPALRLVTRREEPALMQTPAGELYD KGIQSAQQDSIKKANMKENKAYSFKS QIIRLRLKEVSTRHLKVAARLGLGLKL VAFPTAHMLFTWNILRPMAHSSDAPDQC LVHNHTFSPPLHSPFHQLY
5848	19749	A	5896	421	3	VSSIQMGAVNLLGGGLDGLGSDLGGGY AGSPAVGQSFISSVQATCAPSPPTPAVV

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						SSGLNDLSELSTWIGNAGGYVAPKAVW LPAVKAGLSSGTFTTRQGHITYAMDF TNKALQHMDSAIQFTKNSFGVIPSCIT
5849	19750	A	5897	384	1	PRASRFIHEAGIVFLPMRHTHTPKKFTFC EVAGVQFSENVVKLIHRRKHTGERPFYSR QSCSVFPHSYDLAKNHEHATGDRPFYC HLCHAFKEDHLQRLKGGQICLEVVRTR RRRKDDAPPHYPPPCI
5850	19751	A	5898	429	2	QDLAAQSLTQVLTPESHKRNKANTPEPQ KQERYKGIYVKEKLYRARHDESLNWT SCDHYESQCKGCGDGRHPNCGKLNLMK STVQHVVVHVLPQPTCNNGVAFADD TDFRAHPSTHLGKESYKCDQYCKILSQS LY
5851	19752	A	5899	424	1	GTMLQALAAHDAGSRAHVLSLQQDGI EQHMDFDSRYTLLELFASTSSSEHCHMA FEGIHLFPQIPGKLLFSLVKRYLCVTSLL DQLNSPELGAQDQSSPCATREKSRGR ELEFSMAVGNLISELVRSMGVANLSEH V
5852	19753	A	5900	135	459	YFMLEAEHVVISYVCSENLMVVVNRKFC LIGLIHIQEFYFFFMPEHRAIQAGVQVC DLACLQPPPPGLKRCCLIPSSSSRDYRC APPVP
5853	19754	A	5901	418	10	GRSPKQDRLWSESVHLSFPQADLSGG SAPASSYEPQSQRSSPSSNRQSGSTSTR NSSQKGSVLSIKQKGRKELYMEKLQEH LIKAKFTIKKKFSQNLVAVQIYVFKCV YFGLSAYQLPRGYPTRVLGNFLTK
5854	19755	A	5902	402	2	GYRHPSELSEKSDGFGQEPKQPVTLSLV RSNRKGEVGFPPEDRRINVDVTRARRLV TVICDVRTVSSHAFKPLVBYFTQHGSEV RTAFEYLDIVPDNYSHEDSQSSQAAT RPQGGPTSTRTEKQREGMY
5855	19756	A	5903	346	1	GICPLSHIKMTDARQIYENKGGKSPK DTGKEPGHSEAKTGPPQVLGAVPAQPEA PQPGPNTAAPVDGSPKAGLAPETTETP AGASETAQATDLSLSPGSEKANCSPED PMY
5856	19757	A	5904	139	212	EVLENDDISHHHHHHHHHHSNKS
5857	19758	A	5905	2	345	PCGCGWRCALLLSAAVAKSKSGPTPL PCSGHICIGRFSKGRGICDQSDDEE NCTANMLCSTARVYCKGKCLCDKSEYIC DQGNQCNDSDEESSCSQGVGVCGFK KA
5858	19759	A	5906	432	17	PQTTPHRTFGGGAJAVLLAVGGQFLLC WSPYFPHLVVALSAQPISTGQVESVVT WIGYFCFTSNPPFFYGLNRIQRLGSKO FVCFKDAPEEELRLPSREGSIEENFLQ FLQGTCPCPYKSVWSRPLPCIAAALRV
5859	19760	A	5907	407	1	PYACGECGKSYRQSSSIVSHRRIHSGVR PHHCECGEFPFSKYDILIHQRVHSGER PYKCSRCGKSFHSCLTAHQRIHTGMR PYBCSECGISFIHSCLITQQRVHLGTR PYMCSECGKSFQSCRLIKHRSV
5860	19761	A	5908	419	3	VLAKKTIITKSARDCHFGNLIHLSTNL VASIQRPDKHSIFGNHVDNLDLFSRSS AKNYDNGCAKLFHFTYETKINPMGKPY

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						GYKECCGKLRKKKGLSLHQRIKNGEKPF ECTACRKTFSKKSHLIVHWRTYGVY
5861	19762	A	5909	441	57	KVMGIKSSSLFQQLVDITQEFYEVTLINS QKSCBQKIREANQVLQKQKRTSLAPCH DRIQSSSELQSLIQHSSLETTDGPQPW LFPKSSGHRKKTVDKCHSIGLQIAVDQ RKLHLVLSKKIKIRV
5862	19763	A	5910	3	317	CLLMLRRWRSSKSGKQRRLQATPSSWEST KTADQGGDRDSGSRHCSSPHPQSKST TTSSVPAARSGAQEAQCGPRKQTSRP QVSTRQCAAPPARHKLENDA
5863	19764	A	5911	183	1	QNSDSKDSLNRVASRDHAKPNLTCHVSP AIQTGTSISESSIPSVSDTSTPRRSRQ LPPCI
5864	19765	A	5912	395	1	KTIQFNICVKVPFHRFSNSNKDKIRYAGD KTFCKECCGKS FHVLSRLTQHKRIHIGE NPYTCEEQGFANWSSILTKHKRIHARE KPYKCEECCGKPTRSSHLTKHKRIHIGE KPYICECCGKGFANWSSSTPV
5865	19766	A	5913	449	2	FGSHLEKDEKQBELVDRAIKPSTEATL BSIQRLQYKRAESSRPEDIKMTKAQI ANRKAVALQKALLYESIHRPVTIKNERQ VMKLVDRYLRVQILSRANTPIIEEE EGSEASNVKDFPMVKNKTDPSAMVWR PLGSSARDP
5866	19767	A	5914	464	23	SAH/TETRSKSPDYSLSLNGPSAPAPV APPARVAPPERRKCFVLQASLSRPPET ELEAVPKGRQSESEPQSSSKPSAKSSL SQISSAATSHGGPFGKGGQQRDPILGP TVPYTEALPVFHHFPAQTHHKEKPYLPP LYCGROG
5867	19768	A	5915	366	1	LVSFINPFTSVLATLVVEAVLGFKANIM NEKCVVENAEKILGYLNTNVLSRDLPP EVMFNSHLTTKDYMEYNVINTVKEDQFS ALGLDPCLLDELDKSVQGTGLAFIAPN EAMTHSPACI
5868	19769	A	5916	246	366	TSVKQQMPGAVAHACNPSTLEGQGGRI TRSGVRDQFCQH
5869	19770	A	5917	400	3	NDNAPEFYQSVYKVTYLERAFNGTLVIK LDATDPODGTNGD IVYSFRFPVIEAVVY APTINPWGELTKKGLDPEKKLYEIS VKAWDKGNLFWGHCITLVLEVLDVNDNA PEVITITSLSLPREDTQPCI
5870	19771	A	5918	410	200	CTFIPQVVKCRFLNDRVSSCCPGNSQTP GIKSSYLSLPEKNDLRPVILLPCPLSH ISSKQPYFLPFSYR
5871	19772	A	5919	214	407	MYFYIDRASLSPRLKCTVVTIAHCSLE LLCSRDLPASASQSAQITGIRHHIWLKT HFYSSFKT
5872	19773	A	5920	476	39	VFYGLFVGSTGRIGLPLTREGTSHPLRG LHAAALNGRIAVPLTRNKEGCAEFS ANDDVALFCGSHSLAALPAWGTQDEGT LEFTLTQSQAAPLAPQAGWHGDFTHV DTPEGHNSMVRKGGQTULLNSVPVTD AQPHM
5873	19774	A	5921	430	2	SLRPSSTGSPSGGLSEEPAAKDLNRM PLGVCQEVSGSGPHTSSPLFNKAVPLR PSSSTMILFRTKSGPAIGKAVSGARE

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5887	19788	A	5936	410	126	FGGLCTDTKRKLPEWPFSCI PICYKKGGRARWLTVPVIPSWDYRKHQA QLI FVFI/VETGPHRVAAQSPELMTSGDP LAYNFLCSYPNEVFRSQAASDLQFVLR NLEPPDAGNV
5888	19789	A	5937	426	1	DATPHBTDIEAQDQEGGLTRAKVITVTVL DVNDNAPEFYMTSATSSVSEDSLPQTII GLPNVHRDSQNAFTTCSLPEDLPFKL EKSVDNYRLVTIRALLREQFSFINITL TAKDGNFSLSTDAHLLQVADINDNAP CT
5889	19790	A	5938	438	3	ADPTKGLHLKNGSVCVRAPGVSGQNSVN LKNKQKQALPSGGITPSLNDGTTPSPKQV SKESKABQAESKRVP/LPEGCPGGAASDL QSKHLPTAKPASQEHVRCSAITGTESE KESAQLSGASTPKESPSRGPAPPGENKVV SPVV
5890	19791	A	5939	3	191	YSVCMRSLKRLRQEDRTSGGGGSCTE PVVNTLRISNKKTKKREKQGGHSHN WYCNLK
5891	19792	A	5940	399	1	QYSDNDMSWKVTRAAAECLDAVVSTRH EMLPPEYTKTSPALITRPFKERENVDKQ VCHAHSLPKQTSFVQSWLGLDAMDQD GTP/LAMLQSQVANI/VKAVHKMKESVK TQCCFTLLTL/VNVLGAVY
5892	19793	A	5941	411	3	SPCEGPRFQCKSGKRGKVCVQQRD CRDWSDELLKVCWGAQCIPLAGLSILPS PSWYLGSRPSAPCDPTFCQPLRGFWC RPMASHAFRPPQASGLHLKVLNACPSQ VLKNYVPSHKLGLSSFLPRSDEH
5893	19794	A	5943	431	26	KAVVGIPGDMGPFGLTVRFGDGLGPNP GVQGQKEPGVGLGLKGLPLGLPGS PEEKSGIVPGVPGHGAIGPPGQGITR GEPGPPGLPGSVGSFGVPGIGPPGARGP FVGQGPGLSGPLVIKGEVSRVR
5894	19795	A	5944	396	3	PLPVELIRVFAPLIDFWGSLFPRGARIS ODLKHYIHLIAYASVETCKKNKRVRS INKDELKSTSKAVETVBNLCNENKAS ELVAELSTLYQCIRFPVAVGLKVDVN TVSEPRYQLQIDHTPTV
5895	19796	A	5945	465	32	ERVTLADITVVCTLLIMYKQVLEPSFRQ AFPNINRWFLTCINQGPRAVLGEVKLC EKMQPDAKPAETOPKDT/PRKKGSR EEKQKQFABKBEKKAAAPAEEMDSC EQAKAAEPKADPPAHMKSTFVLDDCI AAAL
5896	19797	A	5946	414	2	ATF/PVCRTRKEIRNNYVDIQPVQEPFAQ ACGNHGIIIIITASTSTGCI/PAGSSLGR GVNDKVALEAEMLLNLRHGGTVVEY KQDQIVFMALANGVSIKTKGPVTLHTQ TAILYDEQIVKNCKENSHVDEQVY
5897	19798	A	5947	411	1	EPCVVRRIASVSQTDEDDGESRYLLSR RRRARSADCSVQTDDELSAEWEQPVRR RRSRLPRHSDSGSKGDEATASSSSAA TVRMSSVGIQTTSDCSVQTEPDQI/PRV SPAIIHTAATDPKVI/VRYISAPCI
5898	19799	A	5948	153	409	LPFFPILLPFPSPRYVGLSPKLCGS GVI/IAHCSLELLGSSNPPTASRVFLY

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						LSLCLPVFFEMESCSVAQAGSQNRDLGSLQ
5899	19800	A	5949	21	447	RAAAMSSRNFRFLSSHRELYFGVDLFSGNLVVEEPADREQLCRAKACVLTVDLVL EDPLELHKIRIHVLDTNMNSPLFPAGDV QLHIFPEFLTGPARTFLPNAQDDGSGNG ILSYLSPSQHFRFLDMGSRVDGSEYPEL VL
5900	19801	A	5950	268	19	QDNWYYCVPPEYCKTKLTLAMFLAVN YLSQDFYFFPIFFLDGVSICHPGSAVA RSQFLTATSSSCVOGQRPSCLSHCIAARL
5901	19802	A	5951	389	3	QQMDLARGQGTAKTQQQLLQTHCKEN LLQQQLQVQGGIMPPLMIPIFFHIDRDLA ANAVVQQGFLFPFGITYTKPGDNYPVQFI PSTMAAAASGLSLPLQLQLYAAQLASH QVSPGAKMPSTPQPMY
5902	19803	A	5952	2308	307	RRRPARKKTVWRDGGPHQGL/YPLPLSA VTQ/PTQPGHGPRALGKRELESWGRRP GK/GQTHRRKTRGTASPAVYFSVWGD/ SGGCPMTGKGAKQORAGLGAAFPNLESG EQGTGRGAQDSQGHGGKGRRGQHPPG ND/PRGVSQMGSVSHPEARPTGGTGT /ENLORTWRHQQLVGOTGNLLETGSWS GSGSWRGVVLSPQSGVTTQMGSLAGR/ YGPARRAVELSPAGQGLRGRGWSGE PQETESGVKGG*GSMPLSHGGEQ/PRA AGQKQSLQMLPGGPPCMS/SGMGGPQO LLESEGAGSPGGGGRHKGGRVAVTTTP REGD/RGQSPGGHTLQLFPCLMS*RTQ GQGSRTVQHQEWGEGREGEAGSDQSR ALGIA*ICPHTLRPTSMPEQSTAPAFGQ PPGPPSWGHRGHQGMVGGRCPPG/IQG RGRAQLGSTVG*RDG/QRG*MQGRDQGG PRSNAGVGVSCSHTSK*IPSSSLCT*N SSHGPAAG/QLMWSSPFIHSPGETNTPH TLTEPHSVPGWCMDTLRRHGAGQGHPGM ARSGTGBGQ/QRGRY*ERGREGRGQKQ KKQLKEPG*RAAPTLEKATRLPLRCCLR KVQKPKQGDVGS*LLKVFAPGALGK PQRTCRGADFFHALGSLNSVHVSCT NSGFGACM
5903	19804	A	5953	461	117	HRDITGPTAQGLPSPSPFPKQKQAPT TPSS\H*P*TNRHDTGLSGPVQVPGADW KPLINAP*LPELARGEPKCRDQVDPDPYV WLPSAPLHCVTWATSPQLSDLLSYPRR KQA
5904	19805	A	5954	845	610	PFETGSY/SVAQVGAQMCNFGSLQSQPP RLKRSCHLSPSSSDYRGAPPLARFFF FCIFYRNGVSPCCPMS*TPELQ
5905	19806	A	5955	1	378	KTPVSDR\ATKCCSESLGNRRPCPSALE AYETYVPKRFNARTFTLEADICTLSDE RQINKHTALASLVKHKPKARQEQKKAUM DDFADPVEKRCMADDKTCFVEEG*TLV AASQAALGLLHRIK*
5906	19807	A	5956	723	343	GQCEGICPSFCPIVTPATREAEAGESLEL RRRLH*ASITVLPHS\KQQRSLCSDFI RLILVIFSGMFLVFTLMGALFLHRRKCYR SNKGESPVREASPCCRSCPREEGSTIP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
5907	19808	A	5957	55	491	IOEDYRKPEFACSP AQRPNHNNWPT*LLPHFTNEGGQVTEA RCLKNQAR\CLVPMQKVENAMPGT**PS AEVTPPVCNQHWPQVBGIPSS/APAFQ WPLTMGHPC\WESAPRODASTSPRPGTA SHCPSAVAFQERGS SPCTPHSDSGLCL LPDLLEAP
5908	19809	A	5958	2	413	KKPDQ\AE\REHLCTSTAWSGRNTDNG EELHGGKRVMERLKAVKIANQCNDPSL OMQLVTEILNRYLYFYEREYDAGTIOVL NOLIQIKRIEDLPNLESSIEFEQIT*HFH NTLEHLRLGRESFESBQIYEGLLLYE
5909	19810	A	5959	871	564	WNCHATFGSHLN*ANRLRPVNSG/LLM/ PSBGKAKKESTLMVGVINPD\MKKGKRL LLHSDGKDEYVWNAHGPILG\HPLTLQ CPITIKIKKKL**PKSGRTADGPDHSRIK V*VTFLGKEPTTDEVLASGKENNE*VTE TC*IDMN*VLOGQTWNLQR
5910	19811	A	5960	390	271	GINFPSRN\SLTIT*SRLV*NSWAQVIV LPWTSRVLGFQA
5911	19812	A	5961	333	922	GLSCRVRFGRTLSCPPCPIRLHSEVETIQ TLQKKGIEDLYSRLGKQPPPGIGAPAA LTSQRRLSKGSFPTSRRLSLQSEFPFG PDIMRRLSLSGSSITSGQRLAKSGVTEA GDVGRM\IQNRSHVSPFHGQFPWLSLCSO NMLSLDOON*ARKIPTLG*KA\GGHGE CSSIIVKSQTYVNCCLCGVSSAAYHLH L
5912	19813	A	5962	705	387	CVAQTGVQ*HDLGSLQPLPFGFKQSHL SLPSSNDYRRVTRLPNF)*FFVTDFC HIAQAVLQL\SSNNLEPASQSAQVVG VSHRARPRTLIDIQABIFDLKPSG
5913	19814	A	5963	425	182	ASNG*DSVGQVGFSEFGAGYVNLVFLKC \LEHGSSWVGVTQFSRCHLSPLSTRKG NSLTPTCSRVRQCLALLMLTHGSRTH
5914	19815	A	5964	388	14	PPMYTQLCSIRSTQACPCVFFSRDE/SL ALLPRVLNSWVQAILLWPPKYVG*QA QWLTIVIPALWEAMAGGLLEPRSSRPAN ATTQDLSTKENKTKSLGASDAELCVH WRLLKI
5915	19816	A	5965	1	373	DQGVKGVINLLLAAYTQDVSALRRFAL SMWDSQADYDSRTALNVSQAQVIEV KPL\LSACKWHPFKDRWNTTWDETH FGHHDFVKILQEQYQVYTP*GDSNGKE HHTVKNLDGLS
5916	19817	A	5966	3	329	HEETSRYEYIELIHYHVPYAVKQSFDER YSLSQSTLEQVGH*GFVSSMVVYKTF PGSCRGSTALFSSLYFLDPPQVFLSLK EQELGDFF/EDFDPVKWKLPOEEP
5917	19818	A	5967	2	47	MEDRLVRGIPCPQHNARQCPAVPGIQ AYGAAPFEDLQVDFTRMSKCRGNKYLLV LGRTYSG*VEAYPTRTEKAREVTRVLLR DLLPRFELPLRIGSDNRPAFADLVQKA AKILRITWKLHAAYNQSSGKVERMNQ IKNSLGKVCQETGLKNIQALPMVLFKIR CITTSKRAGYSPYEILYHRPPPLILGLPG TP*ELGRIETLQRLQALGKLTQ:1/YS SKWVSLSPSVHLSRGDRVWIKWNV



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						SLCPANKGPQTVVLSPPPTAVKVE*IPSWIHSHVKP*TA
5918	19819	A	5968	2	150	KQGT*QSSLLSYFEKLQPPQPSA/TS TSKQDPPLATRLWLARGSDDH
5919	19820	A	5969	3	371	HEGKSGPWITGVVLVAGVGVAMKILLCLL CLILLRVRSRCRRKAARALQNEAALAVT D*SPDSRLLPAPHPVPQSRAPCLC RLCMVCLLDSPPSPFFCHPTSPQTLAA KDSAAADTLHV
5920	19821	A	5970	396	58	YKVLGKGPVTGMLNVSFSAASSCLSF LINS*AP*PGIFLGNVFTLPPTFVVGQ AGLELLTSGDLPSASQ/ARITGVSHCA QPHALTSQYLEQCLAPSRLISVSLILR
5921	19822	A	5971	442	120	ICMKGLALSPRLDSSASNTVQWMP RFKSSYGLSLP/RSDYRCPTPEMARSG NGV*P/PMVETGSW*AAQGLELLSSN LPP/SAFQAGITSGHCTRPVFLVC
5922	19823	A	5972	459	434	MWLPWFSTISPSPPPT*VSSNNHPCA VPRAYPGADIPGPGWQRLPPPIRLGSGP PBSCLLTTILCSKHPGNCPLTQNPRLSP GPRPCLYSTPSPPP*AQL/YAAPSP*L YTVVRKALIR
5923	19824	A	5973	681	1758	VANKQIPDIAKATYICINPKEKRSYLK T*MLHRE*IKKQIIEFNIGSHLAPNM GSDPPTFQEDIDALATFSGCLPEKR ARPMVHGHDEIIPPRORAIQWGEDGRPH YLFYTGKQSYISLHSDVYGMILLNLBKHQ SELQAKSLLEPKTVTRDVIGSRMLIKE LEEMLVKLSLDLYMQFIRLLEKILLTSQ CGAAEEEPVQRPFRSVTLESKQKQLEPV QYDEQGMAFSKSEGRKRTAKAEIVYKH GSGRIKXNGIDYQLYFPTQDREQLMFP FHFVDRLGKHDTVCTVSGGGRSAQAGAI RIAMAKALCSFVTEDEVWMKQAGLLT DPRVREKPKQGEARRKFTWKCR
5924	19825	A	5974	1232	980	SLSLSPRLCSGVTAHCSLRLPASSNSC FSASQVAGTIGACHHVLVVFLEVTG/ HHVGTGLELLT*/VICPPWPKVLQQLQ A
5925	19826	A	5975	1	259	LTSYDYKRALPCLVNFVYVFLKREELA LLPKLFWNGA*ATLLP*BPKIPLQAAQ VAMLRLLKFPACLPACLPAYLPPLPSFI PP
5926	19827	A	5976	24	223	PVLQTISTNESSVSHARAEFLDQNLQ /MLGTVTYTCNPS/TLG*GGRIT*QGE FKTSIGNTARPC
5927	19828	A	5977	395	136	GSWDYTHVPEASANF/LVETGPRVIA* AGLELLGNPTTSASQAKITAMSHCTWPS SXY*CHYNARFGSLHKRSGMTIYKSYK RQN
5928	19829	A	5978	1	785	GTRLKSGINTKALQAVYSNMSNPDDVP PBGWNRTRHVIILMTD/GSBGTSLLSQ PHILRPACGP*VHL*HYTHGWGPRCDS* LAVHLSCDPS*GILPKPCDQLSLTLPQ AHPAMCIPAFSQFIFLISYPHGPVSSAG LHNMGGDPTTVIDEIRDLLYIGKDRGNP RSDYLG*PA*DPAPHPLKRWTLTLPFY PSDVTYVFGVGLVWQVWNLALAKKND

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						QHVFKVDMRNLEDVIFYQMIGREITQGNKEPNSQVPLK
5929	19830	A	5979	2	419	KALAPIDSDSDSGSQNKLT* KBEITILNAIKSIYDSMBVKISTLTGVWKKLPI LIEDFEVFK\ADLVSIARERELEVBKEL/LQSDDKT
5930	19831	A	5981	1	154	KRC*HMLTWCMFVG/PTPRAEAGGSPE TGNLRL*CTIMSVSNHCTPAWAT
5931	19832	A	5982	12	311	RKSLNIVGQNTLRNKRCHTNVFPOTIF FFLLEL*LGQC**VNVSEFFFFFEFCFV LFFVFVCVVFVFCFCFF/GCLFVVFL /VYFLEFCIVIMCYTLR*YV*TVMLF FVCMIFVLYLCFHY*LFLFFVVFVFLF IOGVFVVFYELFCIVIMCYTLR
5932	19833	A	5983	3	203	IGQKEASDETT*GSAD/PKRSNGPRDR ARQIYNPSPGKYSNLGNFNYERSLGK YRWRPLGHRKS
5933	19834	A	5984	368	138	STVGKMLSGCHPCYRE/TI/RBQKQSM *QISLSYFKKLPQPPQPSATTALISQQ PSASRONPPAKRL*LABGSYDH
5934	19835	A	5985	2	155	LANF*TYFC/RDKCLVPLRLVSNWPQ VILPPWPVKVLGLQMSPCAPRHS
5935	19836	A	5986	325	403	FIYYLFFLLSYLITITALLPSSSF*R*V VYHVMVLLKVVICHFF/LFFSFRSLI LYLFFLEW/YLLIFVLEFFIQSFSLPF FTLFYLFFNDYCFDLIFFLCIYYHYH QSYFTS*FIYYLFFLLSYLITITALLP LSSPSI
5936	19837	A	5987	81	651	KLVAGCRLSQTDVFRKPSVHSLAVC LRANYFTSQPNV*MQVTILTRCVHRSKH LGTVSYSSWYIKLFPKSHFIYLFTRR SLAPVAPGVQWLDLGLQPPPGPKRFS CLS/LPR*LDYRHPPRLANF*FLVEK GFCHVGQGLELLASSDLPTSASQAGI TGVTRAPSPQKATINLILGGQPHI
5937	19838	A	5988	301	341	FCFCFCNRSVSLW*WHAFFPCANF*LF IYLYFLVETGFSHVQASLKLILLDDLP AASQSAGIPGMSHHDGLF
5938	19839	A	5989	71	1252	TKEQSLRSQQLGVQRQSRHLKPGGGG APSARGVGSWSIATRLGPVSTANMSR PVRNRKVVDDYSGQSGDDADEYGRDGGP PTKKIRSSSPREKRNRRSGKNQSDSDSD SDKQWVTKKDSISAWQSGEKEKHN VQQRQASKAASKQRBMMDVQSESE QSEEDAPQQRDQSGSDEDFLEDDDDSD DYSSSK/NRQKDG*SVCT*KKKKQNAQ TQTKYSDAKSSERQSGSP\QASQAS KEKTPSPKKEIDREPSPPEKKTSTSDPP EKSDEGSEDEAPSGED*K*NSGRFHY *KKKKKKKKKKKEKBEPT*DRTWFLWL DSWGQCFCFPFVESNISLSLSPFFFFFK ANHCNCKCLS YLFVYNSLCQPSPFPMKA MSN
5939	19840	A	5990	630	316	RNVNSVA\QAG\IQNCILGSTGNPRPP GF\K*PSCLSLSSWDYPTHTATMSKFL YF*NRGFTMLARLVSNMLVLS*PSDD PASAAQSAGITGMSHRAQPTYS
5940	19841	A	5991	2	182	WQBQKAR/CLRDVWTANCTAALLTIARG

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						R\NIPCPMKENVRKGPPTTPEYYSAV IMQVILKF*HATTGMNPDDEVISEVQS QKDK*RIILSCNNAGNS
5941	19842	A	5992	79	278	EAK*RVNGCSEKPTNIMYTYVTLNLSTV/ IKPAHCAHVP*KLKYKIIITTIK*RWG LTLPLRLVSNNAQVILLPWPPKILGLQ A
5942	19843	A	5993	22	274	AJDEHRANGVQPM*ARJENPTGCT/ MPSASORAGITGVSH*GCPFFSLNKKI WRSH*VAQAGQRLFRE*TPOLSCYSCS LPSN*DYTSAPLCPPYDT
5943	19844	A	5994	347	195	YMFTHHTHTHTHTHTHTHTP,E,KHKA DNEV*KSNNV*IKPKQSQSCFS
5944	19845	A	5995	1	122	RYELEDELHQTQTQLHALKENYQLR* SSHVSIPST*GYRHVSPCANF/SSLT MFPSSLVSSCAQVILWPYKVLGL*ALK ENNYQLRTIIIDCTLNNNF
5945	19846	A	5996	365	229	RPPPCPANF*PIVETGPHHVGRAGLE/ LTSSDLPAALHGVFYA
5946	19847	A	5997	357	17	ILVDKINNWNLFQNNLVC*RGWGYK* DRSFIILKTVAB*WVYGGSLY*SLSSY YLE/C*ROGLTMLPRVLNSWHQAILLP WPSLLLCILEVFQNRLEKKKNGKPM TS
5947	19848	A	5998	1	207	PIILNLFOKIEARGILNSFYASVTLG PKPORDIR/ITTY*FILLT*NLNKL SNQOLYTKRITY
5948	19849	A	5999	603	269	EDRVLLPLPAKSAVANPLPATASW/ VQSPHPLSPRNDHREVPSPHAFPCCV CL*ROGLSLPLGLVLSNAQVILPPNF/ PKVLGITSMHSHARPLSFYTGHFYKQK
5949	19850	A	6000	3	150	DYRHAFIHLATFK/FFCRD/RGLSVLP GLVNSWQTVLP*PPKALGLQA
5950	19851	A	6001	365	62	ATTACSLNLGLSSNPATASATRIAGTIG EAMSYF*ISSTLTHFSYT/C*LEHML IFKFFVDEVVYQAQSLLELSSSDPPAL VSQNFRTGVSHCTEPV
5951	19852	A	6002	537	236	DRVSLCCPGNSAVARQLTATSAFR/VQ *SSCLSLPPSCDYRSAPPCANFLSFCR DEGGLPOLPLRVLSNNAQAIHPPOPPS VMTGVINGTWPKPLS
5952	19853	A	6003	22	368	NFFLQNKENTKKITF*BRKHLMGRST/ LSYFQGLRPPTTSQQPSTWRQDPPPAK R/LATYGLDDR
5953	19854	A	6004	327	335	NGSIFIFNNYPAPF/CKKPKFN/TLHL WADVAHICHLSTLRQSGRIA*QGSPE ATLANWED*LLCNV
5954	19855	A	6005	2	367	WQFLKKLHFKLIGVGFV/PLGLTYKSK WGHVHASTCTQMFITVLFILIVK*KQPK CPSMEK*IDM*FVHMLEYRAIKENKLI HATWMNLNTMLSEISQITQITCMNLLH KMFVKVTETES
5955	19856	A	6006	1	176	PGFKQFFCLSFWRGTFTMGPHVGC*A GLGLLMSGDPPASASQSGITG/VSHCA WTY
5956	19857	A	6007	1	289	EVLAKIPIR/FFVEIGKLIQDLKDTUPR IA*ITLTKKTEMGRIVHSDLVAYIVAV IKMVMYVM*RDRIHQ/NERLEISEIDS

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						QNNFMNVPTRMQCLF
5957	19858	A	6008	439	223	FFSPGSH/SIT*ARVQM/PHHSSTQPEP PSLKQSSHLSLPSSSDYRCAPPHPADLC RDWVSPCCPGWSQTLGLK
5958	19859	A	6009	1	252	NVVIS*PRDPPALASQSAGITGMSHAQ LFFLN/CIS/ELISSTVTPGLKESACLG LPKCWHYRRPQHPACTVLYLQFQSDPQ LK
5959	19860	A	6010	131	514	FWPYSLSGGSLSPEN/VEKVPETIHH VHSLPLGTTLDLRS/EPTCTERKLA/KDK VNPFLTQMAAMKVCIDAKVVR*LKCSARN WKRLK/VFDEALWAALDEED*RSSCRKET STLLQSTPLLVSYALPCTP
5960	19861	A	6011	625	141	ETGSEFVTHAGVKNINISLHPQPRPK *FSYFSLLLSGMDYRHVPPRPANLVYPL *RGGFPMSLQASLEF/LDSK*IPPCLO PS/AKVGLQVSHRPSKVTFFHQRAGEG DVVSHVSVRGKSIIDRGNQCCHRSIPC VFEBQKGGQCYCIESKEETSRI
5961	19862	A	6012	302	42	GLAMLPLRPGTGLKSSCLSLPSSMDY KIIILS*PAVY/C*FLRNK
5962	19863	A	6013	363	82	VSVLSPLSLKTKVNYAVASASPTIAKI KQLKCPMSMDQMK*IHIIHMEYSA/I KQKINSYSTTWMLEIMLEISISQAY RGKHMLYGI
5963	19864	A	6014	329	99	HLFGRITYFQVASSPFLFRDVSLSLCP GWSAVA*SHFATSG/FRPSACLGLPKC /NDTREPPRPANVLPSPRVTH
5964	19865	A	6015	324	238	LAMLRLVSNNSWPCATLLPLPKVLGLQ A
5965	19866	A	6016	2	308	FWKAIAGIEGDSSEKCRQ/SKIKTKKK FISIDAMRNHDS*EKVQSIWFMIQIPT PRDDF/EGLKTSVEKRTEDVVKTAQ*E LKVDRT*DEELLLLDQQRK
5966	19867	A	6017	2	457	FFFLRWNL/DSVAQAQVWRDLGSLCAP PRGTFPSCSLSPSSMDYRPLPRPANF FYF**RGFTMLARMVIS*PRDLPALA SQSAGITDVSHRAERVISQRIVSVMN KPLPEIHIPTCIINLSLRNHRSVAGLRN SLIVMLSLITHG
5967	19868	A	6018	389	142	AHMLFAAQGDSSIIMVAPLFTVVKWE QSKPLADEWSGF*HIVTEY/YAIKR REILTHATTSLKALCVI*ALTKGRTL
5968	19869	A	6019	384	232	LNLPSSWDYKRAPSGHA/NFSYF*RDG LTML/PGWPQVQMPFKGL*LQA
5969	19870	A	6020	333	84	GLIDKQATTTKSTSLSLT/IPSRC SLICRGSSSDSPASC/SQPPASVAGITDT CHAHITFVFLVK/VRHVAGKANTKPR LH
5970	19871	A	6021	106	366	DTISFFFLKAPIEPWFILIFIFFFFFFI FFFI*FFFLFLFLEFLFYFVF/IFFPIL LCLFFFLNLLFYLFFF/SLFFLFCFV FCFFF*FCYFYFLFLELFFFLFLLF IFFFGSSFLFLEFLFLELFCFVCFE F
5971	19872	A	6022	384	18	REKKFGPGTGKPKKKGGPKFGPKGPKK RGKKKGGP/NSFFPGGGKTPGKNP*R GFPPENQKKRKKKFGQGGKGNP GPI

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						PLGPKAGGGFTPGKGGKGGKGNNGKSK OTKKALSRTHS
5972	19873	A	6023	3	191	LVKCKIRSWBETWVKTW/RFPYDVMH/ TYNPNPLGGQGRWIA*AQEFKTSLGNVV KPHLYKKKI
5973	19874	A	6024	364	142	TINGLITLHNFKINGHTLSTWYTFHLL CVCVYIICLC\CIYVSVCLCVCYTHI QYTY*INKHIC*BLEAK
5974	19875	A	6026	338	102	WGFTTLARLVSSK*HLVICHLDLPKFN YRHEPFCPLAFELIPVOT**VYIPGYRR Y/C*YRHMKNHNRVNMSVGLN*
5975	19876	A	6027	99	77	RRICTPTPTAPASIAKGWK*PKDFLIN EWINTWMCIHMRGKFP/P/VAKTSMELED VFHEITSKQKDEHYIY*PLSPTVYKGA
5976	19877	A	6028	2	328	TITYYGAIRIYTSDSSTETQAREE*SE IF*VLK/EKKKI*PKLLYSGLSFKSK GEIK/YF*GKQN/LKEFFSSRPVLQML KVVLQREGLYRSETQTYKKEKASEKE
5977	19878	A	6029	8	241	GFAPLPRLECSNTMAHSSSLNLSGSSNS PASANFISF/LETRFGHVAQAVL*FLSS SNPDPSPSPSVBITQVSHHARP
5978	19879	A	6030	108	362	CCYLMVTEISAHONPAQQLA/HTAFP* KTFFLKVSWTGVAHV*KPSTLGG*GGR TS*SQKFKTSLGIMRPSLQIKKKVKPKI YP
5979	19880	A	6031	1520	77	ASSSSSSSVLLSS*NDPNNYIVLW/ CL*IE*AASSSIYVPGICYIYHLL CVCVCICMCIVNCICIYSIC*YIVNSI YYIHY
5980	19881	A	6032	405	100	BGFFLPPRGGGGR/PGPPLTPGGGPNP RPKPPQKMGKPGPPGGGPF*WVLLSPS LPGGQVESPGAVSGPRQVPSPSGRPFSP TAVGTVTFTLSKKKKQV
5981	19882	A	6033	42	309	CDKFFHRASNHYYVSITYWVEGICVCVC VCVCVMILC*AY/CGCLGIMWFLVL *CI/CYCCY*SSLFVILICFLMCFVSY ERRFILEA
5982	19883	A	6034	397	2	KGPPF*GGPDPF\*PRGPPQKNPFPPP GGGPPPKNGVGGPPQKAPFFGPKRGA PQKGGPPGGGPPRGEKSLCPNPNMENT PRGLKGGPPPPPPPPPPPPPPPPPPVLR STGLRAPQSVFIVELVDMG
5983	19884	A	6035	343	2	LWPFQKSFKAAPFFFFFGLFISDFTF HLLMAYVFEIPLFL*SPKIK*ITYY VTF*PLQSPSLFSLFVVLNLL*SLLY SE*LIRTYRFLIT*PQ*DTETLFFYYS IP
5984	19885	A	6036	319	68	SLGEICAPK*FPFPAQKGGPQKFPSC FSPSPVKTRPRAPK*KGPP*GKKPYVA NPGKI/GPPKGSFKRPLFFPPPPPPPP F
5985	19886	A	6037	419	191	RIHTIPITALFAVAKR/WOSKYPLVDE/ MDKIWIYHTMED*AYGKKEIMSHARTN INLKNIMLSISQSQKDKYFPFI
5986	19887	A	6038	434	401	YGNKPSFLSKV*YFCGGLVLVFFPPKKK /FFFFNPHRVVPLLYVF*TGRRGVFFK PPPLEKI*FFFLTRVNLGPPRGFF*GAPF FFFFFFFFFFFFFFFFFFFFFFFF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
5987	19888	A	6039	12	346	*NFFPMN\ IFTVL SPSPVRKSLTVTQAGVQW\CNLGS/QPP\ LPPSPK*FSCLSLQSNADYRCLPSCLSN FCIF/M*RRGFSMLARLVMS*PQ/CDP PASASQSGAGITGVSH/SHLV*NA*SKFT ESHF
5988	19889	A	6040	275	45	KDVCHQNKIVOPLHWQVGLKASTGPH DPSILLGLTGYPRIMK*THIK/PCIRMF AEALFLISKK*KLPCKLADK
5989	19890	A	6041	355	1	PGTIKRNFFFIFFPKNYF/FPLIYIFPK KKVLFF*KKKIFFFLIPNKILWVFFF FFFFFFFFCPRFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFLVTRHLF EMRKGN
5990	19891	A	6042	635	209	PLNFKRTFFFLRQSPFTLVAQAGQWHD GSPQPPPPPRK*FSCLSLPRSMDDHRPP PRPANLVF/DPLVETGFRKVSQCDLILL T/S/GDLPALASQSGAGITGVSHCARPTL EFLKVKEMIFCSTTVKAVLDHANFLILR FSIT
5991	19892	A	6043	12	348	KSRYSSTICLPSSVVCNRTISLQVSYV LVVYLFEEF/CFLAKREPGCPPLGVQSP GLGSINFLLO*QQSGLFPQGNVGL APPSPPNPGFFPRKKGVSPCGPNRPAISK F
5992	19893	A	6044	192	1	IFHRECT/HITL/TALDNN*PMLGIM AYAYNPNT.*G*GRRIV*AAQAKSSLGN MTRPCLYKK
5993	19894	A	6045	338	42	WKTAW/FLKLLD/WNYC*DPAILLLGI YPKELKAGT*TDLRSMFTASLEPAIAKR WKQNVDLNKLKQNECRQPIWAKVBNVNL PSWFGWSLQHRLQNGF
5994	19895	A	6046	300	3	RLDCHYLHSHHTHTHTNPAGIYTHH/ HCWNLHTHNPGLLGVALDL*MQPLNLR GWSMGEGQAWPCPGHVMMLGDPGKMI LKPPIMVCLQGGSSYDG
5995	19896	A	6047	332	3	SLESAGPT*YHMYFYIYKIK/YIYKSI FILLFL*IFFFFDLFFIFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFLKSP KRVLYPGGCGNQPKNSLLLLKYLVC
5996	19897	A	6048	2	152	KSLKISWT*WLMVUSRY/WGSLKFGFR LRLQ*AVIAPLHSSI/GDWARPYL
5997	19898	A	6049	1	288	PIITYVLLLLFFFTDSHSVT/RL*CSGA FSTHONLCIPGPGDSSADS/RVAGVAP ACLE*PYRGSGPATLAFRALDPGLPLH PGFSLQRPSCSRGG
5998	19899	A	6050	358	1	FSISILITFDPLGGFLKFFARFYGWDFL RPFFFYR*PFGPKGSFIPPHVF*RIW FLLSSWFLKWSFDQFTLKRFFFFFFFF FPKGFFYKRVFFFPFFFSNLLSSQG KGVWLI
5999	19900	A	6051	308	45	ADLSAEL*TRREWDIDPKVLKEX/NKG QPKLIYPSKLSLNR/NRISFPDQKQL REFTTRLVL*EMLKGLHMBAGQGYLPS *KHTKV
6000	19901	A	6052	2	124	IFCVIVETGPHWVAQGL*LLSSGSPPA S/DLPNAGITCVSH*AGITCVSH
6001	19902	A	6053	1	330	LC*PGKSR\FLTIS*SLCVGLPKCDYRR

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						EPLHLVFFVFFFFFT*TYLKQPYLNPRK IFGNFFPLLKNFFPGVPPKIQPSPIPNL PSLVVFNMFVFKRVLOEKIFRGFFFP
6002	19903	A	6054	34	293	SPILFLCLLRHQSGCHPSNTAVAQSELT AASNSWAQAILPHSWDYRHAPH/LNLFL GNSHAALPRFDSNF*PQAILLPQPVVLG LQA
6003	19904	A	6055	319	217	YHPTFTGMAISKGRKIGDNKCC*GCRE IQMLVCC*WQYKMWLL/WKTVMSLKG IK/L*ELPYCPAIP/L*GIQVRWSKPIPH SSEG
6004	19905	A	6056	341	151	VHAGGSPES/REFETNLNKAARLHYKK *ISQMMWCIPAVPATGAGPSLHFNLYS PNLFGCDY
6005	19906	A	6057	2	558	FFFFLMSFTLLAQAGVQCNLSLQPLP PRFKRPSCLSLPSSWDYRHPV/RIANF FVFLVEMOGLHVQQAISLELLASGDP DPDLR*LAFQSLGITGV/HLAQIPLF /CLETESPSVAQVGVQCNLSLQPLPP /GSE*PSCGLGPSND/YRHALTWPANF /SIFSRDGVSPSWGNSQMDDL
6006	19907	A	6058	320	21	ETCMTNRHPSVNTTK/SENGLASVYLT LPTISKTSKTSGLPASKEVNRYLGTCAI RHFVFTFLMLPV/EGGTMLPRVNSN WQVILPFWPKVLGLQA
6007	19908	A	6059	294	50	CYFSLSFGL*QPLINQSPVTLSSHCGR DTTE*SNWSVI/PGIGVXSS*E/TRGLAN MPRQVYNNSWAQAILMPNLKNLEVQT
6008	19909	A	6060	616	354	ERVSPCHFGNSAVALQPTAALTNS/VK QSSHLSLLNSWDYKCMPELLANF/KPFC RNE/SLMLPRLTSNPAQVICPP*PPK VLGLHA
6009	19910	A	6061	214	11	AASTRPSAWQPPILGSEEPICPATTFSG RCTQQ/LH*ERAMTMVAVLNKRGKVG KRLRNRLVAMSV
6010	19911	A	6062	349	54	QSKSAFFPKRINRISDSSEGYGQSKLKT FWNGKFTLDAIKNIGNSSEVKIATLWG V/WDDFEGFRTSVKEVAADVC/ETARQL EVBPESVTG*QQSHVQP
6011	19912	A	6063	332	3	SQPASGQISRVQSTLRCLKMSVQQVKS CYKCTATYLCAKFNSHPSGSGVCNRPV SYFTTISIRSKLL/WFGWVHTCNPSAL ESQOGCNT*QQGCTSNWVTPVRSRA
6012	19913	A	6064	174	416	NNBELPCEFTTITFTFTFTFTFTFTFT FTFTFTFTFTFTFTFTFTFTFTFTFTFT FTFTFTFTFTFTFTFTFTFTFTFTFTFT FTFTFTFTFTFTFTFTFTFTFTFTFTFT
6013	19914	A	6065	826	571	DGSHSLA/VLECSGVTSACHNHLPGSS DSVASAS*VAGTTGTTCNHAHLTF/VVFL VETRPHNIGQAGLELLVTHPPNP/KKILG LQA
6014	19915	A	6066	1	284	GTSFFF*NRVLCCPG*RAVPQ/VSWLTA ALTSWAQGS*NNRLKP/HMLSPFNFKP QGLTMLPKGALNSWAQAILQPPQM*LG LQACTYANSLGP
6015	19916	A	6067	36	384	VSKNKPTHLFLFFFSKTSWSVT/VLEC SGVTSACHYLRLPGRREGAASAL*LSAT TWLCKVALPLGDLGALCRNPWAGVKG SSRESPLGEARGELFPWQVIRLNGR

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6016	19917	A	6068	393	116	GEPA PQPIFFRY*QNKDFNL*RTF*HKYMKC PAK\LIIFIEKGPSRFQPG*HLSSSN LPALASQAGISGINPGGRARFPLFFFF FFSLLLLSF
6017	19918	A	6069	53	280	FFRFCCF/LLESESHSVA*ARVHWRLG PG/LKRFACKLPSN*WYRHTPTHPANF CIPTRDQWEL*PSWS*VEDLK
6018	19919	A	6070	3	377	HEEFGCATVKGREFFKFLMRSLITVYR LVSNWQAQALPQ*MEHTIIPSTORLH MVK\RYQWCAVAHAYNPRLLGS*QOKA A*AEFETS LGVYMRFC LHKLNKNSFOT VAHPCGSSC
6019	19920	A	6071	337	3	RESQAFSSKKKKKGFTWVFEQRCERG KGARQQSHLRKSTIV*EIASAJALRRHM PGVFPQKPGG/WPGVVVHT*NPRTLGR CGNIT*AELETS LGNPEKPCLYKKYL V
6020	19921	A	6072	1007	628	FLLAHSFHSVAQAGVQWQDLGSLQALP PGFMFSCSLSPSSNDHRRLEPRLANF\ FIFLVATGPHRSQWVLIS*PCDFPASA SQSAGTI/GARKVP*IFVYMYFGVRKH SILMSMPQHDLGYKI
6021	19922	A	6073	27	364	NGLPSVSTPLSLRWADISRATSLPWL LFWMKCFMLLSPNLELSGK*VCCR* HLQSCIT*QWRYWSGLVTHACNPSITG SQGGWVASV*EPETSLCWAKPCLYKKY E
6022	19923	A	6074	2	68	ARACSHGVVALTASCPFLQLDYKCLQYS FVCFVFFFTKSNFVT\RLKCNGLPSVN* NFNFLGFLTRQA*ASREAGTTGTGYHA* *ILLESSTRL
6023	19924	A	6075	330	49	KRRFALVQAGVQARDLRSQPLFFVFS CLSLPSSRDYRCPAS/RPS*PFLELTS GDLPTSASQAGIIGMSHCAQPLIYFL PQIKVILFFS
6024	19925	A	6076	2	267	ARGVEVKUGTKQKPLNMRRLTVHGWK CKLIQLP/LWRLPKVKEELPYHLAILP LGIYFKQMKISL\KYICSYI*IVDHFV *ALLPLGIYFKQMKISINIMFLYITDC RSFCIGTLLL
6025	19926	A	6077	379	236	PPFQVTRVPPRGRVHKDPPPHHFPFP PQEQPRTVPVATHPGESQNHLENSSL LEPWWVYSSLLPQCA*EPHII
6026	19927	A	6078	2	290	BRSLSPPLEDGSLTAKLTWEPFSPH PPQ*RSFP*PKKKKKKKKSPGPKF/HK FKTGKPKDPVYL*RGHMPFFKFF*LKP GLPFF*GTKPKV
6027	19928	A	6079	1241	1487	KMYCIPFVE*KPLCSALPRLLLKNS*P TVCSNISGQPPHG*IMPSIIL\PLFLET VFHSV\TRVGQVMPDHGSLQPGPGLK* SSCLTASQSTQIIIGVSHANPSPITFEI FKRLAYSMSADGW*KSPMKLDLGAKK KLSFAPRG
6028	19929	A	6080	333	1	LCHHVQLSFKFFVMEVSLGCGPMFPK* FSLHLPKQCDYRHDPPHAFFFSLS\ *PPCRDVSMLPRLVLKNSQAILL*PP KVFFLVFCFLRRVSPHHAEPYVSSC



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6029	19930	A	6081	2	239	ARGKTYINRKDISFCPCGHNWAI I / RST/Q P*TSGLKRSSSHINRPNNSWDYRCMPSHL NF* IFRDGGGLASLPRLGTGWLKS
6030	19931	A	6082	323	185	SACLGWPKC/WDYRREELCLVSR*VLNS *AQAI CLPWPPKVLGLQA
6031	19932	A	6083	296	2	GERILEECTYARSHRAETISLHCSLVS K/HVAQVVKWDPDCSQSMPPRF*F SCVSVSVSSWDYGLPLPCAGLHWRNVT LALQGLPTTSLALV
6032	19933	A	6084	443	1	QKPK* KQTWSSSTLSQSKRMKKL LSV ITFFKT*GEBEEEEKKKR\XEB*EK*K EPSQKKEVEEVEVEDERRGRK* KYDMEV KEEKKDKGEKESGEEK* KESAAAVR* VDS/SELVTFAVLPGDSEEEQMMVFA
6033	19934	A	6085	328	1	SNILYFKAQVTKHYSLTCSPTYPGIS QAIKANFSPCTVG*LPSSNAYRHLPPCL DNF*IFCRG\RSILCRLLSNMLQGVKLC QEFFQFLGCHARFQAGFLSHCLV
6034	19935	A	6086	299	46	LDLHL LSLCLSLPRDRVSLCYLGNSSV A*S*L*TW\*TPVILSLRLK\SSHLNLP SSWDYRVVSSN*PQGLLPRSPKVLHLL
6035	19936	A	6087	266	48	GTEIVKQMSRSGADRVIVYLVQSPLEIN GIL/HLGIVAHCTPNSNGSGRGRIT*G QEFKSSLSLSPKWDYEL
6036	19937	A	6088	2	185	ARVTMLERLISNS\GPK*SSHGLRKCW DYRCEPPCPAEISFISGYLTRSGIAGS YCNSV
6037	19938	A	6089	520	297	LGVRDPLHLFPPTS/WNYRLPSPCEA/N FPILVETN*FHHVQAGFERHLSGDLPT SASQ\SAETTGMTYRQPAAGS
6038	19939	A	6090	388	187	SOHLGKLSREEDCL/RLIVPDQS\QOHSK TPLSKK*F*K*AWVN*HMPVVPAIQEAE VGSLEPRKSLQ
6039	19940	A	6091	188	329	TLGLKRFPCLSLR*FIYFFFRDVLVLYY PGWKA VGIHRRDYSMLYLELLASXDS/ SCLSLRSGWDYCVWLIFPGCM*CKRQDL SIIIPWQSLIGQ
6040	19941	A	6092	124	342	RPAPWTQNPISAKGNITWA*AA RVAG IT*GT*QRAQVMFVFLARMGFCHVQAG LYPKI IILYDKLSHYKCSHLQMRGALET YSGIYSLFTIYLV
6041	19942	A	6093	169	2	SH*FPTSSTTRSIWT\GAVAHTCNPSSW GE*GGRMA*QDKIETSLVNMTRPHLYPR A
6042	19943	A	6094	2	324	FFFLRWSL/DSVAQAGVQWRDLGSLQAP PRGPT*PSCSLSPSSDYERPLPRPANT FYF*ARGFTMLARNVIS*PRDLPAJA SOSAGITGMSHARPAVYILTSTSN
6043	19944	A	6095	76	340	LRKRCFSGVYFFIHRWTPELLPLNDFLM NFYFRIVFRFMKKLQ\WPGAVAIAYNP STLGG*GGRIS*AGEFKTSPGNIVRDFI STKNM
6044	19945	A	6096	349	84	FLLSL*DTISLCHPGQSAVVRTNSQL KQSSHRSLLSSWDCRVPPCPVNFVFC RDE/SLAMLARLVSNLWDQALVAAGVS VVAROE
6045	19946	A	6097	346	184	LIMLPRLVSN\GLK*SSHGLPKCNDY

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6046	19947	A	6098	378	250	RREPPCLAKISLYITKFFHLSLPI FKQFSCLSLPISWDYSREPPQHMS*F LVETRPHRVYSYVP
6047	19948	A	6099	3	225	GFKRFSCLSLSSWDYR/HAPAYLANP/ *FLVEMGFHHIGQAGLELLTSGDPPTIA SQSAGITQVSHHAQPLIIF
6048	19949	A	6100	1129	457	YCVSSKRYRTLSFSLTAAALLTKLAS/V QKVG/VQWRDLQ/LQPPPO/ETKLSCLSL LPSGW/DYGHVPHDA*FCVF*WEMGV PCWLR/LVANS*PSGGRPPSASQSAGS LQGLL/HRAPEH*F*TS*PLGEGKTL ETIYIKTKTFYQFCIVCLKLH/RMEFAL VAQAGM/QWHDLGSLQPLPQPKNFSCLSL LPSS*DYRYW/HYHPALEHKEAPSPES PCTH
6049	19950	A	6101	3	296	ETIQAALLITIVLGLYRTLLQAS*YL*SA FTISDGIYGSTFLAA/TGLHGLHVIIGS TFLTICFIRQLIFHTSKHHFGFEDA* YWHFVDEO*LFNLG
6050	19951	A	6102	1	749	RREGLFRTIILITLSLTIGSLNAGLL FFTOFYSKMHIE/TANISYTN*ALSI TLIATSLTSAYSTRIILLTLTGPRPPT LWFKENN/PALLNP/ITIVYAGSLFAG FLITWNLSPSPFQYITLVLKGLALAV TFLGLLTALDLYLTKKLKSPLCITFY FSNILGFYPSITHTPTPY/LGLLTSQNL PLLLLGLT/LEKLLP/NTISQHOISTS ITSTKK/GILKVFYLSFFFLILITLLI T
6051	19952	A	6103	377	1	SKAFQPPGF*APYGLKACCFPPGFRGV WAPSGFWARPPIGYFPQALIGAPVWSP GGPPKPGPP/GPFGVPLKGGKRLGIGOP FPGSPGFLTPGSKKKKSTKKKQPQKKI TPIDTSCSRTIVM
6052	19953	A	6104	1001	531	FFLRKSFITLVAQAGM/QWCDLGSQPPPP GFKQFSCLGLSSWDYRHYVPTLANFSV FLVEM/GFSMLARLVST*PQ/CDPFAP AQSAAGITQMSHCAQLPKPIFNYL* AIDSVTTSISLANDWPSSENRLLGYMGKPS KFKQKQKMBYRLAPS
6053	19954	A	6105	376	117	CSDNKSVRSQSLTAAAPS*/VKQSSCHL SLSSCHN/YRCQPRHANFVLCVLP* RWALAMLPILVLNCPQAVLPNPPKEM GLQA
6054	19955	A	6106	689	433	LCHPGMSAVVQSWLATSPSLV/KPSSH LSLLSSWDYRCTSPCANPFVFFY* R*GSTM*PRLWNSWQAILPPRPKVLGLQ A
6055	19956	A	6107	2	176	AREYPANFFVCLFFLILCRDG/DFITML RLIGSNWLKRSRSLSPKW*DDREPPH QAY
6056	19957	A	6108	328	69	LYIFSRG*RRVFCCHKNSAVAQSLTA ASTFRTQVLSLIGRWDRHVP/PHADL/ SFYRDGVSPPCCSG*SQTCAILLPNPPKV LOPQE
6057	19958	A	6109	777	329	FLEKSHSVAQAGVQWRDLQSLQFPFFG FKRFSCLSPSPSWDYRRPRPA/NFFV FLVETG/TILARLVNS*PRDPASAS

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						QSAGITGVTYPRPALTONPSNLTPGEEN RKPNDPDCSVRYIA.LS.TRQRSP.TALLHV ILFQOMIQLV
6058	19959	A	6110	345	309	ASLIFV*LVEMRFLHSGISLFPNSGKNGP TAFSDQPPG\SSVSFKGAIITIIINKINK* IQHTVYIQIEVQNNHNSLQPLNPELNR FSRLSLSSWDHRRMPHPSANF*NFKN
6059	19960	A	6111	332	3	RKVLVCPGLLSAVAGFQPARSAFQVHP LFLFAFVANSPGAPAFKPPQCP*KK KEFERKKGRKERE/EEEEEEEEEE EEEEEGEGEEEEEPYLRAGK/VKS.PRA
6060	19961	A	6112	498	191	STDRVLICQKARVQKCDPSLKPFPQGP K*FLCLSLPKSNWYSHAPCLANF*FL VETGFCVHVGAGLELLASDPPALASQS VEITGVSHHAWPMQYFQI
6061	19962	A	6113	1381	172	RNDSKAILSKKNGAGGITLPSFKLYK ATVTKTA*YHKK/NH/DVD*NNRINLIE MRPCHYNF\LIFDEPDKNQWAMDSLEN KSCWDNPAIWKRLDADAFLMPYTKINS RWIK/DLNVKPKTVKILEDNPGSTIQDI GTGKDFMTKTPKTATEAKIKHNDLIL KSC.TAKETIKRVNRQLTEWKKIVANYAS EKGKSSITYT*FKQI*KK/NHPIKKWAK DNRRHFSKEDLCQSQSY/VKK/CASLL ISRMQLETTTRVHLTFVQALISNEN KCM*GCGEKNLHCHWKKZ/LGLVQPL WKTUW/RIKTEIPENPAISLLGIYPKE* KS/C/CYKDTCTRMFVAA/CP.SVTDWK KMWYIHTREYTYAIKRNKTDWAMLMV ILALCEAEVGSLEVRSSRPAPWPTW
6062	19963	A	6114	3	155	HEKKISQVWCMPEVVF/TLIMWL*EDS LSPRKRLQ*SYDCTTVLEANATE
6063	19964	A	6115	47	368	STPFSAPFLCLAF/YRQRVULCQPDGGA V\IQHTYSLPT*LSILKQD*PLNLLGT/ WSSRRVAACFENQYRRNGVS/MLPRLV LNSWTQVILLPWPPKV/LGLQA
6064	19965	A	6116	1	592	RQIFLLECGGATSAHNLHLPGSSNSP ASVS*VAGTGVRRHQAQLFVLVLETF HHVGQDGLDLL/NLMHPPRPVKVL*LQ G
6065	19966	A	6117	1	306	LWKTLMQVFLKKNILLFPFAIVPLGIY PNNKLYVHKKTCTQICIGALFIKAT* KQPTCSSIGW/TKLWYIQTMEYISTP ERNPSSSHENTWELKCI
6066	19967	A	6118	2	284	QTGVHHHQ/VLL*PRTFGSRDSKSA SQVAGTTGQHQHARLNFPSFPI.SFFF PFSLGKTLGLGLEFFPRKLQMSGPKLIL RLYLONPENEG
6067	19968	A	6119	2	315	SRVAGITGVGLHARLIPVF/CEFFFLIE RDPLFVPRVFGQPNLG*LKFLPLGLPL FSGLTLPKTDG*GAPLQPRVNEWIF*KK G/V*YOGDWFELDLRGSPPF
6068	19969	A	6120	42	392	LQWRNLCSLQPLPPVFKGFSCLR.LSS* DYR/HAPPRIG*FCIFSRRIVFLGHVR AGSRNS*PDGSA.PQASQAGITG/VS HHHTWAPHFLFPINS.GCSTQNR*QVHKV GDKETS
6069	19970	A	6121	2	202	VHLSQNGQKPCF*MIWKIKRHHIDTME

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, _ =possible nucleotide insertion)
						YVAATKKDKRMSP\ETTLIGERTQWKT KRLILSLIRGS
6070	19971	A	6122	355	161	FIXYLFFFFFFFLLLLLFLSFLFFF XIXXXXXXXLXVPTGMIS*LVVCLVYM NVYM*LYMP
6071	19972	A	6123	1	133	LC*PGWSR\PLTS*SACVGLPKMDYRR EPLHLVFF\FFFFFFFTL
6072	19973	A	6124	3	212	HPLGSSWDYRCT*PCLANF/SCCCO*R LGLTMLPRLASSNWTQVILLNLKPLAQ NLSLNNFYIDDLK
6073	19974	A	6125	156	2	ALLTHAKNKALWLGVAHDCMLSTLEG *GGWIT*G*EFNLSLGNVKKHLY
6074	19975	A	6126	345	34	HPSTTHRVFCSL*S*SSQPARVKNHLS SEHFGITGVNHHMLLFPKKNY/CILIK IETGS*YVACAGLELLSSNPISGSES AGFTGMSHGIRPVSPLKMS
6075	19976	A	6127	2	328	ARAYLPLCFITPTPTVSVIYFIML*G LI*LNKRYLAHPK*Y*LNVSYSVSFCKT HFFPRHKEKALIQGVVAHACNPSTLGG QGGWIT*GPEFTTILTSMEKRLYY
6076	19977	A	6128	1	341	GTRKFSYDYGKGGPDKRNRLLESTPFY FETLSCSVLLCEVTSSQL/CNSPFFPDL PSSNDPPSSASRAEHTTGACHEAQMP* FFVETGPDWS*TPG/LLAIVLPRSPRML ELQA
6077	19978	A	6129	264	2	TAISENKVASRSEHRRHML*LQVI/LI ALQHRSDRDLNSH*KN*KKRMLGEVAHA CHPSTMGQGGWIS*GQQQTSLSNMVK PRA
6078	19979	A	6130	1392	1157	LSLPKWNYRREFFPCNALCCFGWS*TPR LK*SSPLGLPKMDYR/R*TTAPGLPFI SKSLRSPAYSCTVCTQLSHH
6079	19980	A	6131	383	108	NRLCSQPHHVVDSVLESCCVTQGV QNHDLSSLQSPPPRFKRPSLK*LGAIL LLPSSNDYRCTPPHPAN/LCRF*HGPVC LYMGKEVTP
6080	19981	A	6132	307	1	LKTLPALCESHRSVSQNRNLSLQPP LRFKRLSYLSLPS*DHSH*AIQANF/ CIFSRDRETGFHRYQENLIMLVQSS GLGFSIFATLLAVMLV
6081	19982	A	6133	351	66	RNSFTMLHRLLLKS*LQ/CDPPASASQS AGMTGMSHHTRLHNL*TAANNLTQSHK FYSFISLTPHFAINVTHIFLYTTSINI VCIPLSPKPYARI
6082	19983	A	6134	2118	1392	FFCKGR*IFIQCPDWG/DLCV*QEKIQ KCTHTGDKTV*LP*VKEPLTKI*ROI HNSNDLQGLSKEMDQCH*QANFKF FLFVVFYLRSL/NSVQAGVQNRDLG SLQPPVPGFKQF/SCLSLPSNDYRPP PRPANFC/IFE*RWGFTMLARMYSIS*P RNPTASASAGITGVSHCTRQEFKVK GVHPHLLPSGCLFLFYVFLYACLLYS VYPLRQOESRKISKIEMELTTH
6083	19984	A	6135	383	47	HLFNFNYTYSHYNYLYPFLHLPLPSP KIFFFFT*KIIFFLIKNFV*NLSE*K KIF/IFSTY*FWPP*NF*KKPPFFFF FFFFFFFFFF*QTLFGGCGYNTKL
6084	19985	A	6136	2	196	TRPSILVTALYLYIFITTMQ*/LTHH

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6099	20000	A	6152	367	1	NKNVPYGPATSLDLDL*EK*KNMSTKNT YK*MIQALFIIITKNWLSIKRRMTKQIM VYSNRYYSTIKNELP IOTRI PTPWAEAGGSFPCR/LQ/CPN*PWC SCTPAMAPGSPFVSKKKHMQFHRMGHV SSANWPCQADVRNLRAQGYVRRERFFPG LPMAAGGRDEVRICLTVCTACGEDHPGS HLAQRSGOFF
6100	20001	A	6153	441	38	TLMPGALTESKQVQ*ENEMVQAKRL/ QVNRKCPVLSYN*POVAQPVQKLNK LGHEVLSHRPVYLSLSLPTDYTHFFKCTNI FLKEKRFYNQODANAPQSFES*SA/D FCTTRINTPTISHWEKIVDYNRSYFD
6101	20002	A	6154	308	121	GESFPAREKTFPKENDYRMTSFPWGSVL /CKIHGLMLRLV*NSNPQAILLWFP KVLGLQA
6102	20003	A	6155	1	420	QNLQPHNKTLRQF/LYKVKHMLSPATP LLDIT*GRCKPCPYK/ESIC/RMFIARL FTIAKKLKLKSCGAG*INKV*DIYTT EYSAIKSNKQLTHITTWIKLSTPSE *SGT*BTACFTMLLIHESRKNITVTEN RSMF
6103	20004	A	6156	77	415	TLGLKPTSSSHLSLSKOWDYRQEPDPCPT SEANFTFFFFFGFFPWSIS*LRQFFVE W*/PTMLERLVNNSWQARLILP/ASAS QSVYIGKSHRAPQKLTFFFLQGNFP FQPGQCGPGBSNVTEP*TLGLAFOL NLSKCLKYQDSPTAGKLEIFFFKWGV SPSCASRVLNQPR
6104	20005	A	6157	436	206	LMYITHMEVYSALKKQALTHITTSWM SLENMINEIKQKHKRANI*PHLYEIPR KESRMEVNGQGRGIMEFTVY
6105	20006	A	6158	416	50	RFFTHPPAGEFFSPPPPNIFFFPP* KFWOQGGKSPQKFFPLPPQNGVLCP PPHKK*FFPPDEKTVEDPLVWQRP QS*FFLCYPLSFFLYCYIFFFFVFF HPLFFFFFTIR
6106	20007	A	6159	443	145	FFFFSIRFLVUVVLYQS*EYLCEFTM* *IGVLFLFLRICKFFFLVLVGLFGMFL /YFATASPOLFFFCFFIFFFFFFF FFFFFFFFFFFPCGK
6107	20008	A	6160	322	2	TQDKRKHRAHLYKARKSARD*RSVL HR*K*KVQRNEY*PGTHTICLALSG NNL*DA/ISQK*WTFV*TLNENGA SRGQETSLANTVKPDAMANAW
6108	20009	A	6161	421	57	FCBKPTGKNVAVNTV*PTTKOLEY/NI NI/DKTVACCKTDSYERSSMTGKMLA NSIAWYTKIPGRKSKQINQTSLSFFK KL*QPLQYSATIALIRQOPTSRDPSF AKRLRLPGSGDH
6109	20010	A	6162	333	41	CAWACHLVGAALNAPTGLSRFHEPG WSCRTAGGGRLELSVFFVQMGSCINQ VGFFCICFR/DRGLAMFRLVNS*TOG ICPPWPPKVLGLQA
6110	20011	A	6163	2	423	KNNTRSQCFENTLKERTLSNLTKE RRDTNY*YWE*NMDDTVESD LKRIIRN TT*ETLHKFDNL
6111	20012	A	6164	434	5	ICHIFFSISKLNLIRPVSRLFFSINF

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						EGPELYYL*THNP**GRCLSF,FLQNI CIGFFPNSFMOI*SYFIRISLFI PVSPI LLG\FVQIFIVSINILYLSI*LRFFSF FLSLFLFFYYTILSPRVHIVQVSYI RIHF
6112	20013	A	6165	1238	1017	ETGSHSVTQAGVQLHNSSSLQPA*PRLK *SSVLSLSSWDYRRTPQPA*\FCIFG RDKVSCCPWERTPEFR
6113	20014	A	6166	504	210	FFFTSRSDGQSLQ*PLGLKSSCLSR TLPMSWD/YRV/PPHPAKKYKNTFF VETEFHHVACQGLKVLDSNSPVSASQS VGITSISHCQPILCQF
6114	20015	A	6167	258	65	YKTKNTTISLTSFSS**TQLTFF*NTTY YYY/CRDE/SLAMLRPLVSNWPQVILL PWPPKVVLEQV
6115	20016	A	6168	1	156	LARMVIS*PHDPAPASQAGTGVSH CAQLFFFFFWRQPRFFLRAGGQGRDLGK VKPLLSGVRPFLS*TLPTBGRKSGPTG FG*VLRE*FGSH\PVSSW*QSAGITG VSHCAQLFFFFFWRQPRFFLRAGQGR
6116	20017	A	6169	3	285	HASAHASGNILSYVGSFISLTAA\LI IMI*EAFASKRNVLI VEEPS INLE*LYG CPPPYHTFEEPPYIKSRIRRLSDQDA ARKETOOQAD
6117	20018	A	6170	645	15	LEFTYCSFNRNFSNLFWERDSINPLG/ ISLPHSKITNPYYT\IKDALSLSL HSLKLDLSPHETS*GPOAYSL/OPT PLNNPSPHARPPEWIFPYCAVHNSGSGP LTLNGLVL\ALL\SLIHPKQ*FPHDPS YPNKQRH*YFGLPLRPTTFIDFLGRDPSF IGNRESGGQPVSYPTTIGQVASVLYFT TILILIPTISLIENKILKWA
6118	20019	A	6171	409	25	YTFPGKIFPKSNFGSKLFFPPFF/FP FGPFP* KFFFGPKLNFQGGFFFPFP PKKRRFSKNPLVFPSPFKKVPFPFP PLNFADPRVFLKAPPFFFFFFFGG EVNWLSEALDCKSKDRG
6119	20020	A	6172	73	52	VOLLKCRTHIF*DKVLLCHPGWSTVARS *LTATSRSSCLSPSSWDYRRVPCILAS F/SF*YIALNN*A*AILLPQPSKVLGL* AVHNSPSTLGG
6120	20021	A	6173	325	470	ITVTFLLATTFKGR/SLALLPLRV LNSHQAFLPPMPKVLGLQ
6121	20022	A	6174	2	228	TLEDNS*TRCKTIQSSSTFWVITQAA CITLLS**PKLWYVYTKSYQMTWAI FLIAKNWQPPCLSVSE*INLWYI*TM E*YPLKRNELSGHEKTM/MEM*ITLLI ERSQS*KAVVCLHKKHIVDYSSYIINC OKLEATEMSFSKRMNK
6122	20023	A	6175	3	408	RYLLTALRDQITPVSYSVHVPSSDGGQ KDNKNCW*RG*KMGSLNHC*W*CMVOP LWKAQWFLK/DVKERRAILFLGIYPREM KTYVHAKTCHITFLALFLYVHLNALIS VMDNMLGHPIETISRDYSYVNCIL
6123	20024	A	6176	2	237	VWVWLLIPVLLAAWEARAGLLEGSREL *W*TMPLHYSIGNRRLCLKCKKCKFK VFPPQKKKKKKKKKKGGAL
6124	20025	A	6177	387	154	AVVOWRDLSSLQAPPFGFE*FSCLSL\W

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						DYRHKLITSGDLFASASQSGITGVSHC AQLPLSLFVFLTHQRKFAVALS
6125	20026	A	6178	1	239	FFFFEMBCLTVSQAGVQWYNLHSLQPLP PGFRQFSC/LSLPSSWD*RVPTSRPAKF /CVIP*DGVSQCQPGMSAVVQPPHLH
6126	20027	A	6179	325	50	RKFLTLWRVSPFSLRLSSDWMPTPHR HIGGLKVTQSDSNIGLQK*PERHTQ KNV*PNV\WEPNAKSS*HPLKLTITVYPL STWHTYTSL
6127	20028	A	6180	157	338	SOHPGRPRQACSSSSVREDQPCQRFPF HLYKN*KBITQVWVHMPPEAQDY/LEPG RSRLQ
6128	20029	A	6181	3	273	HKKQSKLETFWKGPPT*DVTKNIDEL/W RGVKIPILTGWVEKLPTLNNFEVFKT SLEBITETVYVVEIGRELELEVPEVDTEL LQSHKRT
6129	20030	A	6182	2	359	YYPALPLGLGTHPK*KNSTYQMHTCTHWF TAVLFTIAKINQL*CSSMGWIKKM/W MHTHTLHITMTBYVPIK/NBILSPAA TWMLGVIIITBIIQAQKKTKGIPSHLY VGAKIFDYM
6130	20031	A	6183	3	211	NFGKLSVSINQDCFFATCFPFQMGRCPT LPL*SPYGGQALPLITPSVGTQIFPLKLM /PEVTHHFFHSP*EPLTAALAQPSLPL SLLDVF/RDKGLFCHLQGSADV*SLTLTA ALNS\LVTLQSLCPSFLSSNDYRRMLFCL GNF*IFRLKMLKSLTIFLFFHSH
6131	20032	A	6184	707	384	LQTFPYNRVKCVKNKSTQGFYIYSRIY MHANRHGKYEL/WIIKK*PMRGR*AVQL RMKVVKIKQNTHLKGVVVGYNLSTLG GQGGRT*AOBFKTSLGNARLHLYT
6132	20033	A	6185	720	363	FFFWGRL*TLF*/QTGSHSVACSQVQ WHHESLLQ*TSGLQSSHLSQSSWDH RCAPPRVANFFLDFCRDRVCVAQAGLEL LASSNPPTVASQSAGITGGSHTWPFWD ILGINYWG
6133	20034	A	6186	439	66	KPKTLGSKKVNSEPRVPGK/PWVGSL GGP*MGSGKP/S*NPSPPPLFKTRFG FFPFG*RGHYGGFLQPPFGGKFTFPF SPPKMGHKKKIPQKKKKKKRKKRNI GSWTSSETVGNPAFW
6134	20035	A	6187	83	287	NKMKFTAFNPF/CSFLQSSHTVQQGVQ WHDHSSLQ*TPGLKSSSLPTCDNRRK PPIHLVCFEYRL
6135	20036	A	6188	290	609	RRNDPPFFKYPFPRVLCVCHQGS*V/ K*SSHSPFPCSNDRHCV/PMHPAN/FN PFHTDKSLTWLPRLVNSNAQVILWLPL P*VLGFMAGSPCQPPSPQFCIEAV
6136	20037	A	6189	2	371	RYTFEKVFAKYSLELNDLSLILSKSGY LWKKRSLFS*Q*SYXNFSGLAIYCMH *KRPLGTSIL/PTR*VETGPHHVDQGL ELLTSCRTLASAY*SAGITGISHCAESQ STLKXYIPGSI
6137	20038	A	6190	531	205	RWRFAIWAQAGVQV/HDLGSLQPLP*F K*FICLRQSRWDYRCAPLRPA/NPFVF LVETGPHHFGOT/NLOLLTSGDPPASAS QSAGITGVSH*ARPVVFIIITALLYK
6138	20039	A	6191	52	375	NRCTSLPLPPFFPKKZWCPCPPGGGWRN



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						LK*MRP(LPPGLKEFSCLTTRRSGN*GP FPPLQBNPQVFRKGVPHCNPG*POTPD PRELARI(TSPRGDGGRRPPPRVK
6139	20040	A	6192	3	158	FFFLLNCDLKKETG/WLGVVAHACNPS TLGRRGGWITR*ELKCTSLANMAEY
6140	20041	A	6193	2	54	FFFETESHVAQGVQWCDLGLSLQPPPL GLKEFSCLSLSSMDYRHTPPHIANLFF F/SEIATGGRHVGQGLELLTSGQPEA SASQSAITGVNHRAMPVEFK*RVSPC RPNHSAVV
6141	20042	A	6194	1	323	FILPSSWDCMAPP/RDOWLYFINETG FHRVGRAGLQLLTADLPASAS*GAGIA DGVSLTQCSMLPMLCECRGVILARYNLHL PAACGLKFCRCDLSCPANTPSRK
6142	20043	A	6195	619	243	SPETGSCSGAQGVQWHDLSLQ*LLGL K*SSYLSLISNWDYRCA/PPRLANLFF VQAGSCHLAQGLELMSCHLPAVLSQN AGITGVSHHARLAVAMKRTPLYGLPSRI SNLCVLLKFLFFLY
6143	20044	A	6196	385	19	GGHFGAQELSPGVQLFRLHPLSNMGF KRPPMPGP*FF/VEL*KRGFPGRVPP PSLFP/SDLPPAPPKGVQSLRCPKPT FFFFFDDKEC/RLSCPANFCIPSRDGV SPC*PWSRTPDQ
6144	20045	A	6197	498	437	ENLQSSINLVDAKXNPERLISGNRDF TVKMPNSLTIINACGELTHKRS* TWOTSLLSYF*KLLQLAPLLATTLLIS KEP*TSR/QDRLLABG*D
6145	20046	A	6198	79	394	SVKILALFFFFFGENFCAPQVELKGN LG*INPDPPLGLKNFSLGT/LPKKWEELGG HPPPPSKFFFLFF*KKGMAPPSCQWFKT LGLNQFACLTLPKQGNLRREGP
6146	20047	A	6199	2	313	SASHSAGTIGESHCAWFMPTVYSLVLNF FFFLEKKPPEVTQLEGGQGNLG/SMEPS PSGLKGFCLGPPKKWELRAPP*CPGYF WFF*KKGLPIRPGRFKSVF
6147	20048	A	6200	62	732	APQCARKGTC/GRTSSPAGALP/EVILA PSGPPIPA*\GSSS/PASVAPYPPQAT G/SPTTPGELRNGWSKGLDHPNRTF YCWESSEP/PPN*GQS*APGGVNSEGRG Q/LPPSGIARCV*TPSHVPHPLAAPP SLPHPGASRAPP/TGSDLSASVASAP GRGHP*GTHMVQAGQKPKHGRAS* GSSCSKRTSLPSRQSGPQSRCCFHP RONHSRC
6148	20049	A	6201	424	7	KMKKSPISCVTRDPQITMT*HYTGI KMANV/RLTGNTKC*GYGAKGLTQC* WECKIV*PLRKTAWQFSQ/LKIV*/PY DPAIALPGIOLC*KCTS\KKNCM*IFTT ALFINAKKKQKPRYPSIGENKYLLEH
6149	20050	A	6202	371	144	EWALPRRTNF*\FFVETRSLHVAQGVK LLGSSVSPISPSPSAVITGVSYCAQPYG HPPELSFSLIEYXIYIDFF
6150	20051	A	6203	409	110	LRRSS*ICHGNSAMVDSWPT*FKP*LL GLSDPITSASRVDYRGMPCCPRNFIFD M*FI*CVVCV/RTWGLIVLPRIVSNFNP EVLHHPGSKVLEIQV
6151	20052	A	6204	15	221	KASREMOETTTTRYYSIPRLAQNMLI

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						NTSCW/RKSRQTRTLC*W*EGKMVQPL SKGIWPLYIQAEYP
6152	20053	A	6205	23	371	KVACTCMFTIVLFTIVKL*NQSRCPSTD DWIKH/WLCVCIYSSVCVCLYVCIDR* IERHDIYVYIMEYIALK*/DEIMPSAA TRVKLDAII*S*ITQNVKCCIVSTHSGN LKWST
6153	20054	A	6206	113	417	SAVITLLVYLLNOLKTYV*KTICQIFTA ALFTIAK*KLKCPGSLKIN*CKEM SYQANKRSYARNLWSSKIMRNLCILL RERSEKSKAYCVIPTI
6154	20055	A	6207	510	167	GLGQAISSPSLPSQGTGAYGFGFFFFFK R*DLVCCPG/SINLVASSQSSCLSLPKH WDHCEPPCLAFFFFLL*RGGLAMLDR LPLLEKALASGGGMAKKCIRYCSFKIHL QAQ
6155	20056	A	6208	418	40	SYTHTHTHTHTHTHTHIP**LTGS/RLQ GICRKGSRKHPRGLSQLP
6156	20057	A	6209	1	258	SGPILS*VPSVRDPENRTV*LTWQPLP APLEF\CPRLSD
6157	20058	A	6210	229	310	DFSEAKSRQCGGGISNNHHPGVILKPV IQHF*DGVLCCPGNSAVV*SQLP*LPR LK*SSQLSLPR/SWDYRHVLQ/HPANCF VFFVEMSLAMLKPLVSNWALAILLPQ PKVDDWLEHHTWMLVITYATTTP
6158	20059	A	6211	496	1	CGQSEFELLSINSFPGSLKGGVKNR PGAGPTLAKPFPSPDPLQPRGCGFP VSRGGSQKDRVPKKNFTFFFS*DRVSL WPDGPGARKPSMLPVASTS\R*VQSSCP PLWFPGPPTMVSYFFF\KRDQLPMLPR LV*FNFPQVILLSPKVLRLQARA
6159	20060	A	6212	3	340	VTAGIIIFPMI*EAFASNRKVLIV*EPS I*SLQV/*WRGLLLGSPPPYHTIEEPG YVTSKRKRKESNPPKLASSQPHGLHDF KKKRGGPPKRLLEGAPFGGNGHREFF P
6160	20061	A	6213	60	493	KSQCNFFCFETESRSV*QAGIQWHFSS LQPPPPGFEVLSYL/SLKSNFSGYP*DF FCNGPPCS*GPRIETTYICVIPSSWDYR RLPHPANFCVF\IKTVSGWQSTPDLR
6161	20062	A	6214	414	1	LCNGRPGLLVSPPLGSELIPCLPR*KL GPRVL*\KGGPPL*SSPAPFF*SMESH SVT\RLKCSRAILLVHNCGLGPGSDPPP SAS*VAGSLNAGQVBAVSHEDALQ PROHSBTPSQQNDQNTKLTQYLP
6162	20063	A	6215	2	403	SLLEPLVQLRLCLCFEFLKGFNFAP DKRWGEFG*\LKPMLPG*INTFSQTLR RSGD*RKTPHGVLNLF*EXTGFSNLGR GGLKPPPSGINTPAMPKGVGITGTGTPPP PPVFCPLGFCENTLRAKKKFI
6163	20064	A	6216	2	388	KMEQTLWKTDEFLTILNIIYPSYPAPA DLGIYPNELKT/C/CTINICI*KSIAPL FIVARTWKQGPCPLRDGNLKLGIQAL EYYS*KRNEL*NNHMYKLLIPLLR QEDRFSLGVRQPKDKGEM
6164	20065	A	6217	363	302	NKEFKTILANFGEPPPL*KRGS\MLAR VVLNSLFHDSPPPASQKAGIPGVSPPPR PLFFFFLLETYSYHVAQAQQLISNYDL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						KLPSCLSLDITWDYRH*PPYPVFKLLNS TYIAC
6165	20066	A	6218	576	6	RAVLRLGLVLLLTAKITFFLPFPPROSLAL LPRVGVQW\HDL\GSL\QPL\PPG\FKQ FS\CLSLPSSWDYRPPPPRANF*\FSV ETGFPHVQAVLELLTSSDLPALASQSA GTTDLQSESTLWQSSGLDKPPCHKVNDG PTEERACLLSYSAGRKTKYHL*PEQGS EPPHHGIDILSLPQASHIAQTTPAHT
6166	20067	A	6219	44	496	GPRVDPVRPRVRLNS*PRDPPTSGSAG ITGV\SSHEARP*NIPF*KLGISPIAVFW GFLFLFFVFCFFFPWKGGFLVAQVEGK \NPKFGLIEFSPSGVKKEFFNPPEGMD \YGLAPP*PGVIFWVLKGVSFPCRAWV QTSGLSWINRLNP
6167	20068	A	6220	1	421	QRRLTATISRETSFTLVAQGVQKRDLG SLQHLPPGGQGFPCLSLLST\TGNCSTV QAGVQWCHLGS*\PLPPLGLKPSSHLSPS SSWDYRL*KPHQGS*\VCVT\GAASPEP NTMTANWKPPDIRMKETLLPSSSEKX L
6168	20069	A	6221	3	36	AYCTVKPSP*PLTGALSALLMTSGLAN* PQFHSITLLILGLANTITTYQ*WRDVT RSTYVQGHPTPVQGLRYGLMFTISE AFPLAGFP*AFVHSRGTPTQLGDWPP TGITPLNPL*VPLLN\TNE*LA*GVST *AHDP
6169	20070	A	6222	895	13	ANSNANN*FELATQIAPSGRIPLTDSHL GLLKAVHAPF\AGLIVIAAVLLKNGGL MLYTASHSFSNPLTK\HIAYPFVLSLI EA*FITSLSHLPDKQDLKS\LMAYSS*I SPHSPS*LTPILIQTF\H\SPNGAGQFS IIAHGTYHAYITYSA*ANFKITERTSQC ACINPAQAQLSNS*LQILGLFE*LPRQA \SLTMGLTPPLINPTGENCSVASNQFES \WTQISLLLPYRSTILGSQALYSLYIF TTTQWGLTIHNNIKPSFTRENTLMP HLSPIILLSLNPDITTFSS
6170	20071	A	6223	68	405	HSYALVYVPGIRVKVHSKCLYTHW SNSSQVCEBPHALAKRITLAFH*Y IS*GISQLGAVANTONPTLGG*SRN/I QQLKTSANMAKPHLLKKXKNFNPFPK RG
6171	20072	A	6224	591	283	GTSTQAGVQNCNGSQPPPPGPFRRSC LNLPCSDYRVRVPHLANF*\FLVEMGF HHVN/QAGLELLTSSDPPALASQAGIT GMSHCARPVAF*GEKNHSL
6172	20073	A	6225	302	173	GFFSFFLKC\DR\SLTMLLRLVINSWQ VILPLNPPKVLGLQA
6173	20074	A	6226	417	81	TQTRGPPPPPLGPPSPGPERIVPPPRG GVPTQGRFFFLFRQNGPDALEPKB/EGG F*KKPGPLPPF*KTPFFFTNRGNPCPF FVGENPQAPPVVEGGFNPPFKKKKRNDF LS
6174	20075	A	6227	41	474	TDATETFTSKH\HGF*AAA*ZWHFV DVV*LFLVSYI*GSCVPHPA
6175	20076	A	6228	503	28	AAHAPPRVRKVIGH*AFPTQRTNSRI* ILKFPKDKKARILKGAREK/RITYNGA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						PIWLAVNFSVETLQ/A/RREWHDMQMP KEKTFYLRIILYPHKISFIEHRSIKTFPD KQKPRDFISSRPVLQEMLKSNWPGARVHT GNPTLLGG
6176	20077	A	6229	418	175	VSPLSLPLKILFFPKGLKFWREGGPKCP PKKRVLPKK/PPAMP*IPPKPKKSKSL PKRIKWPQGLFKESPPQPYFFFF
6177	20078	A	6230	45	308	ACVRLRH*TDN*QBNLYNQ/HKSLF* KKKKKKKKKKKKKKKKKKKKKKKKGGG FKKKPGGGPISWGGKILIFFFGGKKIN TLGIF
6178	20079	A	6231	440	209	IQHFRGFSRRGLLPENRASPQGHRES SPLKNQD/NKKFS*VWNCIPAI PASPKV EARESLEPGRRRLHLTEALQPG
6179	20080	A	6232	419	2	SSPPPPGGKFF*KKPKGKKFSPPKKKRV FSPP\PPKKFFSPKA*NFPGGGQKFP PPKKGVPKSKPKGVFTPPKKKKGFFFP PGENWGPVRV*KGPPPPFFFFFF
6180	20081	A	6233	448	112	FSLEFNVNLLFKPVQAPCLT QSARITGVSHRTFPLKRTSTPLSATDRN AGQKISKIDIALNNQDHRDIYRNSTQ *QQNTHSFQAARENKIDPLGHHKMLTH /CQSGDQTNWNLKLSNKYARPKQKHTI K
6181	20082	A	6234	2	351	NDQGLI/SDPESYVLRNTFQCAIVARDG DSSDGGQRKLKTPNGKPSLLDAIKTE DSW/EIKISTGVKKLIPILVDDPEGFK TSVEE/VADVMQLSRLEL*VEPEDGTE LLQSHSQT
6182	20083	A	6235	3	252	PHTYNSLLVCHSNLCYQNSLLFFIIT*/ CI/HFHS*AKVSIMKTYTHTHTHTH NHTHFFQATDRKICVNVYMSVAYIHKG LQ
6183	20084	A	6236	3	294	IITF*LEQLSGYIERSTPYECGFDPISF ARVPFSIKFPLVAITFLLLDLRIA/LLL PLP*ALQTTNLPVNASLL*IILALS LAYEGLQKGLD*AE
6184	20085	A	6237	381	121	VVPASF*FFFFYRDR/VSLCYPGWSTCP GLQSSCLGLSHWDYKYDPPHPAFISF LLSSLLNLV*RPVVLLCATVPAPFLDIR EQ
6185	20086	A	6238	395	62	PPFPLPKFPWGGNFF/PLGPFFPLGF ZFGSPADESHSPDP*HFRAPKXPPG GLFPQKKGDMFFPKKRVFFPLGGFSK FNGGPPFLGPKKKRFXIKGPKKFCF
6186	20087	A	6239	1066	761	SPFLRNSFILVTDGQVQCLSSQLQDLP PGFK*FSCLSLPSSWHRPPRLANFC IF/M*RWGFQMLARPVNS*P/CSDPPT PASQAGITGLSHRAMRLVFL
6187	20088	A	6240	390	27	GELPTIYIAPASPKGVSGGSPPSRV KFFPLEVPPPPPGC*PGFFFYINPGG ARVP*QQIRFFSLRW\PERPTRKPNHL QVGLRI CLSPETGGVIKVPFGSLKLLK KKRAASRSN
6188	20089	A	6241	366	1	KIKNFDRI/TSKGA*SVV/RNLPTKKS PEPNPFGVCTPTFKKLTPEV/SKLF KF*KGILPNSFF*SSIALINPFPYDSK KKKTKKNIYRAISLNNIDKIHRYK*QT

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6203	20104	A	6256	2	305	QWCHSSTLHNSNGERETVSSSLKLPKAWN PRHMLLCPTTSFILRWGPIYVAQAGPDT RGHIAL/LA*ASPSVGLITSKQQRVRPVH DIACFHRSTMTFSAENFN
6204	20105	A	6257	335	3	GPFQSPPPGVTPILSCFTPPKQGNRGP PRRGKFWIFPKKNGSGS*KKRVLFDPDG VPPRPLKKGGLNGGAWAKIFFFFFLRQ SRSFTQSGWQCNLSLQPPPGZK*P
6205	20106	A	6258	219	2	PTLSSQKQDKAQLYSPLATTCKDERLV TLNS/WGCVVAYVTPSTLGGQKRWVT AQKFETSLENTVKPPSC
6206	20107	A	6259	306	117	SPFLIGSSDPLTISALSSMDYRCNPSRLA NF*PFVVCVMGSSYIVQ/SWPQ*ILLSN PPKVLRLQT
6207	20108	A	6260	572	269	ETDITLSVAQARVGSLGSLFAPPPGPT PFSCLSCSS*DYRLRPDPA/NFVFSV EMGF\TVLARIVSIS*PRDPPPSGLP*G ALGLPGVSLRPAICLLK
6208	20109	A	6261	357	116	FAQAGLETMGSSSPASASQSVGTGMS HCA\RLLLFFQGRM*GG/LK*FSCLSL LSSWNYRHEPPIHNPALCIPS FNTISY
6209	20110	A	6262	3	337	HERHERHERHQSAZITGVSHVAGGIG LNNFFLFLEFAGSCTVT*T/GV*WHDH GPO*PQIPRPF*SSHLSLHSSWYRHVP P*LGQAQCATMPG*FIFCRDISEINK
6210	20111	A	6263	515	150	FLWSSFTLVQAQGIQWQVSSLQPLPPG PKQFFCLSLPESWYRCPPCTPI*PL LVEMGHVHVOAGLLELITSQDLPASASQ SAGITQISHRAPROTFL*AAAGGCKQV FLLRLVLNGL
6211	20112	A	6264	1	296	GTSPLPSFLP/LLGPLKPLFPQTVSHC RPGMSAVA*SLTAPSI\FGLKPSQSL RLSSWDYRCPIINF\SLPMLRPLVNS* PQAILPTOPPKPLQLQA
6212	20113	A	6266	298	182	LHFPEVSKIITGLRARRKCL*VLETTA KIWKLIH*ICKYLSIDEMIKMWIHTV EYSAIGNKRI/PVITVIMYIMENIMLS EIN**QDKCKMIALL*GIYIQ
6213	20114	A	6267	402	234	PPPLPLKPNPPPPKPNPPKKKLIIFP/ SPVNLAPPKEP*KGPPPPPPPPPPPP FF
6214	20115	A	6268	125	17	KQAQMLTPVPIPALREA/ESAGG*LEPR SSRPAAAI
6215	20116	A	6269	1109	454	GSGAGDTMTNPTALFQAQDPFPPPPT ALSGGCKPFPFPPPPAGGCTPDPPT AATAPGADKSGAGCPFYLMRELPOST ELTGSTNLITHYNLEQANYKPKOKKVS KLSNFLPDLPGMIDLPQSHDNSSLSLI EKPPITLSSFNPTITGTM/VRI.DPPHMP VAGAVSSDAYASQEEB*AAQATEPYPG SCPPNTI*FRSQEEEKKRG
6216	20117	A	6270	111	86	VVGITGVSHCAWSRNGTITHCWBCSKV /QPLRKTV*QPLMLKI\PYQMI*PLGI YLKKNKAYIHMKTLK*MFSLFLBIAK/ TWKQKPYPSASEWIN*LDSPSLYNLWGS RTPDLK
6217	20118	A	6271	2	222	RSRCSNSQTSACYKSPLYLPLKS/GGPK ILERM*PIYFLIPYVVTIFENQRYFYIY

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6218	20119	A	6272	787	470	NLKRTGTYTVLYKMYKSF LPFFFSFFFTGSHCWNERESLGAQVGVQ*CDLRSLQPPPPRLKQSHSLSPSSW DYRCAPP*LDKFFFCPCRDGFIEVAQA GLKLLSSG\NLPAVSPPSAGITLL
6219	20120	A	6273	2	322	FCMTAAIDSSSSHGSRKSLKTLWKRFF SLLDAIKNTCDSEEV/KVST*TEVWKK LTPFLTDOPR/KESVEEVIAELLVVE ITRETELVEVDVTELLQPHQOT
6220	20121	A	6274	175	406	KNSLGGPNTGEGKKITFSLNFFFSLE ALIFVGRISFVPPPKIRFFSKMSRNL /CPVGEFFPKTRPPVNFPSL*RRSYFF SPFG*IMPP*GIFLKADPPFFFFFLRE RREVSMLPRLMNSHWQVTPPPWPPKVR VLLGIVDVQ
6221	20122	A	6275	2	181	PRVGRVGRHKKKSPVCHWQWKL*P LWKTVMRVLTKL\IELPYYP/ATKLL* SYPLE
6222	20123	A	6276	397	47	PPPSKNFPPFPQKDFPLGGLKKSPPPK K\FFFKKTPKCNFPPPSFFKKPPPAFI KTPLLKKKKFFPPPKPGPPPKFFKKDP PLFFFFFFFFFFITAP*KITKSPYFYFF TKTFYL
6223	20124	A	6277	2	264	ETESHVAQSGSGGALLAHRSLNQGST NPPETAS*VAGTTACDHAHMP*FLV EMGSHVAQAELELLSSDDP\POSFKI LGQA
6224	20125	A	6278	3	204	IRCYRKTFYERKHGQGLSLSYFKLL PQP\PL*ATILISQSLISQDPPPV KR* *LLEG*DDC
6225	20126	A	6279	57	306	INKANRDL/GTIDFLFLTKVRKQV TKTESKIRN*ESILHVE*EDTGHVRAAA VCRDMTYLGEKLTDEVDK\IIREAKYN
6226	20127	A	6280	419	18	SSSSPRACMFVYEWCTQKCVNIVEYMC VFYV*LVLMCCMNVCAK\C*SACV*M CVICEVCVM*GLSVICBGVCM
6227	20128	A	6281	459	235	FLRNVSCCHGMSAVVGS\IMDAENS* AQVILPSSWDYRPVTHSPARTNPFYQ/ CGNKOMCVTHSIVIFSLQ
6228	20129	A	6282	505	470	GVP*GQEFPSLSHNGRCPCLLKCKINP AMWOKL*PRQKFRITQI/LALAPQG QQRNVFFS/NKKKKINPNC*IALR
6229	20130	A	6283	206	374	GGGGGKKGNWGGGKKGGKKIFFF*SP PRFFSPPPYKGGGFFPPPPPPPPNFF FPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP LPMGHSIDLMMVHIV
6230	20131	A	6284	431	269	YIKGGPPPEITFLIF*YIYILILIFFF FFFFFFFFFFF*FUCIKVLPNHI QR*TYISLPHMLM\YTHLFLFCIC SLFTIIVVYIIV*LYOCTVKALCNSL LVSLDKYIKNNYCKO
6231	20132	A	6285	298	44	YLFPPFF*VELVFLCFPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP CPSLSLFLKLYFLKYNFIQGLGNLHFN NI
6232	20133	A	6286	386	1	ANLHKVNFVNFITLNPFLPVNFGFI FLVW*RVYLSHRGFYVFPQNLRFPPFF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						SF*VG\FFFFFLLFFFFFFFFFFF FFFFFFFFLLCIAIVFY*INVISYFTKY IEEPRTRGRTRGRTRG
6233	20134	A	6287	190	134	LEFGNRPQFSRMILRGSGLQWRYADM VKIAKT*YLRNTPHKVIALIGDSCDGS GQKRLKTPWKGFS\LDANGIHNSQEEI KAKLTGVMKK*IPVLKDFEGERTSVE K/V/TADMVKIAKT\LELEVEP\EDVT* LLERILP
6234	20135	A	6288	394	2	RRQASLSCGGLHPVRSRLCLLPKQANA MAGAPPASLPPCSLLSDCASNO*DSV GVGPSKPGVGYHLLVERPLSPLEKGSIR VGVARFSRCRLSPLSLRKGN*LP\TFC ASRVROCLTLLQALGALHP
6235	20136	A	6289	233	58	DRVSLCRPRMHWVSRTLT\VASTSR/LQ AILPQPP*LGQQAANRSPRSPKLTG LRG
6236	20137	A	6290	385	48	TLQYLCTPTSTV*KKKGPENTRYW*QCG ANRILFQ*WQVKVAQTLWKPVWHYTVL NLNTRIVYDGMPLLGTNNAYMCCIC\ YQRTFRMFIALPFIETPK*KGHKLTIV VG
6237	20138	A	6291	273	36	ENGRWTPQGG*IHPS*GIDPVYLPVPG TSSSSCASNSHLLKAPGSRPA\PMFDL GFKPQGPSSNPACRRRLPFGD
6238	20139	A	6292	394	5	AKLYFSINPLVFSKQ*ELKANFENLHL OFFSNINSLMLIK*ALLQDFPLVHNVT NKICDTSKDTTLLPMYLMFVFKMTFFS LKAYI\WSGTVHTYNTSTLGRGRMWT *GQFKISLANMVLASLY
6239	20140	A	6293	536	190	RRSFALAVQAGVQNRDLSSLQPPPPRFK RFSCLSLPSSWNYRHAPPRPANFVFLVE TGLHVGQAGLELLTSGDPPVLAQK\A GMTGVSHRVQPD*GHGGRLSSQPPWEA KTGGSPEVLSRPA
6240	20141	A	6294	2	238	HEADLGTQVLTHSTMTMYFVHYCQPP *ILYGTINT*PPVVKNDPIHKT/SPC LQASTAINPQLSHINC\NPKDTPH
6241	20142	A	6295	2	447	FFFLNGVSLFCPL/WSNGALLGLSLAT SCLLGQVQVILLCLSLPSSGKQVCAYPH LG*FLYF*ASDGGFSPCWFG*VNSN*PQ VHEFWAPALGITSMSHCCPACTHCTF PHFRQNHMLFFFLGLGLSPPPPSQ FLEGGKPGN
6242	20143	A	6296	2	133	AEGREERERERERERERERERERER R*VEEREGGVPLRTYR
6243	20144	A	6297	3	244	HDYSSFLAPPALGYRMLHPATFIFYEY FIF/YFL*FSQDFVILC\LGWQTPRLIN QASCLGLQKMDYRCEDQCLAECDS
6244	20145	A	6298	1	361	GTRRSANLARLVNSGPO/CYLPALASQ RAGITGVSH*GCPFFSLKKRNRSHCVA QAGVQVFRG*TPGLSCFSCSLPNS*DY KCAPLCP*DTVF*VRAVSEVPLTITY ROEGAGVNA
6245	20146	A	6299	3	348	HRRHRLRELINLFFFFFFFGKKIFFFP GKGNGGPF*FAGFASRPQGIPLPYPP* KW\DWGWPWPCRGDFWF*KKTPSILA RVNLNSPFWGLSPYPPKGVRFPGGTR



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6246	20147	A	6300	1	436	PGPV VDGEFSCLSLPSQWDCRASPCFANF/S VFVAVIGIFRYVQAGLELLTSQDLASA SQSPGITGMASHCTPRKH* DANSSVVL GDFRIDYFQISRKAQMITLGYNPWAEHS LMAQAGIRVLEAPRLMISQVDLLPAPHP SSGRRG
6247	20148	A	6301	370	70	PKG*STPLASASRSAGITAVIL*SHCT SDPM*LRKPHKTHSTSTPP/CPFPQK ILIFVQPGQKGNLS*LKPLLSWLRLK PCLTL*RGGDYDGFPPD/SYFCFPYK GV*PCGPGGNS*PASASRSAGITAVIL
6248	20149	A	6302	1	285	KIFFPLTYLFRDRVSVCYPSASTVVK/S L*SWLIAASN/CLGSK*PSHLSLGLGHA LLVDNFNL*RRRLRQERLVNSNSWAQAI LSSQPKALELKT
6249	20150	A	6303	194	351	GTFCICKPVQ/WLDTVAYTCTPSTLGG RDGRVT*ADPFETSLGNTVREHVVYK
6250	20151	A	6304	354	211	YRIMP/S*LADEFFIKRDSLPMANVL NL*AQAILLPQPPKVLGLQE
6251	20152	A	6305	1	346	GTSSLQLTSLHSSPTASYPPKHLHRLT ELLSSVIMARVLSVSPATSS/PILQPH IYPCWIMFTHSSGSGKPSQTHHTHTY HTHTRMCAHSGSHATLFP*HPLPHKHA YLLW
6252	20153	A	6306	395	177	WLTATWYIHTVDYFLAKRSDDLHSPW MNLQGMLESEKQ/SQR*HVV*PYLYNN VERMKSKQKWTVLMLPE
6253	20154	A	6307	2	718	GVLPTWFGMSKRTFDLV/HPTPSASQIAG ITGKSHRALP/KFAPLTSSQVMILALH GTTAVVFSKLS*F*EPMTCAVFSVVTG SCHINSFRIQTCL*YYSVFTSCFYCSMI EKLTTGIS*QKEHLPFSQSSDIFKLAY LIFPW/CUVEMESHVSQAGVQNMNLS LQPLPRFK*FSCLSLPSGGDYKPCPPH MANFCIFSRDGLPC*PGW/S*TPDLRM DPPGLRFPQSAGDLTGMEA
6254	20155	A	6308	377	67	PPPKKIFFFSQTLFFFWGGCPQIAPPPK KFFF*KNPQGFPPPPKPKKKIFFFFPPK FLPQKFF*KP/LSFFFFFFFFFFF FFFFFPTI*LIPIGSLP
6255	20156	A	6309	1	362	QTYAMHITLIFGVK/LTFLPQRLGL SQWPRRYSDYPAVTT*NLGCVGSPIS LTALILITFMIREAPASTRQELIVEPS INLS*LLGCPPPYHT*EPGYLKPKRRK KESDPPKLW
6256	20157	A	6310	2	411	VLPITMIRAGAGSLERSSRLQ*AMIT/ HCTPPNAT
6257	20158	A	6311	59	334	THAGCNLSYAGSFISLTAVALITPMI* EA/FASKRKVLIVKEPSINLE*LYGCPP PYHTFE*PVYIKSRQKRKESNPPLVSS QPHGLHDL
6258	20159	A	6312	3	22	KPSP*PIAGALLDLMTSGLSM*FNHS ITLLILCLINTLSIYQ*WRDVTRESTY QGHHTPPVQKGLRYGILLFITSEV/FP AGYF/WPFTHSLTPTPOI*GHWPPTGI TPLNPL*VPLIANTFVLLALGVISIT*HID P



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6275	20176	A	6329	346	1	SHCAQP*VCFHYCLTFPSLQ LPFKKKKKKISRGLFPFQLPKKKKDNRES L/TFSSETMPGRQWSKIFKVLGRKKQPQ QPRIISLAKLFLKSEDFL/ETQKLRFFV ASRPALQAMLKEVL*REGK*YRSLFKKG KALK
6276	20177	A	6330	349	77	HTTPKKKH/N/RKKIKLOVLRYNKVDEN SMSGH*QCPSDECDAGVFMASHQ/F DRHYCKKYCTLYCFNKPEDKAKQCSLE PRLSLPAWAT
6277	20178	A	6331	319	46	RPRRPETK*ALAK*KDI/PMCSWKORHN TVIMLILSKLKNRPNAITIKISTE PHR NKLILAIWCKGPRIAKTT*KGIKLEE LLYLISRP
6278	20179	A	6332	496	309	DRATAF*ROSTFLSL/RAGMOWHDLSEL QPPPPGFK*FSCPSLQSSWDYRCPSPRT G*F/CIF\VEMGFHHGGQAGLELLTSGD LPASASQASGITGVSHCTWNPNTINNK
6279	20180	A	6333	3	173	HHHSRL/TFRCSVLGTSSHVA*AGLEL LGSSNPDLASCNPGITYGSHYANPDIP VF
6280	20181	A	6334	339	153	FSPPPPPFFKGFPPPPPPPPF/SF*PLRG GGPPPPFGPGVRPPPPPVVWSCPPPV VLASFPPS
6281	20182	A	6335	32	331	QLIHSVTVFLSLFDESYPLENLSLFLIA FKLGVNS*YTLISFRYLLHP*RLNPF FFP/CIRQGLPVILRLVNSWAQIQCP WPKVGRGLRAWGPGLSL
6282	20183	A	6336	226	177	DGVSLLLRL/GGATSNCHDLPGSGD SPVSAS*VTQLQYVFCIGLGFPTTTRL SAYLGTGKLTALNTPPGLLDS
6283	20184	A	6337	302	59	KMLNNTIMCNRYTL/RKRSRPHVOTSS VSFYFKLPPQGHSAASTLISQPPSSSK QDPPAAK*L*FVEGRLIAFPNNVF
6284	20185	A	6338	197	28	AEKVRFSVAITVHLGSHSL**SKNKL/W LQMVDHNCNPTSLGGGRGIA*AAQAPT G
6285	20186	A	6339	46	317	EVPSSISSQISLFSGDFSSVPLEELSNL FFMFCPEHIVTCERVTSNYS/YKWAQ EFSYP*IF/CFRGLTMLPGLSLNSWAQ VIIPQPPK
6286	20187	A	6340	4	276	QTLRGITVQITKNLSSTMMASRCKK NL*SANGMGWENNYQPILYSAKISFKN GVHKTFTFN/KQIKN/FITSTLV*EIL KRWLQAG
6287	20188	A	6341	485	2	GWVFLRTSSRSVAQAQVQNCGLGSLQA PPAGFTFPRSLGLSSNDGSPPPHPA NEFFVFFVETGTRHVSQGLDANVUSI* PREPPASASQASGITGVSHRAPPKSKIL LAGSRSSIQMPFVKFPQKLVVNFQK TKDFLNPYSRILLHTSQIHSSC
6288	20189	A	6342	2	339	EDLRVLKKEGYSNINIVVNHQDPLMN SNGSVTVVALQAS*YLCLQAS*ASSQ SWTS/VTLAAVSFORISNOEHIPVYQGE ENQTDVWTLANGSKDDFLIDRCGCLVY HL
6289	20190	A	6343	181	12	RWGLPSGWDYRSMPLHPVNF*YI/CMRQ DFTVLRLIINSQPPVILLRWPPKVLGL

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6290	20191	A	6344	3	295	QA YVHLSCF*FLATNKAAMNIRLLMTCA IFPR*RSRKEMAGS*GS/SLFNVRNCL TIFSHDCTTL/HS/HQONGV/PVLPP HOHLI*SIPLVFDILIGI
6291	20192	A	6345	334	8	KPSNPGGEGPP*KKQPKVFPSTWKKRNF SPKKKKKI*CPQKPKGPPWGAFAFKKK N*NPGRSPQL*KKRGLIGPTLLPPSS QRPPKKKKKK/GPPKGLLAFOGKKFF FFFLKKNFLFFKGGKTLAEPFFGGGLPL PG
6292	20193	A	6346	68	256	WVA\PIVTHCNNTLGGRRGRIT*QRF KTSIGNIVGPHLYKLNKKKKKKRQKPL GGGFSPL
6293	20194	A	6347	385	60	KKKKKRNTPYDAAI/PSLTSKRFKSG SSRDICTPMFIA/AITKRWK*LKCPMSV NI/VKKMMFIMMQY*SAKKKILS*MH LKDVNLSERMLSQSKNFCMTLLIGI
6294	20195	A	6348	234	61	CHRIETIRKNTL/MDVVVHTCNPTSLG GGDTWIA*QRFKMSLSNTAKPCLYKXY KN
6295	20196	A	6349	2	358	FLSLGIHNPCLVNTTESKLSKRLTYFF FFFLBETFPFCSPA*RPW/PNLG*LKFP PPGSKETPAUTLPKIVNNKHAPHANF FLRENGV*FFPGGGKTLDLGGPTRLM FGKGGH
6296	20197	A	6350	346	27	KW*SLWKAUQFLKIAIH*PYDSVPP LIG/IYPT*MTT*ITYTG*TMLAASF IMAKNTRENSNIFNNPIDKLVNHYIMEY **AFKRN*LLINFT*MLKC*LF
6297	20198	A	6351	36	158	KNSVFSQE*LYYL/RQERNLSGGIGCR EPINCHYTPAMAT
6298	20199	A	6352	2	146	RSSHLSLPSSEYRREP/H/LANCFIF CRDR/SFTMLPSLVANS*IQTLIL
6299	20200	A	6353	74	303	EPSTCGIYLSFSIYKIC*/WFGVAQ ACKISTLEG*GGNIT*AQFTSLGNMMK PCVFSKKKKKKKPHPGGGGRKK
6300	20201	A	6354	3	210	NNKINTLKNLFFRFRVLCPFDNSTA VHSRLTAAS/TLGKQTSCLSLVSS*DH RCMPCLALRRKKT
6301	20202	A	6355	2	627	GRVGGFLVPMRDLAKASRGQQGVKGE MKPSVSCVCGGV*CLSKFKLN*L/WPG TVHATCSFSLGGGGWIA*AQEFETSL DNVVK\PCLY
6302	20203	A	6356	584	166	RGHNVAGAQVQWRDLSLQPPPPGFK* FHLSPSSNDVLRPPHILANT*FLVE TFPHVQAGLELPTGLDPAVQASQ ITGVY/HQAKQLL*KLINPSTGFW ELLEANGRCPSVVMGDDIALNCFPHFVS S
6303	20204	A	6357	448	202	FTTLVSECI*DIHDSNKKDV*ISTLTGAW KIWLIPTLVNGFEG/FT*VEEVATDVV EIARESELEVEPEDVTIKLLKSHDKS
6304	20205	A	6358	3	237	DRSLI*P*PGLK*SYLSPSGNDHGR A*PHPANFCLFT/V*QRGLDLA*HD PASASQGN*ITGMSHRAGPLTF
6305	20206	A	6359	49	242	SSYLSL*P*PGLR*SYLSPSSDHK HA*PHPANFCLFT/V*QRGLDLASHD

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6306	20207	A	6360	508	223	PPASASOSTLTGMSHRVWPLTF FVTQAGAR*LDLSSLQLPPPGFKQFSC SLPSSGMYYRHVP/STPLVF/CFPSRDF HHVGQAGLELLTT*STCGLRSAGITGL SHRAQQERGFEP
6307	20208	A	6361	2	595	ATVVG*GTHFLIPW/QKPIIPDHSQEH NVPIITGSKDLQNVNIIPCILFGPVTSQ LPRIITRIGEDYDERVLPSITTEILKSV VARFDAGELITQRELVRQVSDLAERA ATTGLLDDVSLTHLTREKPTENAEAK OVAQODAEVA/RNSLATAGDGLMEKCL EAAEDITYQLSRSNINLPAGQSVLLQ LPO
6308	20209	A	6362	1	259	LESPLYLLYYK*SS*PLRLKRLITFIF ETECPCPA\QLECSGTISAACHLCQGS GNSPAPAYRVVGTDSFRITHCILCTIP SE
6309	20210	A	6363	60	221	NITKIGWVAHTCNPSITGARGGRIT*V* EFKTSLDNIVK\PCTPPKSLIKILN
6310	20211	A	6364	1	393	RPRRPQTGVQWNLGSLQPPHFGFKRS CLDLPSSGDYRHTPPCANFSGFS/HHV GLKLFDSDDLPPWPKFGLARHSHKRC T*RSKGRRIADPLER
6311	20212	A	6365	19	85	CINSKINQSSRIITLCKNWQPL*RALMQ CLIKLNIHPYDSALPLHFPYQK*RH NHN\YPTSMFTTALPTAN*RQSKCL SIGQMMK*CHITVQ*NSGI*HE*IN SKINQSSRIITLCKNWQPL
6312	20213	A	6366	2	298	PPRLARVQKPLFFVFLV*DRVTLGHP WTAVV*SQLTMTLARENRLPSGMDYRH VPQRLAD*VFL/CR/DRGFSLVLGIVSN SRPQEV*ATSPSQSLLS
6313	20214	A	6367	67	636	QDNKKGIRYLFFVYFQSPALVAQAGVQW HDLGSLQPLSP*FKQFSCSLSPSS*DYR HAPPRPANFL/QFLVETEFHHVQAGLE LLTSGD*PASTSQAGITGVSHCTGPRI RFLKTFSHLEAPGGFPEKROPLRSERLQ FRAPPQTAPCAHAYLLGCVSHLEMGCRN IDIPELSFFLCPLQCLTYRGKSP
6314	20215	A	6368	3	251	RSRHCTPAWAPLSTQDHFYVYFFLHFL IGSLFIFACFVSSYFIEFSYCL\YFFVD SFGFYRTMK*NLANSYFKLSAILLQ FKGLVHAHAKYCKANFFCGVPVASKN /TGLMEKQWQCPDL*EALLFKPG WYDHKEPPRLANFCI/FLVETQGHIG QAGLALLT/S/GDPPASAGALE*LGGS SCI
6315	20216	A	6369	333	193	FKGLVHAHAKYCKANFFCGVPVASKN /TGLMEKQWQCPDL*EALLFKPG WYDHKEPPRLANFCI/FLVETQGHIG QAGLALLT/S/GDPPASAGALE*LGGS SCI
6316	20217	A	6370	36	369	RPTRPMPRHHFVUGQA/PRSPGLK*SAC LSLSKCDYRHEPP/*PG*FSFFTYIYI YFFLFFSFSFLEEMGFHHVQAGLELL C*NDPPASASYSRIIGVSHQARPPFF FF
6317	20218	A	6371	2	375	DTQMIDRNIRN/CSTQSIRKLIQIRIM *YHLSVSRMAITKTIHKC*RCGKK\H C*WQCKLVQPL*KTIORFVKQTENNINI *PSNSKN/WKSAC*RDICTAMCITT*FI RAEHGGS\PCNPSTLG
6318	20219	A	6372	75	372	NGNSQKKKKKKKKCOOPFLKKSGGNL

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						PPGGAKIGFPLAGGGKPFPGGFLKKNPP LOGAPL/GPPPPPKRPRGKTKP*GG*R GKNPAKPNLGGKILKP
6319	20220	A	6373	605	350	ISTGTCLMGFLAALFTLAKL/WKAT*PS FNR*KKMKCYIYASYSAIKK\DAILSFA ITWMLLENIMLSEISQTHDKCCMISLI CAT
6320	20221	A	6374	167	378	KKSQGTGNTKPPATIKYLSMGG*KRLL TGFLKKKSLGGGAGVTILLT\WRTFST KINDPDGGGDHILSQ
6321	20222	A	6375	994	747	VSLALSPRLCNGYISAHNLRFPQSN SPASAS*VAGAHHTQLTFVPLVETOFH HVQOAGLRL/NLWLNPPWPKVIGLQA
6322	20223	A	6376	1956	1592	HEFEMESYSYVAGVQ*HDLGLLQPLFP RFKQLSCLSLP/RYNDDCLAPPCLANF/ *YLVKMGFRHVQAGLKLASSDAPASA FQSAGITGMSHRARPISAFKIQATIGEG GVSELIRKINI
6323	20224	A	6377	94	402	KTORIQRKISICLIRRVDRRM/WLCTVA HTYYPNLTGGQDORIA*GLEFSTSLNT TRPRLYRKKKKKNVQANPLNSNPLRLR LRREIRAKESF
6324	20225	A	6378	463	146	GKLGPPKGSILKPPPPFFFL*/R/F/HFP PRGTTPFPFKPKKSPPGGGASPPFPL GRVPRNPFPPGGGSP*RGPGTPALP PGQKQETLFPKKKKKKKKYMLI
6325	20226	A	6379	3	207	LEYQVAQNTCTISSRTQLVAEKASVFFV DKIVLS\TMQGL*EAKAEDGFPVPG*YG LAVSLKFOSTRP
6326	20227	A	6380	328	70	RPRRLGLPRSDYRHEPLHPDOLLVET MSHYVAQAGLKL\ITGVSHARPH/YR F*LGHG*SLVRRPNTISYSLCLGFPWM EVSD
6327	20228	A	6381	13	77	VIFLLQPPK*SSCSPLNPDQYRRVFPY PANF*PS/CRHSLTMLPRLLF*TLQAC ATIPS
6328	20229	A	6382	342	77	KGQQFYPHLFFFFFFF*KDSPLPRVEC CORTSAPCNT*LFQSNDFP/ASHATVGG KLPRKRGAFPS*GGGFFFFF*M*IKHSV LNSSRN
6329	20230	A	6383	1	208	RGVVDKI FYLFPETDSQSVT*AGV*WIN FGSLQLPLPPGPK*PS*PQVI\TCLDLPK CNYRREPLCPY
6330	20231	A	6384	277	50	LVLKLGKRSISF I*NPFGQLAKTLLK KMGASLT/LPNFKTNYKATVKTV*YN HGH*YRHGFSIGLSILFH
6331	20232	A	6385	2	354	AAASTNPRDR/L/LCHGHSAAVQS*L TAVSTIN*AGGIG/SSHLSLMSLDVRY APPLILAVLLCCPGWPNOWPOVILLSP PKALGYRCBPCCAPLLNFFFFIGRL NPPCCPGWSA
6332	20233	A	6386	2	188	FFKYICY/CINAYMCFYFINIYSLIYL *THIYKIYAIYINTYL*TYICLIYIK YIYIYR**TYICLIYKIYIYR
6333	20234	A	6387	2	241	NATKCR*G*RRGTGAG*WDCRASGL *KTQQPLISITY/PYGPAISLLEIDPS ELKTYVHTKTRT*LFIAASFITKN
6334	20235	A	6388	142	429	YCVCIYIYFLVLIFFCTFFYSSHL

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						LIFSPPFFLLRRGVCFSPRGGGGKYLGL WRFFPPPE*IKGNVYIYA\QQYYSAIKON EILSFAATWMELEAIMISEIRQAQNDKH YMSLICGLIKK
6335	20236	A	6389	468	250	VHRKTPPCPIIIFFFF/CRQ*VLPMLPKL VSNWNPQATLLPWPSTLVFQALTPGNK NFKNWFLLMWSNLIK
6336	20237	A	6390	616	1084	LCLQYAGISVQCPDGVQPFHNVSTY EDYLRRLKTSLSFFWRRSPALVAGAVQ WCDLGLQALPPGPK*FSCGLLGSNDY RHPWHPANFVLLVEMGFIVGQAGLEL LTSGDPPASASQSANITGMSHRTQEQ\Y FLNLKFTSPGELLCLK
6337	20238	A	6391	415	200	SPPPRFFFFFCPPKKNFFPPPRSNKFFF *RGPFFFFFFFKTTPF/YFFFKPPFP /RFKNPPKIFFFFNRPKNPGGGGKKK PPGPGGSPWGP*PPPKKKPPPPKKNP PLFGCKKKKKKKKRAAER*NPRARQVF FFPPPPPLGFWAG
6338	20239	A	6392	3	117	ELKPSHH\DY*VGRTYGRDITSRGDKP LAVCKTFFSPLS
6339	20240	A	6393	3	204	DRVSLCRPGMSAVA*S*LATSNS*\VK QSYHLSIP*SGSDYSCVF*PPLG*LVIL LRQPPKVLQQA
6340	20241	A	6394	501	187	AGVWVHEGLWCPPPPLKRSLSLPS S*DHRAEYPCRAE*KIFF\VETRSHYV AQTSLEFLDSSNPPTSASQAGI*GMS HCAQPMQTFSLVKIGTNPLIF
6341	20242	A	6395	3	393	HACGAIMNSKPHAVTQYTFPLLM*SVLIT TT\VLILLFVTLINDGITILLTDNRNT TLFYPSGGGDPILYQHLF*FSGHAGG*I L/LLPGFOTISHIVTYSGKKEPFGYIG MV*ANISIGLLGIIV*AHHI
6342	20243	A	6396	101	135	FDSPTGIIVPGWQTRSLNIVYLTTLT SFSIMPS*FLIFFCRDG/SLTILPRLV SNSNPQAILSPQHOMGLQA
6343	20244	A	6397	395	187	SSYLSLLGINSYRVPHPANPLFFCRD GVVYFFFC\KGMAMRLVLNSAQVI LLL*PSKVLGLQA
6344	20245	A	6398	35	334	QNETLSKTKIKRKKKKKKRGGPLKK PLKOPKLTACKKPPSLKG/WRKSNL GLEKKKPPGCKKKNPPTKIKSPKPK KKF*RSKGEKQPNQGC
6345	20246	A	6399	464	146	HQIREFQRTPIRMSPKRSTLSHF1KK QLVMNRSFIFKQWIS*QKPCQMARDD*H NIMTVQKQINQIR\ILCPAKLSFENR EIKPFLGKYKLREFTA*FIFKG
6346	20247	A	6400	723	632	FFN*DKILLCHPDNSAVARQPTAATF RVO\QSAACGLPSSNDHRHIPSCLATF* *KRGFAFLPRLLSNFQAQAILPPWPDV \LGLQA
6347	20248	A	6401	522	46	FFPPFLSFFFFSKIPQSLGLVFF*NR VWVFCQWRAIR*PPFPA/APDLSGNS /SCINLPSTWYRISGMVPPKAR*IPPE IFFFFFF/CROSLALSPL/VVOMQVQA ILLPOPPE*LRQVQPVGVV
6348	20249	A	6402	103	261	NIPPTCLIKKKKKKKKKKKKKKKKK KKK/IK*KKKKNVGSGVKKKKKGLGD

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6349	20250	A	6403	146	384	GFLPSLSGKHLKSLFLFTESHHPVAQA \DLGSLKPLPPGFK*FSC\SLPRSWDYR RVPPCSVMFCVSPY*PG*SQIPDLR
6350	20251	A	6404	3	395	ETESHVVAQAQGVQWNNPGLQPPPPKFK RFPYLSLSPSSDHRHNPCCANSAFVSVE IGL/LMAQAHLQLLTPGDPPT*TSQSA RTTGASHRARFSLKFLISFVSSLLHG LFFSVLASWILRLSQVFCC
6351	20252	A	6405	30	205	CLTRPAEPRTRKHTLRKPYECKQCG KFFSCSKNLI VHEKTHKVTWGIQ*VMW LFL
6352	20253	A	6406	3	444	ARKITGV*TSKITVFLVT/DELAEKIK KAIPPTIVPNK*DN*ELNLTQVKDPEK EDYKILMKETQDTR/WKDISSWIRII NIVKVAVLSKAIYRFAICIKIRVIFKT ECHWKKKIWIGKVAHACNPITLENQGRRLSARSIRLS
6353	20254	A	6407	480	307	QHDSPSAKKPPQKPDKS/HPSRS/RHFP PPPPPC*TPPPPP*YPPKPGENGARPPP QG
6354	20255	A	6408	923	833	KAMKHFLYKTRAFFRHVTAHLIDQSIYK TELLYVTSFIAIFALLWYKGEPM/L/WP GAAAHTCNPSTIGD*GRTA*AQEFKTS LGS*NTKTP*CLSAV
6355	20256	A	6409	382	152	ECSTGLARHCILCLSSDFP/SLFHNVS LGSNSGS*VAELIGLCHNVLI FVSAK LFLGRVFNLSPTTQSNFSK
6356	20257	A	6410	553	173	CLLIYNTPLPKKKKKKKKKKKKKKKK AR/WDP*K*RAP*NPVKTGGGF
6357	20258	A	6411	38	562	FLRQGL/DSALQGVQWNRSSORADPP GLGRSSH\PASLAWSAVA*SRLAATST FRVQVILLSQPP*LGIGSCSI TQGVQV QWRDLGSLQPPLPFGFKRLSCLSLPSN*D YRRLPFRPDSSITFSRKFFQSPQARNLP PTPBLKPQQPVDPSPSELHLSWSGNK CHFLWFLCP
6358	20259	A	6412	414	144	FFFETESHSAKLECI/SAHCHNLHFPQS SKSPASAS*VAGTTSVCYHAQLI FVFLA DTGFYHVGQGDPLMFCCPPRPXVLGLP RLPLICP
6359	20260	A	6413	3	455	AEAGGLLRPRSSRLQ/CSQP*SHFCTPA WAT
6360	20261	A	6414	462	162	TQGPLFLPHPPGAPGVPVLGWEVRPPP APGKPPFPFKQVNSPWHGGQPSIPPP LEO*AKSP*PFKGLVNTKGPFPFPHP QQENPTFPFKKKKKV/N
6361	20262	A	6415	499	0	HFTSKHHFGFEAA*Y*YHFDVVV*LFL YVSIY**GGH
6362	20263	A	6416	187	236	MCHINGIMQFFFFFPFENVPFCPPARI GN*R/WPNIG*LKPFPDGLTFLSCLTPP RSWNKRPPPPARVIFLEFNKKGVFPLLP GRV*IPHTPELATITNLVSVIDLLILN VSYKWDHNVFFFFF
6363	20264	A	6417	158	412	SSDPSRRSLFSF/CFFFLERFEFFAPR VEWGPNFCLTTPPPGKKHFFAPSLRGGDYHILPHGVPVIFGTLRKAGFSPCGPG GS*PPPGKKHFFAPSLRGGDYHILPH GPVIFGTLRKAGFSPCGEGGS



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6364	20265	A	6418	457	11	HTGSGPYRCSBQK/APTQKSAITNHQK PQOKGRKSMQ*LRI*ESFFD*SHQLRHN RSSMNTIMVMGPPGTLVGEKPYRCNEYF KPSFLKISLVYRDLTRITGQAHWPMP VISALWEAENGSRLEVGSRRPAWPT
6365	20266	A	6419	103	376	SALSLILGITFFFF*IFLETGSHPIAQAG VQM/PIHTCDHSILQPTTGLKPPSSCLS LSSSDYRHPVPVPRTSACPECTILRS G SVATVLRKAKAGSGLEVRSLKLACATQ GAPCLTKKKCDPOD
6366	20267	A	6420	463	6	FFPNPHKKQKQCTP/PPKAPQQQKYTA DP/QDPFGNDPKAQYKKSAPATYPAAS SSPSSPSS/RPPSTAAR/LRVPL*GSPD GLVGNRPFPFPGGAQHPPPTDWKRP HEGLQSLGASPPGIS*EPQLARLVNSWA TRDL
6367	20268	A	6421	1	479	RGFAVLPSAVEFFSSSKSHLDLETSPKA YKKGAPCSAPGSLQASLPGRNQNPFS NFFGVLF*DKISLCCQGN SAVIQS*LTV ASTSPGSDPPPTTTPPPHAPDTWDRHVP PHAKFYIFPYDR/SPTMLPLVNSWA QTVCLSSFLVMLLSLWLSLP
6368	20269	A	6422	11	242	FEITFSAVEFGSDHSILQTQFFG/SSD PPTLDS*VAGTTGHHHHQLMF*LFVEI GSPCLKWSVYSASESEPLYA
6369	20270	A	6423	488	335	SCQLAPWESIQSGSLRWLTPVLPALR EA/EBAGG*LEPRSSRPWAI
6370	20271	A	6424	454	229	RCPPASASQAGTTGVSHRL/VSLFL IVM*AEGCYLSGIWTRLNKNPFP*RK RQIQVKSTRSDIFFFYFL
6371	20272	A	6425	1575	1309	FESESHSVT/RETCSTGISVAHCSHRL GSSDSPASASRVAGITGVHHAQLILFL LVELEFHHVGDGLELLT*VTHPPWPP KVLGLQA
6372	20273	A	6426	276	437	CPHPPEPNDQWGPPPLGNS*IFWKRG PPFVPGIILNPWQKFFANPPKTLG
6373	20274	A	6427	445	240	RFRADHL/RSVG*DPGQGGT/LRLRK IQKISWVWHA GTLWPFNRDGSRLSL RTQMLGSWACSEGF
6374	20275	A	6428	114	450	LLLLLFESESCSVAQA/PSAVL/WILL GSL*PLLPGFQKFLSLILLSIWEYRGLP PYPANFFKFLVSMGFHHVCAGLELLTS GOLLASASQHSGITDVSRAQPVITFLK GLS
6375	20276	A	6429	380	224	LNCLFTQAGIQRQEGSL*P*SGCLKQ SLSLSPSSWVA/GVLECNKPGH
6376	20277	A	6430	509	228	PIHKGVSPPDPQNFSPFSRHLGGWL PKIDPPKKKVPKPKPRGKKK/PPP*KK KNPSPPDPFGPPPKIINKDDPPPPPP FFFFFFFF
6377	20278	A	6431	3	117	HSWESI*KRGA CFNIFIAQFTIADTN *FMCLSGDE*IKKGLGLYT/MDCWGVK KKETPLATTWIELKVNILSEIGQA*KD KVHVF*NNR
6378	20279	A	6432	417	271	LSKRTKPRNSPQPLPCSF*NDK/WP RVVVHTCNPTLGGGRMIT
6379	20280	A	6433	385	145	TPGKQSSCLHLPEKNDSCSEPPHLANL NF/CKR*YIPVNSKV*TSQEVFSYT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
6380	20281	A	6434	65	383	WPHSSSTFGREVTITPPKPCPMFK LFPNLLKKKKKKKKKKKKKKGGPDKK KP*GDKIKITRQKKKNFFPKRGKKNPQG KPKIKNNFWGGKKMKRP\KKKKCKEKK KKI*KKKGKKKQLAPEKKKGS
6381	20282	A	6435	3	454	EQRTFVRYTYK*TLERHIVRLSKSTL K/EKKKKKKFLAPATERQGIIPPKKIPI ELTVNF*KES*KKKKGAPLPNLLKKKK FPKIKYPAKLTFIRGKKKFPKKGQL GKFTVTRAPLKKITLTVNLKMKKGYLF PONTLYLAINHP
6382	20283	A	6436	424	410	NFFFPQGGGGGGFF*DKPFGNPSGL FFFLGGGKRGPPPPPKG/OTPPPGGL P*KNLGGKKEPKKFPSPFPFGGKKI FF*KPPPPPGFFF*KSPGGGGPPSVKK KKEKHKKKKKKKK*R
6383	20284	A	6437	3	214	EIDCCAAVWPKPKCPSADE*RRKNWYLI TMEYCSATNKNIQSP/VNNWKEVLIIM LS\KKSQAEEKHGI
6384	20285	A	6438	83	420	QSPF*ISCRYS/WLGAHAACDANTLGG GRGGAAWGQKPKTSLGNLEPGPKTADP RTSHGCELRSSSYTYALTGHGSPSTETA RPAPLFPFFFFFFQREDYKSEDLVDDL NK
6385	20286	A	6439	163	289	EMCYTTY/C*DRVLLMLPRLVSNLMAQ ELPPMPKVLRLQA
6386	20287	A	6440	459	431	DKRLRTPLATEKROIKTV/REKLQ SHYVVVKETIRK/CGIFHSWWECKM VOLLWTVSQVFKRLDLYNLATLTIPI COLQIKTSSPKYLMMKVSIIIRKKK YIKNKLCPSTDEMIKI*C*SIHTMEN ERA*K
6387	20288	A	6441	478	36	VFGCRVILVEKLFCEPLEVTPLRLGKQ LEKSL/WNPHDLNLSLHNQPNRNVH QNRIG*RRKS*CSE*R/TMQFINSLT LIN*IPSCHTAMDIIIIAQH/ITHIVEY YSAIKKNEIMCPATNVEALIIIGEIT OKQSIWRSPP
6388	20289	A	6442	464	206	LVORSGIHLFYSSTVPL*GL/HQRNEAD VYRNTMPTAALFLIVQNK*HNYLQTG BKINLGLPYIHTMEYPSVIRKNSHSIT
6389	20290	A	6443	414	216	CYIYTCPLTQQRBSWAT*ASSKEEMIN KLMHIITMD*Y/SSNKINKLQINTTWTN LKSIMTEISL
6390	20291	A	6444	7	411	SPYCLISFASRUGYCMQYLAFLWL LSRNSLHVFQHW/CQV*PL/YETV WQPLTKLNIILLHDSALTLGIY*K/DM KSYVHTKMCQTQIFIAALFIITAKTNRL CSSVGEWRNKLNYLQTMYSYSSVLEK\N ELSSHEKTWRLLRERSQSKAIYCIPO QYDTLEKALNRQ
6391	20292	A	6445	257	419	KSLPFFF/CW*ETGSHVTOVRVOMCH IALQPTQPLKQPSCLSQGSNDYKXHP TOACPY*RP
6392	20293	A	6446	20	417	HQYCFASFFFFNNFFKTSHSVAERAGQ WHLGSLKPLPLRFK*FSCLSLSSWDY RCMPHLDN*\*FLVETGFHHVGAQLR LLTSDDPPALAS*SAGLTGYSERAPVR

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6393	20294	A	6447	371	3	LFLRLRRGLRLQLNGIGRQ VIGQFL/RKTKRYLPYDLPIVLLCIYP R/BKIONLCRH*TCISMPMTALFIITQH* KYPCHSIGEWNLMLHIHTMBEYYAEMK RNKLLIHEKTYMDLKDILFSGGQRVYLK SSLSIKCIRPQ
6394	20295	A	6448	46	332	LSBHLAQSPILLKVCQVILTHQQFFESQ WSIHALSBRKTDANCRCGLKCPMSYIKK BML/WPGAAAHACNLSTLGGQSRHIA*A QEFKTIAPDCLY
6395	20296	A	6449	2	381	LCSLVPTHICISIFLFFFFFKDRALLP/ H/PCWRAGP*SYLTAASNG/VKQSSNL SRGKPLCRANFGSF/CPWFKKKGPTWM PRLV*N/ILLPQPKVRL*AAAHAGGQ GHDHTSLRPQTPLGKQSSNLRSKPLCR ANFGSPWFLVLEKRGSHHVAQASLKQSS CLSLPKLGDYRHEPSHRANMFNRLSLPG LRKADCLYFY
6396	20297	A	6450	2	136	KSVGCRWCG*IGAL/LHCWECBMVOL LQNAVQFLKNCIKVPHY*A/ILPLGIH PNALKATQRCNICAPNFIAALCATAKRC CK/PKCPISDKT*THIMKYDSA*KCKC LLAKRVNIWSPVHCWCBEMVQLQNAV WQFLKCKIVPHY
6397	20298	A	6451	314	72	HLPLTWSGCTKVKSLTGLSNSINPLP LIGIYRTFPFKTAGT/PPFFFLV/PKGT FTKIDHILGHKTRNLILKMI*LLKYIP
6398	20299	A	6452	54	350	LRSFCSALFCFTVLCLGLWSAVA*PR LPAGSSNPPPS/CLPSPSSWDHRLVPPH QVFLEAFFFFFF/CRKGVFVFLPGGV* NSGVKGTFRPNPPKALN
6399	20300	A	6453	368	172	WLTSVT/QRGRPRREGHLRPGA*DPG LR*STHLRLPKYWDYRRSQCPARPVL KEMMFHLG
6400	20301	A	6454	1	365	NILKLANLLNLN/VREBAKERTK*LV LNKNENTTYKDLWNEAKTVLHL*H*VKF IALSA*RIVSNQCSK*ASTLRNKKKSN LNPRLI*QQKSITLKREKSNKPKGSLI RSIKLITRLT
6401	20302	A	6455	364	1	PETRSCSVWRLLGGVQRDGHSLPPLSP RLGQPSHLSPSS*NIHGMPPPCANLLF KYLFLYL/FCFLFVMSQSHVSAQLKF LSSDPSALVQSVATTGMSRRAWQDII LQQQAATAA
6402	20303	A	6456	91	300	GHAHIFGRPRAGDCLGPRVDRDQPOQHE TLTLQK/KNNK*PAWHTPAVPAQZGAG ITGVSHRAPCPDN
6403	20304	A	6457	2	195	RFSCLSLPSSWDYRHEPRLAIPFFP/C FWNFKRGGFPLWARIWVNS*PRIGILL WPPKGNGLRA
6404	20305	A	6458	522	202	TENWRPSLQIFLTAALFLAKKWKQPCP STDEMCHKMYVHKMY*SVIKRNEVLI HSA/KMMIFENMLNEACWERPHIV*FH LYEMSRVGTGETKSLRVVV
6405	20306	A	6459	377	161	EMNIKCPSTDK*VKRY/LYIHTMERCS ALKGNEVLI/HTMTWMTANIMSEKQ SQNTYSMITVVCLE
6406	20307	A	6460	92	484	LLQACFLRTVLIDYHWAERGRVNCVL

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						MRMTVIIIFEDRVLL*HFGHIAVVRSG LISA/VKRSCLKPPKC*DYRCILQOV ETAFTHRSLFNSFLKRSKRVLLNYWKO FSLGFCSDSTGMALLNFS
6407	20308	A	6461	483	192	NGIMLILRANFQSTKRMICLLKSLTF LNCIVLBNWFCSTFNNYLFVCPAVIKHL VMAE/PVAHACNFTSVGGQGFRTA*AQE FETSLGNIIIRPCLY
6408	20309	A	6462	451	98	KQVWGLL*KQVWGLLESINMKLLYDLAV LNLGAVPREKTIIVITKTCTQMTAPF I\IKK*KKNFSIDMKYEERDQWTHVHT QHVLILK*SID/YAPVWNLNMLLSED SQTQKTHHCILSFI
6409	20310	A	6463	395	67	FLKFWCTHWNSS/DILYFVCSLLSNRS HSFPRVHKSPLYHSYALCPHSLAPTYE* AKHMF/RLVNFLELVE/TGRHAAQASPE LPSASNPFTSASQSAQTDDASHRAQTK
6410	20311	A	6464	485	220	FFPFTWSHSVTQARVQCNLGSILVKPLP P\OSSDPTDSAS*VAGIACMSHAPTHEI PSIQARQQHLQGEKKIHLISLPTASQV LRLLA
6411	20312	A	6465	1	371	ISIPPKKYLRINLITTVQQLYEQNYKTD KRNQGRSSNRWDGCSKRIKGLNIRMSVL SNLISVNFVILVIVPASYFVSIT/RLIL KFT*KCSRPRIVPLFHILLPLVVPFVCS FILCRPGASLVK
6412	20313	A	6466	489	175	YKIRIRISRCIK/GLL*LRITTHLFSHH WRGMAEKENADFLGTVAHAFNPSTLG G*GR/WNQFRTSLNANVVKCLY
6413	20314	A	6467	2	367	FGITLQGGIGKGDGERSHAGEGHQL REALKILARVILLBTMIGLYGS*LTLEL PAAAGSAGAPQQTGHPPGSHELA\EPGL GSGAGPAGTGTPTSLRGRKGGHATNYRI VAPRSRDERG
6414	20315	A	6468	472	260	TTLGSGAGSYGRHQPRVANYLFTICDR /SLITLLPRLILNS*L*AILLSRPPKVLV LQT
6415	20316	A	6469	88	435	RGVLLHMLSCPLCKTCFSSPTFHHH* TSFSPSTFFFLGLGNKVSF/CQASGGQGN LG*LKLPLPGLKQFSCPT/LPEKME*QT EPGPVGRHGLSYFPLTRG
6416	20317	A	6470	34	106	EFAPFLNITFYLELWIKLITCFHST AALSTR*KSPTCPSW\INKNWIHMEX YSAIKSNKALTYATTW/NKLENIMLSER SQS*KICI
6417	20318	A	6471	390	92	DFLIDAINENILKVFVYS*FISMCH/HYN *SLGFSNIQKSLIKTIMINVSLSFKY*YL IYFS*KKTF*N*RQGLTILPRLLSNSWA QAILLPWPVKVLELQV
6418	20319	A	6472	414	167	HIRIKTCA*TPSAA*FLIARK*KXPCPT ADEWINKMWVHTIEYSIAIKK\NKLII PWNENLIMLSGTGNTQKATYCMIPFI
6419	20320	A	6473	3	244	TTTTLIGTTIDALFPPELYTTFVTITLL TSLFL*\IRTAYPLRYDQILHLL*KNF LPL/LALLI*HVSIPITSSIPPT
6420	20321	A	6474	12	224	IASORPPFCYDVCV/VKRLCHESIVLIM *KKKKKKKKKKKKKKKKKKKKKKKKR

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6421	20322	A	6475	417	155	GGALGKKKGGGEPLFFH FQSFTENRMLSSSITCSSEIFGKRKSQL M*RPSSL/SY*EKLPLLASTTVISQRPS AL*VQPL/PTAKNL*LTAGSKGHYYPLN SKVFSN
6422	20323	A	6476	1	131	RTRPPTTRTRGRMLTTPVIALREA/EE AGG*LEPKSSRPAMAI
6423	20324	A	6477	830	513	WNSVESLGPADTWLPLFLGPLDIFLLLL IEALCMLNLWPKVSRQL*FEVOMMLA QSPQPTPSDPEKDLPLSLBQVS\G ILFLQ*AGSMPTLSAGSSVRE
6424	20325	A	6478	399	196	SRQSSHLSLSR*RYRCAPWMAFF/SF FLINIFCRDE/SLTMLPRLKLS*PQVI LLEWPKVFLQQA
6425	20326	A	6479	1	411	NTGIMPANTVSIILLIDGELVTVTKCY LRNTFCGFSGSGSHV\QTFWIGSTLLD AIKSL/R/DSREDGKISTLIGLRKK*1P ILMEDLVGFKTSQREGTVDLNL*ELQ VEGPRDETELL*PQDQCMDEKFLMDE
6426	20327	A	6480	381	162	AGFTHEHFFFL*DMVLICHPGYSVA/VQ SWLTVASNSH\VK*SSHLSFPKH*DYLG AVHFRMASNSPGLYLLQ
6427	20328	A	6481	379	85	SILFLFHPINFFFFFF*ANETIIPPPH \RAFKVVRVVGFFLADSVWFIKRLPQY FFFFFPGFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFLSVC GG
6428	20329	A	6482	355	117	PKVILSPPPLPRKHDPREP*SQTNF SIFFLVEKDFPHVAGLKLSSSTPS VAS\QSV*ITQMSPHMLQVLLSL
6429	20330	A	6483	402	97	TAFHLDTYKKS*RYTINQPLYKPLF I IAKN*K*LKCPRAKQIVA/WCHTIT EYYSARKRNVLKYTRLMNLKSLMLCK RSQSDVTVYVIPFCHS
6430	20331	A	6484	714	365	NGFALVAGAQV/QNCDLGSQRLPPIFR QVSCVTLNLS*DYRSMPPHPANFCIFSR DGV*SYWSEWSLTPDLGLPKCCDYRE P PCPANAKSPTVEETHVTYQAYETMLLSD HDESG
6431	20332	A	6485	408	146	LKTETQTETCPPMFIALFELN/REWNQ PQCLSTDEWISQI*YICIMNINSDIKRN BALKHAVICMNLKNNVFFISPTERKKK EKKK
6432	20333	A	6486	243	11	QHSQEQEYSKNFFLSNRVLLCHPGWSA VAH/SRIETALNRF*SGCGLPGLMDY RRVPLLAQANTR*HSL*SCPA
6433	20334	A	6487	403	161	DRVSPRWPNVSNQ*SLK*SAVLSLARC WDRRPPSCDASHKIS\GRGNRQKQNT CMYLLFILPLKCYMCRVMEYFKT
6434	20335	A	6488	292	24	DWRCHMAIPLKGGK*QGCGENTGLRY *W/MECKVAQPIQENV*WFLQRIANIKLS YDPDF/PLLGYPKE*KAGI*TDICMPM LVATLPSG
6435	20336	A	6489	3	203	SSWDRCIPPCIANFLICRDR/SLATML LRLVLNS*TAQVLLPWPCKMGLLVF YGGIVLSYVNIS
6436	20337	A	6490	413	30	RGF/YQPGFLGSPPNGLGFG*EVFLPL PPPPKPGPKGSGPRARGPGQAPPEKE

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						NQRGGGPNRGRGLAKKKGFWFG*GPAKG KKFFFFLGGAGVGLKVLIPIKKKKGFPF PPLFFFFFLQ/TIHPING
6437	20338	A	6491	101	335	SSSFLGFFPKYDYRRREPL/WPS/LWQFF RLNIHLLYNPSPILAVYPREMKICDLI KSCMRMFTVAVF*ITQIWRQNPVF
6438	20339	A	6492	532	127	STVFRARQLPCLHEPGRGSSPVPVFTSI LTTVLPFPSSRYQQNGPCILSSPKLSPS PRLGTQSPFVHKSFPCPLSPKLTVP ALPSTGSPQSLAQKHSLSLLEHTHTP PAPSCNPESWGLDATALSTCTCYG
6439	20340	A	6493	399	1	LCPAPRGGVYRGR/ESSLSWDLGHSVQA SNPLCLPTPASAMVDAPPASLPSRRS ILDCCISSEQGVGMGDAEPGAG*NLIV OCLRLPLEKCSIWAGVSRFSWYLSQLP LARKGKSNPLSPFNEKMRPVVS
6440	20341	A	6494	319	75	KKIWGLPKKKFGLQTRRCKNFFKRPDP PFFFFFFFFF/HVAIFLLFCRDG/IA MLPRLILNSWP*RILOFNLKVPGLQA
6441	20342	A	6495	333	190	LFFFFFFFFFFFFFFFFF*GFFFFIF YSFRDGVLLCHDGSAAADS
6442	20343	A	6496	1	299	LPRLEYSGTITASNSWAPALLPQLIK/ YNYFCOC*GRVTLVPLRLVLSNRQIVL PDPFPPKSAETIGVHHVWPKLIISNEKT TKSCGALLAQQISS
6443	20344	A	6497	51	266	PVVLTPSSNRLKSPPCDARFFVLFCFL LFFPKN/RLAMLLRLVNSWP*VILPP QPPE*LGLOQVQATMLSS
6444	20345	A	6498	366	78	LLAHCHSNNKSLITLNNFATVYQPSN TVTS*F*MSSIMLILSSP/CYGTSHSY LFYALKKIFCED/RGLAVLPSLV*NSWP QVVLGWNPPKELGLQV
6445	20346	A	6499	37	396	FPRPTRPKSSSPAKATQNTTSPKRRK SKQKNGTIVIIIRVKNQRKQEN*KLK Q*N*EQ*KINKISKPLAKLI/KKRVKT *IANIRNERSITT*STDIKRLWKYY* QL
6446	20347	A	6500	706	394	VFLLPELAVQMHNLGSLQPLPPGRRF SCLSLSS*DHRTTPPCPA/NSFVFLVE TRLHAGQVCLKLTSG/DTSPSSASQA GKGMSHRTQPIELFYSVFF
6447	20348	A	6501	403	216	LINLVSPK/NNLY*HYTTVLRVTRVPLSP R*ATVTCYTSWPEAASDPQKMTFPHC DLFLNPH
6448	20349	A	6502	377	116	LEFY*EN*PLNLPLPCLPFPDFNNGSF CHQKKHFFFFFFKSLSV/RLCCGAI PAHCKLCLLGSSDSMKNFLNAPSFPNLA FNGL
6449	20350	A	6503	3	401	CVQHLKASWSSRWAMWAPHSSEQPAGP AAPNGEGLSTRASCGCGCTGYPSASGPP ALCSIS/PRP*LPERRAGLATCSPPCLS LPPPWAPVDEPPRVRVPPAPWRPVPS TTQGLRSASARHRTGRLQLHQ
6450	20351	A	6504	406	55	WPKGTPPFRPRKEGSP/PPFPKVFIL TRQPGQ/KPFFFFPPIFKLTRPGRPP* FPPPPQVRVAKPP*PQSFVPGALFPPP PPPLKGHPPRPGQKKKKKKRKKRTRK RGST

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6451	20352	A	6505	3	281	FFFCDRVLLCHPGWSAMVRVRSRLTATS /SFLGSSDSHACLSSSDYRHLPLLAN FCI FLKRGQFTMLPRPVSNP* AQAMRLP QPPKVLGLQA
6452	20353	A	6506	1	247	LGSLQPPFPFG\SRHSFASASQAGIADN SHRTQSIIVFLKTNKFP* IENMDITLS CTTAYKYELRHSERKICARSLTEKL
6453	20354	A	6507	34	47	FDENLTPRHRLTLKAWNKERMLTARK KKOII*RSSNLGDRLLNEBASWEP* CK KSMQETIQATGOWNDI FPKVLKCKNL\H SKILCPAKLSFKYGBEVIAGFPKPKWRE FTVTKPILOKC*RENQRTFDLTOI
6454	20355	A	6508	403	106	HYVFPSPSPS/YFFSPFGKRGFFPNPF ILVSPGFFPSPLF/KPPPEFFFPFAPLKK IFFSPPERELKFFFKGPPFFFFFFF
6455	20356	A	6509	389	230	LSFFLLFFDRKVSLLCNPGWSAV/VITFLK RSSCPGLPK/SQSHCTKQPGF* KYIYF SFFIK\KR*SLTTLPLRVSSNDQVHS ALMHIPKVLGL*AVAHAYNPSTLGQCSAS WIT
6456	20357	A	6510	101	419	ISPPPPPPFFFLKKFPFFPPGWRGGGPF* LFQTFPFVWKKIFPPFPKVGGFQNSPP PFPFFPPFKKGGFSPVCGFFFTINPKK/ SPFPFPFGVGLGWFPPFPWDP
6457	20358	A	6511	41	376	EWKCTKGGAGGKRAAGAGGATGRTVLA IQARKRPRKREKHPKVSQVAQGVW RDLVLLQLPLPQOLRVSLCHPS/WCCGV VSAH*NPCLPV/IKDGVLPCCAKGS*TP GL
6458	20359	A	6512	2	332	WERVKIATLIGFWK*LI/SGSSRTLMD FERFKTSVEKVIADVVEIARELELEVEP ENVTLLQSHYKTPGTIAFSRLSPDVS LYSQLPETRSHEWQAASKIQPKASTSQ
6459	20360	A	6513	3	294	FFFSBMSLSVTQGVWNNLQSLQPPF PEFKQFSCLSLPSWDYRHAPHLA/NC FCI FNRDGVLPC*LGWVSNSHLGTGNS HCTOPLLALSFLHG
6460	20361	A	6514	1	526	FRLGRKPR*GVN*FVWSRGRPGSVGAE AG/RS*SAPRRLHHAPGATLGLSAG RSSARWIMERASGLSPGGGLGATSRQMS PQTQLNPPDHGDKDCLGRISPGSGKI QAAQGLPFPFTSLAPAQGLRLSLTPWGL QTPSEHSPBGIHLQAATEAVLPSTQN LITKRNLM
6461	20362	A	6515	747	451	QAGVQW*TLASLQFPFPGPK*FSCLSLP SGWDYRVRPPNPNF*FLVEAGTHHFG QAGFELLTSQGPASASQSGAGITGSHH TPLGVIALVGENIQ
6462	20363	A	6516	444	3	EGGGGFPFFPPWGGKPGKIS*/PGGGG SNKPKLPCLPFGGPK/GNPPQKKKKK GFPGGVVAHCNP IIPALWEABAAGLP FDAGRYPGGRREAVREAGPGEQDPE GQV*GDPRGCGAAHPARGHPKA*RGAE GSSPGLPFK
6463	20364	A	6517	257	575	ASSVTWAGVRVCHLSLQLLPLGPK*FS CLSPFGSDWY/GHAPPGPAKFCITYSDG VSLC*PGWSQTPHLR
6464	20365	A	6518	337	389	SQHPV*ISCLDINPALASQASGITGVSL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						RALLFIPFK\MDSCYVPQNGLE/PPELK RSSHGLPKPWYTRHEPQAQPVCRFIRA TKCAYVSTQALSAPVQGPNTPPAKRGL PCQPPQSPCPSLGHQLAGTPPVE
6465	20366	A	6519	61	323	FWMDRVARKGSIRGASLELP LGGSVGGH GSCISMVVGALGHSS\THV*HHTHTHTHT HTHTCTYNHTPSDSKSSILDKEEASG CMT
6466	20367	A	6520	399	101	KIQIKATMKY/HNIPIRMGFPFKLSGG /C*RCRK/IYTLKHQC*KEBTWELWK SVN/RVFLKLNHPLHSEIPLLLGTYP /DMKT*TCM*MTAILLITITS
6467	20368	A	6521	1	276	RTRGFBGLRFFLGFFGTIVLLCCPNASAV E\QSWLLAASASCLW\VK*SFCLSLRG WDYRCIPPCLANF*RR/GSNAQVILPP QSPKALGLQT
6468	20369	A	6522	280	277	GDDPSCSMGGCHCLASRSE*GSVGVGPS KPGAG\YNLLVCYLLRPLEKKSIRVGV QPSRCHOSWLPFDRKNGSPPTCTYNVR
6469	20370	A	6523	2	327	SLFSS*D/YRHIPPHGNFRIPCR/SAL TMLFRLVSYSWQVILLPQPPSVGTST SHCPQPCIMFLKADLNVRQCFRCALAP EPTIQDFPLRDDVAFPCIGASAPWHLA
6470	20371	A	6524	298	414	PGPQSETLTKKKKGSGRLKGSNFTPAGM ESNIFP/CFPLSKSHSACASVON/P*W LTAGSLQAPPPPRFKLPSLL*VALYASP TLSS*DYRCITPPRLNAPCIIPRAGVSP CRSCKAAVFNLLDTRDNFHRQSFRLV AGDGRM
6471	20372	A	6525	376	180	KCKRYPGGVAAHCSFS*DYRHVP/RPG YFLHF*QKHFGQAGLDLPTSGDFPASAS QSAGITGVSHRTQPLNFF
6472	20373	A	6526	415	86	LYLPYDLAIPFLGMYPGRKKCAHTKIC TRIFTVVLFIARK*KRKNPSTREW/I KMNNIYTVSHSVIKRKELLIHASMILV H*/NMIFRNIIILSDRSQMKITYCMVPF T
6473	20374	A	6527	391	166	FFFFRDNFSLSHPGMNAE\S*LTVISN SNSQARLIFPKFLRQGINLLTRLVNS ELQGLISSNPAKVLGLQA
6474	20375	A	6528	544	176	TMRYLTFVGMALIKAKVYT*Q*QGR E/IGTL/LQCR*ECKVLPLNKTWVRF KLIALSLPYAPPLPFLSLGOLFSLGSEN CAQLRSVYRKAVONHQGVSGCAGPQDS SHSAPVAIPTAQ
6475	20376	A	6529	392	139	TYVRNHCK/ALGMVAHANNPSLGGHGG QIT*QGAATKLSHWSGLGRESFMLECY SRSCSCFCSCLPADCTSLTDSKO
6476	20377	A	6530	362	87	NGPPPPFFFCGEIDKLILLLNKCR/RPK IAKIVFKKKNVGLI*HYFKAYYKGT IKLVQFWHKVRKTDQ*SRRESPEIRLHI YVLVNRDASA
6477	20378	A	6531	1	346	APTRPRLKTKLTKLKTINLQLPYDPAPS FLSVYPREMT*RFKICV*MPMASLF MIVTTO/NVPRCLPMGENLNKNR*\*FIT *YHGMKNT\VMHKTWVNSORIMANEK SQSLTY
6478	20379	A	6532	3	294	FFFFRDNFVLYHFGWSAVV*S*LTAAALS







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						KSPLPPEAP/PAPPLTQDCPEFVSNFGG KKKTTP/SAKKKKDPPTS/PSPPRH* I OGPPGFSPPPLEKTTPPKLLGPPKKKK IFPPPGKNTFLKGPPPPPPPPPPPP FSLFPVGVMSRWLRSEADLCGECYS
6508	20409	A	6562	1	356	FFNFPTIYLP/NFNRSLALPRLNGV QMSDLGSLQAFRPLMPFSCSLPSSRD HRRPPPLANFLY*RWGFTMLANVS IS*PO/CDPPASASQ/STGITGICHGTR LIPRNPMA
6509	20410	A	6563	416	84	LSPSSW/DYRPPPCLANFLY*RRG PTMVIS*PHDRPTSASQAGITGVSHL TOPILSFLKSPFFTLNRFNRVCIDSEL LLQCKDFYLQKFNHIAFQETTHCHGVH Y
6510	20411	A	6564	2	51	FVVREMGKTKVLRYSFLKLVKIKK*DS TFWKGCG/GETGNLHKAN/R/SI*QYL KKLYVHFLVFPVIPLEIYLKXKLLST K*LFVAVIVTEK*KKKRG* T
6511	20412	A	6565	2	511	VRN/SCAGL/LHTA*VTPRLTSECKA QQVDETHRN/LQRLQALINRGPILLH NNTCLYAKPMQLKLNELGCEVLPHLSY SPDLSPTNYFFNHLNVLQGHSHSTQGN AENAF*EVFK*SMDFYATGINKLIS/H WKKCAGNOSYED
6512	20413	A	6566	3	248	GDYCT/SMVLVAFIVPK/TWNPUSIS K*TDMMWYLYPVEYILAATKTKPC/SFS ATWMLIEDIMLSKPGTER*ILHVLVLOG R
6513	20414	A	6567	3	258	WRDHSLSHS*PFLKLNPSHLSPLSNWDY RDVPACPANFEKVL*K*GLIMLPRL/LL SSFPPEW*ILSSRLPASSFQSVGITENH CS
6514	20415	A	6568	392	166	GGGGPPRGGLRPPGPPPPFLKNKK*/R PPGGPGPLFPPPGGGEEKFFYLGQGNF H*TRVGPPPLSGGKKCKRG
6515	20416	A	6569	234	411	PGAVMHAYNPNTLGGQGERIS*GQEFK S/LGHTVRPELY
6516	20417	A	6570	1	175	FLQHV*NKQPMDSQYIGKIDMNTLID LEKNVKDL/LITQTEVELSGENKIPIL PG
6517	20418	A	6571	392	140	LPSSWDYRHVPPCPANFVLLVETRLHV SQAGLELPTSASQAGITGVSHARP/E *NSIRKATITQRLGLQVLRKLVRC
6518	20419	A	6572	2	228	RCTQSVATLFLLAGVKKQPCPSIGG WINKL*YILIMEYLVVKK/NDPSSHK TRGNPKILLSKRSQSKA
6519	20420	A	6573	412	100	ALJSHPIGGPGGVPSKIPNPPPCPGQ TPFPKPKLTPRGFARLPFPLPKKLGK EKPFPNG/MGVPLN*IPPPVSHFQVQ NPPSKKKKARGFCLVNPSSS
6520	20421	A	6574	406	257	NKRKKTRKMLDSIVTRRHHSQMRGY SAP IQMAKV\SNRQSPKFWVRQROTSL *HC*ECKIVQSM*TLQKFLPAIVFLC IVHTEKLRFTQOP/CT*IFLAALLMIV/ RTV/XRLVCPMSGWLSKLN*VNLSPSV
6521	20422	A	6575	370	68	EQGSVGRNPSEPGPGYNLLVCR*LRLE KRTIWAGVS*FSRCSLSRLVLRKSGSP

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6522	20423	A	6576	1	259	NP/CTS*VRFSGNLS IDLTDLVLRPSITVT*AVVWCNLSGL*P *PPG/SGDPSASASRVAGTIGQHHRNL IFVIFPVEIWFHRLVYFHTALKNYLRGL NL
6523	20424	A	6577	418	218	KGKRLGRVVPFPCNSTLIG/GQGQWIT* GQAFKTSLSANIVFPLM
6524	20425	A	6578	1	401	EKAGCSYIL*P*H*GRPQEDHLLIGI *DQPOQCSNLSLQRM/ENLSWA*WFG IVAHACNPSTLISGQGRIT
6525	20426	A	6579	3	356	HMDYRHFPPFPV*HFFHLLKQCHSLLA SPNLTGCFPSISITESTLSLFIYLETIV *DLQCSYVNERG/SLCCPCWSRAPGLK RSCLRLFPSSWDYSRLTFPHLANYCILG GEGESS
6526	20427	A	6580	411	158	IGSVAQARVOWMDLSSSDFSAN*APPOL KQSSC/VASLPSRWDT/NKCTPPLDLANF YIFFVETGFPYVARLADCFYPPPL*KMT GSY*VPTMCQIPH*AFYKF*FI*FRVGE DKNSLPAMQHRRLSLQKCKYN
6527	20428	A	6581	399	218	GGABLKVFK*GGGPGSPPLPFPLOKPRE KGPLWFG*GPPFP*GEPASPLKNK*/ PLPG/AGPFPVPPNWGGGFPYPRG*GFG* LPLPG*TLARGKQKDPVFKKKKQ*NVN KKKARK*KS*QEFFFLKTQSCRFPRAK VOGNGSYPKCPQERG
6528	20429	A	6582	392	214	GSSDFPNSTSRVAGTIDEVLPCSPGWS* NSW/VSK*SACGLPKMDYTREPQHLA RSNF
6529	20430	A	6583	390	257	PKRFPFPAPFC*FK/SLGMLPRMTSNW ACAIL*RWPPKVLEKA
6530	20431	A	6584	65	251	HYFNSFNFFLGGSSNHPKTPG*FFFFL TFYKNN/SLTILPRIALNSWAGLILPW PPKGLGL*AOGLILFWPPKGLGL
6531	20432	A	6585	2	143	RHMFCLSSP/SYFL*RRGFVILPRLFS KSWVQVILMFWPKVLGLQA
6532	20433	A	6586	142	334	GRWISQLILNPTTRSVLKGMSW/MACV SETNPA/STLQORGRIT*GLKEFKTSL QNMARPYLYK
6533	20434	A	6587	485	377	RTLSCRFFILSLIFRPNFYCPTILKF/ H*VFLLSFVFCY*GHP/FEFFIKVFFI IFFHFKVFCVKYLLFFILIASTYFF FVNIFSFKKFVSVMFVLLIEMFYGRFT IILR*F
6534	20435	A	6588	241	251	NSLFTKKKKKKQALKEPILRAGGZBG ITTFKQPKSLPCPFTKAGREKCPSP *NWFF*KGPPFFFFFCKE/RSPMTLPR PASNSWAQAIICLPQPPKVUGI
6535	20436	A	6589	429	54	YPLPLSLPTFFPFSFSSPLPSVLGFPLP SI/SSFPLSILFYLLSPPLSPSPSLF LSFFLSRVSFCHPG*SVAQSRLTATS I SWAQAILP/CR/NRDFTLMSRLAINS*P QVIRPFRPPKVLGLQA
6536	20437	A	6590	411	137	KCTGTTTNCSEHLGSDPFTSASRVV GLQAHHIQAC*F*LD*LD*LVNRM ESRHVAQAGRLGLSSDDPFTLASQNAI TEMSHCIF
6537	20438	A	6591	412	196	QPOFPGAKKTSGGGFPI/NGIQPPPG

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6538	20439	A	6592	28	400	AKKYNFFFFFFFFRQALAMLPVRVNPQQT*ATLLPMPKKVL*LQA IMPNCPPKWLITTTTTFF*EQSL/DSV AQAQVQ*HSLGSTATSAFLGFK*PSCPP AFLE*LYRREVPTHTNFCVFNKD/MGF TWLARLVNSG*PO/CNPPASASQASIT QMSHRAQPHLFLVKMEKPPPNFLFLILM NQSIHTIYLLAFYR
6539	20440	A	6593	414	23	OTHLFRRFFPGESDPFFPNAPRLPFLGA LKKNFFPPPRHKNLFLKAPPTFFFFPK RSFFPPQWCAIGLSLQPPPPPRFK*PFC PSLPKKHGYRPLPRPKGF/CTFFFFVZ LVENGPHFVGODGLDLLIS
6540	20441	A	6594	91	274	ILHNS*PLGNYHL/MLGVAHARDLSTL GGGGRRIAGGDDFKTSLGSKQGSISARK KEKKKK
6541	20442	A	6595	391	251	HLKRCSTSSVIREVQIKTTTTTCHFS*K R/SEINMCW*ECQTELGALLIRC*WD SEMVPWLERKEYLKQISTESSWADATP LLDI*P*ERCASLSLRKGGYRPPPEL ASFLIGSYI
6542	20443	A	6596	465	268	ILLCHLGCSAQAQD/LTLCSLKRSSHIL SSSWDSRRGPSHLTKFP/C*RGALNT PSLV*NFPAQAL
6543	20444	A	6597	3	229	CIGSPQPCPOLK*SSHLNLTFRK*LD YRMPPRSANFLFL*RWGRCAVAQGLEL PSSSLPASASCDPQPVLYF
6544	20445	A	6598	122	418	ITVNELCHIMCFTTTTFFPKQMLLGTQAG GGGGKING*LKPKPPRLKGSFWLTLGG WNYGGFPD/HPS*FFFFLGGKGYFCPC PAGGKFFNLKGPFFFA
6545	20446	A	6599	1238	930	FETDSCSFA*AGVOWRNLSSLQTFPPVG SNNSCASAS/RIAGITGTHGHARVIFAL LVETGFHHIGQGWRTPGQAIRPPOPP KVLGITGVTSRARALSKHFV
6546	20447	A	6600	398	78	PSSPFYLFIFROSPPFFARVEKGGHFG FPNPPPSGLKKFFYAPAPPGSKAPGGP PA/RFYLFIFROSPPP/CCPGGGRKGS GFPQPPPPGVKKIPLCPSPPRK*GPRAG PPRPRKI*FFFFSSLFFFFVRRMGFTML PRLVNSGACALCPDPPKVLGLOV
6547	20448	A	6601	3	473	FKKQKKQPPKAGQ/QLNPSKRNKR PGAPRPGPRGPKKGGGGLGSPQSPQGG EKWTLKGGPNLPPRGGGLGARPPPKIG QQFLPKGGQPGGTPPPPLFFFLRLRS PALSPLRECSKAL*AOISS/SPPARVGC PSPPAITRPTGLTVSPGNS
6548	20449	A	6602	398	156	NGRKITDVKPEELGSNVVTRDTLPTGTA GAF/O/RGYGYYNKIVTVKKGSLAGVS TVLAA*VLFSYCLSYREIKIKHQLLRH
6549	20450	A	6603	380	77	PPPKESPPL*NEPPFF*KKKVPPFPGR LPLSLFFFFF/RDRVLCRPGNSAMV HGHGLSPVNFICISTRNAL/SHLPRPIS NTWQAIRDS*PPKVLGLQM
6550	20451	A	6604	352	204	KRGPKI*NPFFG*ROSLIMLPVRVPSNW AOMILPWPWP/KVQGLQA
6551	20452	A	6605	631	357	FFF*DRVLLYHGWSAAR/SLLTTTSA SWV/KQFSCSLSPSS*DYRCAPPCPASF

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						CIFSRDRGFTMARMVSN*PQVIRPPG PPKVLGLQA
6552	20453	A	6606	3	397	VIHKLQRCSAVPLRAPATFLRIGTQT KRNVKCR*P/RETQNNLLDKBQDFKTYQ KATYTKAVWQOEDTIEQWDGIESTEKK FHTQAGGORDSHSDSVRKRRKESLFFP LAKGILLFPANLGGTQKGISIP
6553	20454	A	6607	323	35	YLKTKKQKPGYLAALQGLTFEPSPKNTQL QNRPNCTHTHTHTHTHTHTHTHTHTHTHT RSISFCPSLDSI/SP*VLTSSNSNPPT LKCC*HFTSPCL
6554	20455	A	6608	439	252	LVPPLFFPRSFLLSPPKKRGPKP*F GPPRAPYPPPF/V*RGPPPPFFGAPKKK IFFSPPPG*KCCFF*SPPPG
6555	20456	A	6609	3243	2602	FFFGRDGVLCCPGWSQTPRLQSSSL L/PKC*DDWH/RATSSGLQVFLSICSI ISIFPMPSICDKSTKQPSN/PQRAYILV G*R*VIYLGVLVFLVFLRQHL/NTVA QAGVQWNLSSL*PPPARFKRFSCLILP RSMHRRRLP RPANFPVFLVETQF/TIL ARLVNS*PRDPASASLSAGIMGVNHR TWPILVFLHPSVFFKVLQLEYL
6556	20457	A	6610	81	395	TWAALKLYSTCIFSSSETEPDVDSQSIT DTTACIMEPGLW/YRSILNLT*FFHFF WRDQGITLLRLVWNSQVLSLPPKK VLGLQASATAPNISFILREGIS
6557	20458	A	6611	1	126	GRLRQSNHLNFGRCRCSEFRLHSCPAW ALERDSVSKK/NKNGKRCPLRLKTKLK GEKRIVV*PGGRGCSEPLRHHSCPAWAI ERDSVSKKKMD
6558	20459	A	6612	389	67	YLFMYLF*/DEVLLCHPGMSAVACS*LT AASNSWQVILLNSRFSWTVLLSSKI PVVQGSTPCPCYSWHPKCLQLQGLGL DCSSPKYPGPGSLAARFSLPKWNV
6559	20460	A	6613	1	384	RCFKVZDLKRPFWNTQVDPKSNCKPC KRLKRRGHASLPWWEKRRPGDKGRGW NSAVTSQGT/VEATRWNKSGQSVLP*SL *RERSPV/ELAHF*QRLAMLPLRLVANS PQDISPPWPFALGLQEP
6560	20461	A	6614	385	174	CLRLSALKKPKLNSWY*K*LYINNEY*SA LKT\NKGTLSPAI TWNNLDDILLNEISQ TQDKHWNLSLCTI
6561	20462	A	6615	1	370	NHPPALHSP/LKRRRLPLWALGNIN /FTV*GLRGALANSXYVLHDTYGV SPHFYVLSIGAGFAIGQTH*FPLSG YKKKKKHIRGGGTQNFLLCPALVQREX VNPFFALINLWG
6562	20463	A	6616	3	342	YRHEPPHSAIFALYKL*K*LIYALKTG KVYVYKLYLNKAISKQ\SYNRSLSLT* *PRVKRKS*PGTAGHTCNSTLGSQDG LIA*VQFEINLGNLAKPCLHKKKKGA PV
6563	20464	A	6617	1179	915	FFFETESCLVTQAGVQRDLGSLQSPPS G\SSDPQLI FVLLVHQAGLELLIS*SF ALASQTARI TGVSHHQALVNSDFKSN LFCCL
6564	20465	A	6618	3	390	HASVMEFLPYDAIPLPSIYFKELIARF *DLCPW/FITALFTAKRNRQLNCPSV



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						QPYM
6579	20480	A	6633	740	776	CSFPLKKQTSRAAVQAQVQWCHYSSLQ PSPPTLKKQPPASASQTV/KD*GAYFWCC FFLFLKRWGL/NSVVQAGVALPDLVTV RRLVLPISLWAVEPALWAAQL*LL/SP CPLASQSPRHQTQSPHQKCFPDLGLGLH LALRSSFPGLERPTLRLPPGLASPHI* ATWLSWPLPYK/PPKRWMLV/KADRF PFL*GTRKRSVMQWTHAKTLQETLYSG PEAQAAASYTDF
6580	20481	A	6634	2	296	FFPLKQSPALVQAGVQWCHYSSLQPP PRFK*PSCLSLPSGWD*RHAPPRPAIFV FLVEMGF\TMLATMV\*IS*PGDLPTSA CQSAGITGLSYTRAP
6581	20482	A	6635	407	212	GRPR*TPPTLGGKKKGAAPPPTKKKKPF LGRDSYSQKKPFF*RNKTRPGGGGPP GIPPPPLKG*AKKKGLRGPFPFV*/NK PPPPPPGGNNQNPFFKKKKRSTR*IK IRISRFILYFFFFFLLERGPGCSPRGG GGAPLSYKGLWPPG
6582	20483	A	6636	20	223	PCKKLPQPLQPSAT\TLISQQPILTKRD LLPGKRL*LABGSDDSYQPLVAKYFKIK GLSPGRNKLANI
6583	20484	A	6637	866	647	FFLDRLV/LCHLGWSAVNRSWLTAALTS GLKQSSCLSLPRLDRHREHPQHQAANNIS *SSWDSNMQFRLKTL
6584	20485	A	6638	398	26	KGAAPPNIFLFFFLNFFFFFFFF FFPINFQLCLLYRALHFNKVKVNNNF/ PLNFCAYYHPL*NM*PSYISFQNLKFT LI/PCVFNLSGIYFNVL*IANF**G*LI LPGTLYLKIICYFTTN
6585	20486	A	6639	1	341	NADYRHLPSCSANFFFLNFTGRCQLPRL VLNSCPQVSHHA/KFLFFIFFFLFLEEG GFVGGPRLLEYRGSLQP*LPKLGSTCL TLPGK*N*RGEPLPPARSSFFFIKFFI ET
6586	20487	A	6640	391	118	NANFRKSPSMGRIL*NSLAWYKTLCD/ RKNRSNMQTKPLD*YFFKKLPQPL*PSA NTTLIGRPALTTSRQGLPTAKTL*PAEGF DPMILSLF
6587	20488	A	6641	352	285	KKKKGGGGGGAYSIGTIF/CFFFLNGVF LGPAGVQWQNRSLQPPPPGVKLFFFLS LPSH*GPRHGPFRPGMITYNPF/CPT/V RQGVLLCPGWSQFGLK
6588	20489	A	6642	433	64	TSNFFLDSLFFNFPDLGGGLKGFPS FFFLTKTFFFPDAGQWRYFSSL*PP PPKKQFFFFLSM/WPRGKFFFFFPGL VFAGFHRVAQGLKILSSGNLPTASQS ARITAKSHRTVP
6589	20490	A	6643	424	11	PPSIFLAPPPSRGGGPPPPKKK/OSPP KKKKGGGGGPKNP*PKKKGPPKKTGTF KKNPPQKKKKKNSPPKKGGGPANK*KP PPRPQPFYFLTFYFKIFTYIFLLKFLLF YIIFFFLESKQGRPLAI
6590	20491	A	6644	411	2	PPLRIWLASPPSKIF*PQPLHI/YFSPF PP*KFFFSIKPLILGIGGFFPKFPKPKKS FFPKNPGVF*NPP*KKKIYSSSP*NP ADPKILKTDPPPPPPPPPPFVEGSRV



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						TAQARTERTRTGRTRGRTRG
6591	20492	A	6645	34	381	AKLGTRGAARQREKIRVRI*WKFIEIS QFTEYTKNLI/NVIDKLL*LVYMFSKIT GYKVLNKNINICIPHKHTNOQQKILNMPF IIA*K/TIK*L*INLTGDTQDLYAEIYQ TLKAEI
6592	20493	A	6646	17	448	HFYAKLGTASLS CSGHPV*ASQPLYL PFOASAMADAPFFARLPFPHLSISYCCIS NMQSGVGVGAEPAGAGTLLV*HLRPLE KRST*VAVSRPSTHYSLSRLPLARKQNP OTPCASWVRQCPTLLRLALHGLHPLSNQ SQGD
6593	20494	A	6647	462	336	SLRLPGSNDSPASAS*VAQITGPCHRA RLVEFPLVEMEGLS
6594	20495	A	6648	447	62	KDDIWIATHTNNRWSISLAKRKV*IKYT MKYPYTS IKMA/IKQTNEN* KSSSSIKC W*BCRTMRTLHCW*HITG*PLWKTVM KFI IKINLYPYDPA/TCTQMPFA/ALF IIIKY*KQSKYPSGYCVPA
6595	20496	A	6649	3	1492	LAYARAFDDTNTKRYPDNRVRLKEVF ROFVEACGQALAVNERLIKEDOLEYQEE MKANYREMAKELSRIMEQI/CPPGGED ERLTTFPSHLQRHQWDSNKNKNGSRDQOL VGRGVITSHGQCVGT*CFVICKRLMLSKA NWDGDRAG/ERTNGGRKK*RTTLFLN R/RPTYSKKVHLFF
6596	20497	A	6650	495	170	GAEPFASQAGIAGVS*HARLESFFSL DSGRVNRGTETVLKLYGVTITTI*SIFFF FSFF*WPGLSQLPPLPGFK/LSLSLRN DYRCPAPHLISL
6597	20498	A	6651	9	222	QTTFRPERRNSGDPHTLSL*SSSDYGVVC EHANLIF*K/CFPSGGLALLPRV*NSWA QAVLPFPWPLKVLGLOV
6598	20499	A	6652	241	833	KKTPLAMNNPWPFPFPHPLTKIVQKA G/QNGCLSGHDLSEIRPAQIHNARGE VLGSSSLGKELVFORELDISETHIPE AOEVEMASGHFAFLHVPVPGRAPYCKA SLSASSSLEPTPPRDTAISLRPPSPAPE MLTQHGAAOVEDHPG/G*QSPSPHSQR PSPOKDPQALVIASLSRTERKOASHG TRPG
6599	20500	A	6653	1	398	PPFDIGSHSLTQAAVQ*HDSHGSLHPR LRGFK*SHLSFSPDS*DSRHTPRPAN F/VFVETFLHVPFQALNKNLLPAT/AT SKSARITSVSHVQPVBSIKW*NNISNL IKCFLLPYKKYKCFINTKVFVTV
6600	20501	A	6654	489	282	PAS/WDY/RHNPPLNANCAFLC*RDPS MIPGLVSNWNAWVICLPWPVRLRIQAR ATTPG
6601	20502	A	6655	953	908	SQSCSVS/RLKCSGATSDACNTCLLSS YSSTSAS*VAGTIGARHTQLIFVPLVE MGFPHVHVGPGLELL*VIHLRSRPKVL GL*APSSARGQNSVQ
6602	20503	A	6656	412	44	RISERRKSLGAVHTKDKKYSSSRVTSN PNCARSGASSKQSLFGKKRAPHGPKS F/KDALLVVDGITGVHEHA*QTFVRSRE R*IRPVIPALWEARAGGSRQAQIETILA NTVKRPSSLRA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, - = possible nucleotide deletion, + = possible nucleotide insertion)
6603	20504	A	6657	3	241	FFIFLEARSHSVIVQVGMQCDHSSL* TQ TPGLKRS/PASSFHRAGITGVSHHTYLF L*GH*SHSQGPHPHDLTISRPCPS
6604	20505	A	6658	467	42	FFFFFQKQGFGLFPQLEGKGIIPGPNP CPFGANDSPSTPLONGSGPGGPNP FGLPGI*GGEGP*TPGSGKPSGPGSPK VTPFCWIRERPHGPPPPFFFLRQSL CFAGAGVQWCDLGLPLQPPPPRFKQFCLR NS
6605	20506	A	6659	2	286	KNLKINNT*WLMFVVSAT/SGSLEKPR LRLO*AVIAPLHSLGDRARPVLVSVOY LYFSLSLSLSLSLTHHTHTHTHTKIE LLGCVAELIHHF
6606	20507	A	6660	3	249	LSPRF*GSDTISAHNHLHSSSSPAS VSQVAGITGACHHMLLFVFSVEMGFHH AGQDCILHLL/NLVHPHPQPPKVLGLQA
6607	20508	A	6661	3	1507	PRAPVPFLDSNGENDLMEERKFPERTTV TELPTSHVFSFSEPDIPSSKSTELPVDW SIXTRLLPTSSQPTWADHLKAQEEAQQ LVQHCRAKTVLTPKSIQDPKLSBELRCT FQQSLLIYNLHPALSNLPLFRIGADRM AGKTSFWSNDATLQHVIMSDWSVSFTSL YNLKRKTCYPFYVCTYQPTVLPRAGL AGSDLTALSLPTRELARMHBLF SLPLKESCHKEKTAQSTSLQYGEVLEK ITL/SSSTDLTWTHIDLHNSL*NRDSN CSNF/LRQALSDREDEESPSNLEEMGV QDKIKKPDILSKLRKEKHEVQMDHRPE SVVLVKGINTFTLLNLFINKSLVATSG PQAGLPPTLLSPVAFRGATMOMLGRSV NVKTQALSGYRDQFSLEITQIMPHSLH SLTMLLKSSQSGSFSAVLPHPEPTAVFN ICLQMDKVLDMEVVHRELTYNGLHPNTL EQLSQIPLLGKSSLRNVLDRDYIYNRS
6608	20509	A	6662	326	1	IMI FLFFOTGSRFVA/RLECSGITTHC SINLPGSSNF/PTSA*VTHCRTRVIL NFSVDPGSRHVVKGLLELLDALLPWPP KVLRTRGSTPEFRSGSGSVIRIGFN
6609	20510	A	6663	414	105	QGRVGFVGLNPLSLLHFFKQGLFVLS *KQGVKLSLKLPPPGGFGSPPI*NDP P*NGQRFQNDPGFT/IRKKLLPLAFK STKSGG*NPPSK/HKKI*FSF/CWETE SRSVTQAGVQWHYLSLQPLPPRFK*FS FCKPHKRVFKPLGLVLWVGISNRRKKKT SGGKRNFKA
6610	20511	A	6664	1	407	GCVPVPPAAREAG*IA*TRRT/RLRW AGIVPLHSSVGNKSETLSQKKGAPSKK SLQGVALFLSQLGLPFLQKRRPQFG GGGQLAGYNPPAGKTLVGGPHLSFC SKKAKKELRPWKPRGFNPLINST
6611	20512	A	6665	1	280	FFFF*HRVSLCCPGNSTDLHLLPP*LAR FKRSSHLSLPSSWDYRHTPT/HPGFVVC LPVFCRDRVSFVLPLVSNTPAQAILLC GDRKVMGLQA
6612	20513	A	6666	408	89	WLPNSLILPN*NYFVSYLSDRVSLCRP GSTAVAQ*ELTA/A*TLGLKRSASFHS HSCSLPSSWDYRCTSSHANFPFRKRGF TTLPRILINSWPOVILLPQSQRH

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
6613	20514	A	6667	484	208	ITVVSAMGLTHYSPLNPGEPMTTERKAYO EIDDIH*NLQHLQPALVDRKGPIFLHSH A*PAAQPK\LQRLNKLGRVLPPLPYPS FDLLPLT
6614	20515	A	6668	493	227	PAFVKVPPEKQQRQNSHAGRNHLEMEI LLL*KKKLETESHSVT\RECSGVITZA HCNLLGLGSSDPPTSASDYRLKFPWHLAP SFSFMS
6615	20516	A	6669	2	65	DGVLLTSLGLARLV\NSHPQVINLWPF PKVLQ*QAGLTPGLK
6616	20517	A	6670	403	224	ILL*P*PPLK*/PLPSSWDWRASLCL ANFLFVTVFVGVPRVARAGLKFLGSDPSA SQSAGVTVGVSRPGKFLIKIVL
6617	20518	A	6671	406	162	RSYACQGTOWLDFSSLOP*PPLIKQSS HFSFQSASH/RHPDNYCLP CRNRVYVG QASLELLGSCDLFASASQAGITGSCIL
6618	20519	A	6672	433	32	VVSATLHSTVVVCACTRCVGMCMTLGV CGCECVV*GCVCSTVN*\HTSTGWSEK V*LCVCGCV*LCVACMAF*VSQCVCDDP VCCLPECMRLSPISVA*VCAPMKVS PCP PQLSEIHLLSLNIYINKCVSLSQAMWLF L
6619	20520	A	6673	378	180	NEVIRSYKVSLSFPRIERWINK/I/RWY IYPMEDYSAIKERNVLIHATT*RLKNI TLNERIPDLIPI
6620	20521	A	6674	378	94	PVKNRRTKELHKKDCTMLLVLMIV K/S*KQPKCP*IDENWNRWYTHWVEYC SVSKKEGSPFICYNEDITLINEISHKTN IYNSTYIRYLE
6621	20522	A	6675	1	380	VCSL*VLCRRHSCFONCSL*FSFSFWFF WRQCLPLSPRLCCGPMASHEHNLRLPGS SDSCASASLVAGIRGACHARVIFVTVV EMG\FHCVGQAGLELLT*\VICPPWPFK VLGLQVLATVPGOPHF
6622	20523	A	6676	424	135	SHRMGVKCPKRYNIPFFRD\RV*LCCTGW S*TPELK*SSCLGLPKQDYRHETLRVS Y*F*NSI*OIGVLAMVSKLVLS*AGAI LLFWPMPRVGLQI
6623	20524	A	6677	408	91	HTHFVWPVVLIF**PBR*VILLTPTNIF FLRDRVSPCHPGWSEVQAQSQITAAASN\Y GLKQFHSFVPKCDYRRELP\CMVSLI FLYVILLMWVIRAKKEEYEL
6624	20525	A	6678	1231	217	PYFHNALTFPK\KAFFKCDKTLKRL*I REILLQNRIG*KTDSIR*WGTETAPLK EKFLGTALQPSFLPYMLGHFKKE*GKE FPGTHSWPFPSPFVNLGLSLVNHRRGILH PRVSLQTWPGQEAAMECECONHGTEDTG \GAVLQPG*VT*GHHTPTSEPLVAPPCC TCSGLKABA\GFLKLPKQCC\SEGALPP *SP\PLSACFPELGLRLGSSPGMLHPG WGLFTSPGLKILGRRHPAGPALPQIAQ RPSLKFR*RIKRWGPPELLPAQTCCGASL GPSTAPLLGGQPGWGLG*HDSRWGLTGLA VAPGNEVPSSLSPR*PRGAGPLAHRHVPV RSWG
6625	20526	A	6679	1	178	RGWDYRRRLP/RPG*CFVFLVENGFRV GQDGLYLLTL*SSQSAGITGVSHRARLQ PPIF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
6626	20527	A	6680	3	135	KSEHLRRRPITRQLSTMTFF/TAKYGHLLRGH*HRCQKKPPPPEDR
6627	20528	A	6681	425	107	KGPPPTS/PPPPSPVFFTEKILVPPPPFPFPFKPPPPQNIWFQPKK/IKNFSPPRGEKNFFF*TPPPKYFLGAKKKNFSPPRGEKNFFF
6628	20529	A	6682	424	284	CFLPQGP/PQSGKASPPSFQDNWGLRQALPP/RESFFLELEFFIVQTFGHVHVARGLLELTSDDLPAASQASARITGVSH* A*PFP
6629	20530	A	6683	1290	449	PLSAPFPQDPS*KSSEPRANPLPAP*PNLSWPWPKPRPR*PASS/PP*LPVPPKSPSPPV\PUVATASRQHQPQIT*BLGLSLVLRMTKGTWG*GIPDSIMPLPRRS EPRTCRE*GDRWRWRRRSTGAVSTFSPGFACGGSGA/PAHFGQKLGASARPD/PHYCAAMVLLPSARUVASPAAPPPLPSPQPVH*RFKP/SPY*PP\ALPPLSPFSPSAPHITGSVPY*QGVPP/SBGCPSTSKPLISVRPPTVINGCLPQSQPPKTHTVSRLYREN
6630	20531	A	6684	425	40	EWASLKN*HPP/GANQAVEAVEAPTHCW*GCSIRPLWKTWQCLDKNLICLLYDSTPE*MSRVTQGAACKSFTAVLPMIPPN*KKSPCSTENLQGANLVLVLPAPWA KVGSGLEPSRLRPANATG
6631	20532	A	6685	2	107	SNLTASTSQ/VKRSRLSLFSSGDHRCMBANFFFLKCDVSLPRLSNSTQAILLSLPTKGLLEL*HCSLNLPGSSDPPASAYQVVGTITGACOLIFF
6632	20533	A	6686	12	224	TPFGSTHAGAPFCLANIKEN/L*RLPRLFWNSWPQVILLPWPSKVLGLQVWATVPSPFLIFDRDIDREI
6633	20534	A	6687	404	2	TAARGIITGGPIKLLPRKPADVR/SGSKFTAPFFFFFLGTRTLTEFLIIQN*KQPKRPST/DRINKLWISTIEYISAMKRNKLLIHTTAMNYKIGM/SKRGQSQKSI FSRKTGTGGRNHSQCFLYPLPLRL
6634	20535	A	6688	410	163	PRGNTTPGFSPPREKQKQVFNPPGNTIV*KKGQPP/PQGAQKKGPP*GPPSLFLPPKKKKKGGPPPPPPKKN*PKGNS/SPSPKKKKKFFPPPKKGG*QDEPLKTLFPWGGGKFFFFWKKKEPPLQGGFFFGGGGGGPPFFFFFG
6635	20536	A	6689	205	405	KSPSPSGGPI/IGKRLGAPKPKNMPPPLGPKGNPLALGGGGGAGNHPNPFILLFLGKKNP*KSPSPSGGPP/ANRIGNRGPKTKQIAPPLGAKGKPPPCPRGRGGGQKPPQSPVSPFFGGKKPL
6636	20537	A	6690	3	199	HGSLQH*PPGFKSSSLLEPSSWDHOFQPRPAIF/CFFLILEKGVSPGFFGGPSTPGLKGLDLL
6637	20538	A	6691	8	350	SVCGLP/RCWDYRYPHTA*LAFLCQIIFHMDNIYHSILVVDGLGCFYFLAIIINNV\G*AGLELLTSGDPPTSASQSGITGVSHCTHPYCYFTLTREITTPKEVKILGLCM
6638	20539	A	6692	373	197	LPSSWDYRPM*HMLFFK/FLFLFCRD

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
						E/SLTMI.SRLVSNWAQATLPPQSPKVL GLOV
6639	20540	A	6693	369	100	PMLARMVIS*PRDPFASASQSGITGV SHEARP IYFFK*R*SHAGYSAVPVHRHD PTDDKHNSFLFCFLQTGSCFVQVGMQNHUHTSL*PRTPGFKQYSHPSLPRH*DYK PTFP/HPS*FVQVGMQNHUHTSL
6640	20541	A	6694	12	182	FLSSWNYRCVPHLAN*KKFFFTYDR/SLAVLPGLVSN*TAQVLPQPQKVLGLQA
6641	20542	A	6695	402	248	SSWDYRCAPCPANFKYLL*VGS/HITC*PRFVNSWMDQVLLPFSKPVLRGV
6642	20543	A	6696	301	309	VQRF*DRLLTS PRCHPGKRAVA*SRLTA ISASRLKARSHLSLSLSDYR*VPPGP ANFLHFFCR/DRGFAMLRPLVNSNWTQV ICLLRPPSGITGVGHRARSLTD
6643	20544	A	6697	3	387	PCLANFF/VFFVETGTHYAR*CGRLGLSSALPV*TS*SAQIGQMSHCYC/LQITL LKTESHS(VAQAGVQWHDLSLQPLPPG FM*FFCLSIQSSWDYRRTSFRANFCIFSRDEVLPCEWGS*TDLR
6644	20545	A	6698	1	287	LMFLYQGNAGITGISHAQNSFVFFKD RVLLCCPGWSAVA/HSSITVALTSQAQV IFLQPPG*LGWFCIFSRD/RGFAMMPRLSNSWAQVTRP
6645	20546	A	6699	412	3	FEWSSVAREKCSQTLAKCNHLS SSSPVASRVAQGTQACHTWLFEPF V/FLVETGFVIVQAQGLNNAKAILPOP P*VLGLQARTTTS*SPNSFTRHTSSGSG VGPYAKFHSITVLLLVLLPHLCOVF
6646	20547	A	6700	393	88	OKLYPLTPYAKVN*QNTSLSVTAKNT*FLGNTGVNHSFRFKGFLDM/TPKS ISTKRK*KIKWSSSL/KNFYALQNIK KMKRQPTKYBKHLTLNNW
6647	20548	A	6701	494	239	KAGSHS(VSRLCSCGSIAS)CTFCLLS*NNPLTSASLAAGTGVVHAWLIFVFSV QMFCHVTQAWLLFDCHFSPIKYNLL
6648	20549	A	6702	2	379	RPIWTVWQNPASTKKKQFPFFPKTESPT VPQAGGGGNG*RKFLPPGLKFSGLK RPEAPKQGS CSLMGGLCPLLPF/WSGT PPKR
6649	20550	A	6703	220	47	TGFSGSQTN*EK/TWLTQVAHTCDPSTL GGAGQVT*GQEFKTSRHSLHLITVLSLF
6650	20551	A	6704	80	414	ICYYFIVFAIVLNFQFSSNCRSFFPTFC PFETTSRGAQAQGYNPITALLHPPLG IKQFSLTLTPSS/WARS*KDPCPTWNS VPGYIKNKIGGGA(RRVQTCNQTYSG
6651	20552	A	6705	69	416	NVEKRNNHNIKKTPYFFGFLLYCCKA EVFYLDNPFIFLYFYFFETHCVAQAG VQWNLRLSQPSH/SSSDYRCAPPHLA NFRCDGVS PCWPSW/S*APGLKLHPNP SPKVL
6652	20553	A	6706	373	75	HAQLTFKFFYFRNTFCXAVASTKSNSSD RSE*SKLTFWKLTLILDAIRNISDSL/EEVNMSTFRGV*KKLTPIIMDFEGPDF TRESNHRGARHGGSL

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6653	20554	A	6707	331	379	K*KINKN*KGL/TTLDAKNTCDSSWEVN IST/LTGVNKKL/ITLDGSEGGKLSVE BGNAGVVBIALELELV/SPEYVTKILQ SHKKT
6654	20555	A	6708	578	152	LQENPGSLQPLSP/GPKRFSCLSLFSS WDFRHAPPCSANFVFLVGRGYHNG* GLKLLASDSDPTSAQSAGITGVSHRAQ PLIGPKVNSVKRSVSVPTRILKGNMS YBOL
6655	20556	A	6709	392	146	FFFTSLSPGLECSOTVSAHCHLGSDDS PALPS/RLGSSDSPAVALVLYSPK*Y Y/FHKTONYVLKINILLHVAIPYSFWS C
6656	20557	A	6710	9	393	KSKPCN*KDSQSYRL/LFAQLPTF/SNF FYFLTF*ESHCVIQAQHSOTMAHHT LKLQSSNPPASAPPSMDHRCQPPPLA TFLKIFL*ROWAHVVSQARDNGLIMFER LVFELLGLKRFLLPQS
6657	20558	A	6711	34	387	QDFGLSPFLLPFFPEKGLGGPTCRAGFE SNLME\GGPGLKQFSLGLTPRTNGNR ASRSRAKFWN*KKGKGGPGPPVELETPT LRGPPHLSPPKGNNGGPKPDFFKVG KRAPNP
6658	20559	A	6712	1	188	LQAWHTPVVPAWHA*AGGLR\BRRS RLQ*AVIVLHSLCLGRVRPCLNKNGKS FPPOPLA
6659	20560	A	6713	377	98	SLGLKSSHLNLESMDYRVPVPCFRNW FVVPVFF*RE*GLANLPLVNS*AOV ILPQPSKVGLQARTPRGFFSHLWT LVPNVNVLNI
6660	20561	A	6714	353	229	SSCLGLPKSMDYRHPHAYFYVY**RQ ALV/MLPRL*Y*FLDVM*LPLPHVAP SHLLNSVGMV
6661	20562	A	6715	371	64	ENIGDCTPAATRAKLPRKKI/CYQMF ITTLFTIAKRK*LKCPSSDK*INQWYI HMEY/YALKRNTLVKLNQNPYAL*XV LLRE*KQNP*SVRNIFKTHI
6662	20563	A	6716	462	232	HPNLITIKITPFF/C*DGGLTMLPRLVP NSWAHAILLPOPPK*LGQARACKL
6663	20564	A	6717	425	48	GGGGPPFKARFGFLHPE*TPPTLRPRP PVVFGGFKASPPKKKTPK/PPGGGPP PVFFPFFLSPPFFIPFEKPPPPFFWRG LCPPPPFPKPPFFFWBGKFLPKQK KKKFFQSLSTRSVLHK
6664	20565	A	6718	3	413	GFVTRTSLGUTLY*VISTYCV*ETS* \SVLVYIYIPKDCV/LYNYIIFYIYTC VHISVCMVMYCMYVCMYKA*PANLKF CTQKHLAMGWQMLSVISALWEARE SPEVETNKAOLGPTLSLPRKKKKKKK
6665	20566	A	6719	408	71	SSMDYRC/LPPGPAFPCFSDRGVSPYV PGWSTPD*RSFGGDVMPALVIRIVRP LLKKQHSVSRSSRPANPIW
6666	20567	A	6720	375	57	SVIREMQIKTIMKYPFITPLGIVIKRTE NN/RGNRCREIKACIY*WNGCKMTQLL OKTIN*FLKKINTEL/PYDPAIPPLCM* LRELKTCPLRGLVHAHCNPSTLRG
6667	20568	A	6721	391	164	RISETCT*MPFAALFTV/DONNPDGNTN LWNSYTHMDVDSAIRNEVLLHSSTW

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6668	20569	A	6722	381	278	\RNLNLMISKRGQSPKTPFG SSLQPTTPGLKQSSCLSLSNS\PPRPID *SISLYRQGLTLLRLLSNSWSQAIVLP GPPKALGL*ASKKFLYSNT
6669	20570	A	6723	2	363	QRSLERHPCKKC/CGLVV*VS*RVQYLV YKSSSS*KNLLKRIHGNFLSGIV*HF* KILRTPSFCLCGLHIPINPTTF*IKKE KFKKC*POTNAHPYNPTLGGIGWIT* QDOLDLLTS
6670	20571	A	6724	352	58	HGGATGARFFKVFENLI*PNLVCKDE/SF SILARAVINSWPRVILPWPPK\VVGFQ AKTPLPRLKGFLESPLSKKKKNLAYAR TITAIQIGLIVCFIDQQ
6671	20572	A	6725	383	54	KSSPFFFFEQGLLCPGMSAVVSPLQPK CPRLKQFSPLS/LPSN*EYSCPTTFSL HVCVSIHKYI*YIDQYIFKF/CR/DRT LAMLPRILVSNWSQAII.PP*PPKVLGFQ V
6672	20573	A	6726	3	343	LEV*ARATROE*KINGT*IKYKRVQY SQNDMLIYIQNTKDSAKKLPELVNKFSS PKVNRQNSVVL*NSNKK/SERETKKKL /PFTLAS*RIKYLGINLTKEVKNLGRAQ WVTA
6673	20574	A	6727	3	615	HPSQNI*IQYHTPWHPSSSERVERMNQ TKSLHLKLVKTRLSWTKCLPALKV RTVQKRGVLSFCRGLYRLYSHTVDYI PFTETKSQPVKSYVLGLSSTFSLKAK/ ELFSTDATL/GSSPGTSAPSLGDDVILRS WEEGKLPAWEGPYLVLLTTKTAQT/D NKKMQTHETPVKASPSKSCAIVPRPI PTKLKIKKKKA
6674	20575	A	6728	2	228	SGAT/SVHCNLPFG/SSSDSSASAS*V AGTTGVHTMA*LIPLVLVETGFHPISQA GLELL/NHMCPPMPKVLGLQL
6675	20576	A	6729	98	359	KVEYTVILF*GPKGKPTPLIYLSPSP LKQHLISNFPANRVLCCPDNSVVG*PT AHCNLNLCLSLPSTW\DSRCVPTGAWL RFI
6676	20577	A	6730	10	428	RSTRTDYALREVLPDPRRCRPTGAMS NGRRDRPGAAGSGPKARAEHTRETKGL LPCPCPWSANVA*PRPTATTSRAQSITV SPRLCGGVSNH*HFSRIRQWGLAV LRTLVNLSWLIALLLWPRKVLQLYALA
6677	20578	A	6731	425	158	SCDHDLR*STCLGPKWDEHRCAPKRAL FLF/PNKCPSMTRKINQ*LPGI*KN FCRDDHLLPLSRLLINSWAQGL*CRPL KVLGL
6678	20579	A	6732	431	22	RDRVLLCHPE*SAVV*S*LTITVONSQA GILSSI*DYSCVP/LPVNP*TFPKSVY YFIIFIFEIYPNCALOL/LGVSHRAR PPRI.VLNSWPPQVILPSQPE*LGLEAL ATAPAI PRSNLVVHQYSFSSIPDDL
6679	20580	A	6733	44	414	ATYDLPLFLIDLYPMLERASIRAHICT* RPVATLFTVTKRIANQPTCPSTDE*QNKX WSL/YIMNYPAIKRNEILIHENIMICK RSQSQKAHTE*PHICEISRISKAETED ELVVATHNGKRE
6680	20581	A	6734	375	49	QRLTYICRPSYNTASNMRLS*TNHQIK

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						SACSMCPGRI*GVHAMR PKVMRLSRSH /VARPIATCAQ*VCDRIK/R/SLLTIRE OKIVVKVLKAGTOSOTAKFKNBTFFRNK N
6681	20582	A	6735	381	88	SLFPRLETPGLRPSFFFLFSLSHVGV SVVV*SRLLTALNS*ARFSLNSCVPLH QAHFF\FFCDRI/SLTMPLRLVLSNAQ ALPPPEPLKRGGLQV
6682	20583	A	6736	384	293	AHLSELLSWDCRQWPGLENCVCLG/RV FVCR*GOAWLPRVNSNSWTVLLPLPWP KVLGL*ADQCRPLNGRSGPLPOAASG
6683	20584	A	6737	24	300	NILSAPLCLIS*P*H*YGLVLI*NVQWR FLPLFFPMQMYTHIFPKIRIRPGVVSNA YNPSTLVGGQGR/SHEFKTSLDNIRPR LYQVGNKIR
6684	20585	A	6738	2	353	IHCW*CKRITVTELEKTWQOPIQLNIVL PYIPA/ILPLGIHTREMKTHLYTK/T/C MQMPGVVLFILAKIVFQLVNR*IKL*SI HKVDYHSE/IRNKQLVYAT*INLCKTVL SE*S*STOKTT
6685	20586	A	6739	2	356	IHATTYTNF*HRH/VHTPTHVT/HVYTH NGTHHTHARAWTPAPPTSLILPSPTESP PALQIPNLPLGLSSSHIPAGSSQGEPEE GGCORRAKNR/VHRAEKWETELCAGDMN L
6686	20587	A	6740	3	385	KQATLLMLIHLATTSFVET*QSKTEVH DIFKVLAKKKK*TTTPPKITNPKIAPI HBGRKILV/IVK*OLRDFDISGLVLAHM LKRVL*SKRKGH*QTIINLRVQNSLATA NTQNPTEYQNTVLVGN
6687	20588	A	6741	406	155	TGSCSVTOR*/CNSAVIVHCSLDELQSS NPPASASWIAGTGMCYFQALPSFNLC LQFYCMGCVESRFYLRFTPLQSYTRKQK
6688	20589	A	6742	1	215	LPYSPDLSPDT/Y/HFSKHLNFKLKKR FHNOQDAENAF*KFISQSIDFYAVRIN KLLSHWQKRVDCNGSYFD
6689	20590	A	6743	376	109	YHMEVWNLVLSLGSSTYLRLPSSNDWYCP PP*QANF*K\PPCRDKLMLPRVVLNS *LQAILLRPPKAPQLQLGQPFQFRES GVNN
6690	20591	A	6744	382	148	NIPQFMFDILFC*LIITLSCPASF*SKFP LSSLYFIO*GR/WIGTVAHACNPSTIAG RGOR*A*DBLETSIAHAKRPHL
6691	20592	A	6745	403	209	FLVTHIKLTKLQ*HYAKFKNLDKLDLT FLVTHIKLTKLQ*HYAKFKNLDKLDLT RQKIKLSDNN
6692	20593	A	6746	366	40	QGSVLSLHNVKIVNPKTGCVGHLFPLEN FLSLPQNYVCHSTS/YPLSLPHSILNS FPPSFNHS*Y*HFLKTN*MPDAMAHAC NPSTLGS*GRWIT*DRFPETSLANI
6693	20594	A	6747	392	57	APKKKGGGVVPLYPKSGRKKKPKG/PP PKPKKKLKTGPRKNDKDIKPGGAKFF SPKKKRGAPPGVPPRLF*KPPQATL*GG PKKKKKPQGGGKKGAPKAPLFFFFFL YF
6694	20595	A	6748	376	140	LSDNI/GYSNONGAGRVS*INTPKIKV S\QSKIAKWDLIKPKRLCAKVSNNRVN ROPPENDRI PALASAD\RGFLNKLIG





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6710	20611	A	6764	1	229	P*PHGDCPARKKKKQNDPRIGQPTVT VLLLCFFFFVL*DRVLVGHPPGSSRLYL KIKTKQKQNNIPVCRVGG/LITLPLRLVS NSWPOMVLSPOPINALGLQV
6711	20612	A	6765	580	273	WRQSLTHSVQPGVQWIDLSLQPPPPG FKRFSCLSLPSSWDYRRAPPRPTNF\*Y LVQTEFHVHQAGLRLFTSSDLFTSVSQ SKGTSVSHHQIQDWHFLR
6712	20613	A	6766	220	239	AGEPKAAASTALQVETTLCLKKKKKKK GVSLQGVSSNFRITGGAGSVTSPTIF/CF FFFF*DRVLSGVQWQSLQ*TPGLKRS SSLSLPSSNVEYRHVPLEPA
6713	20614	A	6767	89	387	FLSPSGSQKHILQTLRSTFSPPFPFR EPRGRVGGQCNLQ*MKPPPPG*QPS GLTLT/SNNERNATPPPTINFNIFKKKG NSPWNKRGAKIFGMDP
6714	20615	A	6768	397	223	IRRVGVVIVNQHDKPCD/KVNCVY*1* *WIHKPTHDKT\HRNTHVTHTHVNGHS HTQK
6715	20616	A	6769	3	367	SWKVCSEKPIPSLFF*KHPRVLLRAD QT*VSLATL*HMQLS*AGSVKDEPRS NAPPHKATFLFLEFCTD/SSLTMLPRIV LSTWPGAILPCPPKVLGLPARANSSSL SVFKLTSFCC
6716	20617	A	6770	490	260	FYETESCV*AGVQWLELLTSSDPPA SASQAWITGMSHCARCRQTHLCERF LVSPVTLALLSOLLGLGLHNSRC
6717	20618	A	6771	418	130	PSPRDLNLEFLNPGFLFPFFP*DRVLLC CLGNSAVASN\PDLK*STRLLGLKCLDY RHRPLCPAMDITLSSL*ETGLPCHRP LPAPRTGPGSQ
6718	20619	A	6772	311	314	FVAGELFILLHHVGHACLPFCHDKCFE ASPAMLPY/OPVEL*AT*TGIEVLTPGC RFOAVFLKVGPHOGTPVYLG
6719	20620	A	6773	465	283	CPSLPSSWDYRIPPPRPNF/*YF*YHV GQPGLELPTSSAPPASASQAGITGMSH RAMPK
6720	20621	A	6774	410	91	RDSKLPQPTFRLQSSCLSLPSN*DYR HMLPCLAGWLAGWLACQIDRQTDRTDR QTDRTQDR*TOR*IDSRDR/SIALPRM PDSWQPVNLLPQ/WPPKVRRLWA
6721	20622	A	6775	409	253	LIFAFF\CRDGLATILRLVNS*PQAI LPWPFPKVLGLQARAGVRPDLIS
6722	20623	A	6776	3	278	PPFSLHTMAPLAFPPFGAISAHYNLP PQSSDS PASASQVASTTGACHVQIF\ VSTVEMSHVHGAGLELLT\*VTHLPQ PPKALELQ
6723	20624	A	6777	79	442	RDEDRLHRRCVSACSTPLQGNASTT*G CPGVSDPSLHIL/CFPKKN/SCFAPQA EGGGHNIG*LEPGPGLKQPSCLTPQRI WNNGAPPPPLYFFFLKRGGSPLMPGN A*TS*PRS
6724	20625	A	6778	77	417	HRGLHLSFFLF/SLFFFLKRAALLNPR BQGRGVNWNVCNLSLRGGISKALPS*E AGTKGGRPHPTFLVF*KKTSFSQVQDQ GIDLWARGNPPPGNLWVEIQETLCPG HTF
6725	20626	A	6779	62	235	TQRLRIRRGKCLAYETHARNGSQDLHA

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						GLSCLCCCCCCC/CNCHP*STRKFFKPE
6726	20627	A	6780	908	566	SRMBFRSCCCFNSDLGSPQL/PLGFQK L/SLCLSLP/VAMVYTHAPTHPANT/*FL VETGFFHVSQAGLELPTSGDLPTASQS AGIIGVHKHDAHPECVTQRQLSEANLRRI WQED
6727	20628	A	6781	11	483	TEALLKAVRH/G*HLSLQRLLESFVCL CPAPRGQVARGQAS*SCQGLHPVTSR LLCLPNQAMAGAPPTTSLPFCSLISD CCASNQDQSVGVQSPSEHAGVNLVPCRF LSPLEKRSIRVGVTRFSRCLSLSLSTR KNSLTPCASFVSASPCS
6728	20629	A	6782	225	589	SRKSEKPNFRSCIGVGVPCNCLSLSLP SRSF.RPL/LSLSCVFCVCLGTRVPCAP EGGF/LARRPFFWSASPRVSANVLN/PVCN RFPQSGCLGVCEGLGNVGI\WSEPOGFS FPPHPEQPLC*AGRRRLPNQGGC/LFG AHLRLPAGGCPQSG*SKKVVVTPVLCPHRE W*PQLDAGTERKAGGGGQACLSLGGWP SWPSHPTDTPFRMPVUVAMPRLPLGLN PLL*PAGRNARKKKPETHRRGSRAGSQ PACANDVRLSLPKSGLVSRGELPVC PMAALS/PVABSRGDQNPATSGAANKWVL PACVCSLSLSLLALSFLSLPCLSPVCS CALGHVCPVPERVGLVLGCLSSGQPLPA SLPGCCSRLAIV*PAVPAWGSVYKATNP ASASEPOGFSFPPIHPEQPLC
6729	20630	A	6783	458	170	PCTVITASASQAGITGVSHRTLLVNF KVGSVTTSLG*EVGLRIMP/NI/GRLLDK TGPGSKQHFTLEHAPQSAPSVTHCLGNTQ ELPPLSTAMISQPKR
6730	20631	A	6784	1	192	FFFFG*TLPLSPKAGQWHDLSLQPPH PGFKQFSCSLSP/RG*DYRACATRDGLI FCNFRLED
6731	20632	A	6785	3	246	SLCVQYCYCRACAC*VPRQVSG*VTNGI /CATGFVLLYLCG*QCLCG/C/C*EDPFF YCEQLCVHVCSCVLGRGWSVVCISRL
6732	20633	A	6786	408	128	GPVYKARG*SFPPFGKEKSPFPNPKT PFGGCAVLPFPFMRGRVENSPPGGRK C/QNP*TFPLPHPHGHTQSPFPFKKKK KTSAEPLSVV
6733	20634	A	6787	1	418	LTLGVWNTGDSNKEVYSAFTGANKK LITPLTD/ET*GPKASVREGTAPHLETA RELEVRBAVTEL/LQSHDQT
6734	20635	A	6788	3	237	FFFL*VLTVI/PG*SAEVQS*LTAST S*/VK*SSHLSLPSNDYRMRPPIHPANF FFFFGKSLILHPPGRGGSLPTP
6735	20636	A	6789	282	3	PHPDNF/RFLV*TGCLHVGQGLALLSP GYPPTLASPSAGITGVSHCTRPKRYF*M VLSNKSINRFLCTVLPICLQAPERTGP PPATVILGRGT
6736	20637	A	6790	62	328	FFDRITLCPHPRNSAVIQ/SWLTEASKS W/IX*SSRLGLPKNCNDRHEPLCLDNTT Y*CRQNTLPITLIGCFRVSILPYAKYTGK FWGARG
6737	20638	A	6791	67	353	TNKHITYFLNKKKPKQLTVFFF*REL RGLILANGNFKLRG*SNSPA*PSKVAG1

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						TGPPHQAGLTLVFLERTGFNYVG/RRGP PPPPPKELALQA
6738	20639	A	6792	744	382	MTFKKTAHTFYLYLFTLYLRQSL/DSVA QAGVQWHNLSLQAAPPFGMPFSCLSLL SSWYTRRQCPRA/NEFFYP**RGFTVL ARWVSISSPCDPPASASQAGITGASPR AWPKLHIFKL
6739	20640	A	6793	372	129	RVLPCHSQWTAUVQGS/LIATVSTQA/KR SPHLSIRHVPDPHA/NFKQFFCRDGLIM LPRSVSNFWQAALLPQPPKVLGLQA
6740	20641	A	6794	395	25	QPGFLCFTPRKKPDSFSAVLSF/FP PSL*FS/PLSL*VQEMVSICCPGWSAV/ TPGLK*SSCLSLPKRGYRCAPPHSANL KFFL*R*VLRLMLRGLH\SWVQVVLQ WPPKPSLRACTSKI
6741	20642	A	6795	412	176	KKS*/CLATPSENWVL*NGPLFFFFFL *RRDLAMLRLVNSNKAQVNLPPWPK/ VLGLQAGATMDHSCVQYSSHFAPE
6742	20643	A	6796	444	95	NFVRNCSQFLQSGCTFLHSYQFEL/PC PCQH*IMSVQILTTVIGVYMLRV*ICS AINTFDLPFMEVLI/CHLHIFFGSEVSH FSLLLFLFESGSIYVQGLHLLLSNPS PASAS
6743	20644	A	6797	378	732	FFFLNALSQSQPP/PAPITR/FSHLQLL NSRDYRHLPPRIANF*/FLVETGFRHVG QAGLKLITSGDLALASCTGTIGVTAS PSLDEGVFKALPPVPGTITCLLPWTTGG PFLGPAL
6744	20645	A	6798	444	1	PLCFPPGGGQFLSSHQFPFPPPPKRGKS VGAKKENIPPGFPFFFFKKNFFF*GPY PF/SEPCKARWGPFPFGPSPPPSLVS FLGKKKKKKKIPPETQPPSFGA*WGKK RAPPPGPRAGGRNSFLEGGRGQGRIGGS VREFRAGR
6745	20646	A	6799	462	83	IEPLRPAFLCS*SNPAST*KPHFILPF/ CLPFLSFFFS/SFPFFSFLFPPFFSFP FLIPFLSYSLQCSGWSTVA**GLTIAS/ TYGLKQSSHL/SLPASWFFCLTN*KKIF FRDGGTLMLRLAFLFLNIP
6746	20647	A	6800	433	185	FFPGRRLVEKTRSEJLQGGQPGRQAG LGMKGNPGKQPRPASQAPBQGLAPPP SGGHLYGCGAIONNEGANPLLQGTQSG SVAAAGEVSKAPSDGLMGNMLVKKK/ AGGGGEPQANQETEN*EG*PMSPEGAL LLTSPAANTLPLVPVPPRRGFAPPSFL APQP
6747	20648	A	6801	395	60	IEFLFLFLPLSVQGRMLSHQLLPVNNAT /MSIP*HAFAMTC/SSFLEGGCLGA*ST LLYGYMFSYLRNKQTIQSSSCCIVNGB QPRMRNLFS*FIQHLVSVFLIRATLE GI
6748	20649	A	6802	423	98	RGVPY*PGGLQPPPV/REFFP*FTGRVS VLQNGAAAPTCAQSLPGSWDYRHLHA NMSS*FLYFV*QVFSMLPRLVSNWDQ ATHPSQHPALFFTCVSVKPLATL
6749	20650	A	6803	396	194	SLMKLAHV*VLHTDGGFMHPSAITSCHD IFDSLHATGESSAKICRALYELIMQLME BHP\GEKQTTIA

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6750	20651	A	6804	373	192	FALNPWAGANLPHQTFALSSNPFYF/CVEMGLTVLPRLV*NSWPEAILLLPWHPKVLGLQA
6751	20652	A	6805	370	242	KRGTSKFLFPFSPYSFPFSKFWYQKRVKIAFFFF*DRVSLCHPEWSAVM*S*LSAALIT/CPGLQGSWGYRHLVPLCLANFS\FPC*DGVSWLSRLENWPFCLF*FVQPGQHGNSISTKK
6752	20653	A	6806	464	182	DGFHRPEFPLISS*FLPWPFOKLRIKG*APLAKQIFPPFFFL*RDIVLLCC*GAGTVSYVSWVSRLLTAAS\TAVLKQSSHLGLLSWDYKHEH
6753	20654	A	6807	3	228	YTCAGFFRPSQLCHLGGWAVARSLQTLVALTL/VPPGLK*SSNLGLKCDWYDCEPFFHLACVNFNTVKDVCFSCLIS
6754	20655	A	6808	506	173	NLHLGQLKQFSCSLSPFPRSDRYRPPCTANP\*FLVRMGSRHVQAQGLELLNSGDSAPASQAGTGTGVSHGQISLFKQILITSTRISVILPILTLRLILHDLPCLLKPSL
6755	20656	A	6809	676	397	VSSCPDRQPGHGETLSVLKIQKLARHGGCL*SQLLRSRL*QTRLNSGVGDHSEPRLSHCAP/AWATEQVSVSRCKKQRQLHQKERIPWVRS
6756	20657	A	6810	367	31	QVFGQYISQDLFIYLETSLSLCHPG*SAVARSV*VTPASDSWVKQSRSLSPSSWDYR*VPPYSAHPDVNSFLTYCTISPLTKIEDSWLGTVAHACHSLTLAGHSGQIT
6757	20658	A	6811	469	251	LLSSWK/YQVFPFPHVFTKIL/CRYGRETASCCI*PRLVNVSNWQVILLRQPQPKMLGLLSATMPGPIISVPCPCPCF
6758	20659	A	6812	16	462	ELISYCGFNLHFSNDYKKKKRKRERERKKRKENIGE/HI*DIGVGSIDLILPKAWTTKLNIKDWYHKL/QKLSS*RVAKTNKLKSFCTAEBILITRVKQPMWEKTFPSQTSDKGLISNTYKELQCLNSTETNKQKNFDDLSADRG
6759	20660	A	6813	492	243	SSWDTGCTFSRPDI\IPFLVEIGFGFMALARVLIS*PRDPPASASQSTLVDSRSRYKQYQIHQQVNMNF*NYGWCFFDIPTASVDG
6760	20661	A	6814	32	308	EYTLPHFYLTITGPPFPVPKPTYSHS*YFLSPHTQICQ\PAFRTINTASSTCLSRRTARVPITQDPSLEPLQPPNSLTLPTPLHSPCW
6761	20662	A	6815	97	274	GRFLELK\VRGSLGLANVVIAYNLSLGG*GGRIP\QGFKASLGNIAKSCLYKNKGA
6762	20663	A	6816	74	376	DFFTIVSVFPHLVNLRKDVVLYKSLKYFFAIYRMGNIYKLYTLGGINIQNISMYYTA/IKKD*ILLFAATNM/ELEDIILSEISHQKS\KRCNFSLICGS
6763	20664	A	6817	1	1127	MRTVAPRTVILLLSQALALFETWAGHSNRYFYTAMSRPGRGEPRFIAVGVDVDTQFVRPDSDAASPRMAPRAPWIEQEGPSYWDRETRNMK\ASACTYRENRLIALRYNQSEAGSHTLQRMYGCDVGPGRLLRGYHODAYDGKDYIALNEDLSSNTADTAAQITQRKWEAAREABOLRAYLEGLCVEWLRRYLENGKETLQRA\DPKKTIVTHPIPSDHE

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						ATLRCAALGFYPARTLT\WORDGEDQT QDTELVEITPAGDRTPKMAAVVPSGE EQRYTCHVCHIEGLKPLTPERWDAILLES PTSTIVGHCAWAGAVLASWMSGAVVAT VDV*EGRSSGGKGG\SYSGWRPSPVP QGFWMCLSTALKKP
6764	20665	A	6818	34	382	STAGATHVCMCMCVHSTCVCAKMCVRV KF*TWIDETGAGLSGCCVLVAQTELIYL QFRNSSLSPRECVCAK\CVCAKCMVHS TCVCVCCVCV*V*KRENWPGNVAHCNSSL TLGG
6765	20666	A	6819	1061	305	FFLRWSL/DSVAQAGVQKNDLGSLOAPF RGFTTPFSLSPSWDYRRLPRPANFF YP*RRGFTMLARWVIS*PRDLPASAS QSAGITGVSHRAKRENTILY*HLNFVIK SHKPPDIVFRDL*GPRLLHLENFVL*GAK SHSSCPWLNLSPFPFHAGSHCLSSSFR NGARODLLFNASSHTGLFP\LOLNOTAS RPTSQVPKSLCFFLPWQVFPALPWRQD EGRASVNSPQDPQRPVSCAGFTHSCNLS
6766	20667	A	6820	610	248	ERESHVA*AVVKCHLGLSLQLPPL\GS SDPP\T*AS*VAGTIGVRHRAHLIFVVF IETVSHVAQPTGF*TPGAQAIRLPDPP ENAKITDVKPLCLAHFCYSKHIMVPAP CLSHQVPH
6767	20668	A	6821	3636	3332	TCIGSHATPHCHGHSFSSCKILLF*PFF EM*SHFVAQAGVQCDRLSLPPPL*FK RPSCLSLPSSWDSRRPPLANF\CIFS RDGILSCMPGWSRTPDLR
6768	20669	A	6822	563	146	APGLSFNCYTPGAPAFMPGRLTLFVUD/ NRSIFPTEY/TIHLISSSEDILHS*TIIP LLGLKTDALPRCLNQTTLTGRPGLYYG QCSEICES/N/HSPFIPVLELILLYKFK T*STSTLKHYCKIAQHLPFKLIDGVYT SLQ
6769	20670	A	6823	399	201	KAEPFPAKSNRGGYVLFPS/IRLDHVK WALEPDDIAVLNFMKRRHPQSKS*TILO KNIOFSPDIVOK
6770	20671	A	6824	323	323	LPTVIVITLSPNFFFFGMRILRLTSLPI CMYICICIYVCIIYVCIIYVCYIIIVCIIY /TYINISF*NDRISSFFPPL*IVCVIYH EWIKKI
6771	20672	A	6825	396	122	LEPGSHHPAVKGRGMPSPSGNPGNPGP F*KGKPPSPGGGAPAGGPPSPG*AKKN G*PRGSLP*TIQPPGSP/NGPPGVVT PETLVGFKKRGHPGRGGPPGVPFLPR AKPEKNVNDGGQAHPEDKSPDPRGPRGA KPETLSPKKKKKV
6772	20673	A	6826	414	64	RGVEGGAACIFKGLSVAGKGP/YLSMR SCFRMLLKS*G/QVIATKXHLPTVLR MVGDPVANVRNNAKSLQKIGPILDNST WQSEVKPILKLTQAQDVVKCFAQAL TVLSLA
6773	20674	A	6827	2	519	KTKTCLVEETS*ITGRFLERINKIDKPL VNL*KK\VOVINIRNEKVDTITDRT*K \\IKHYGOLYANKFN/IDEMDFLGRD KLAKLTQSEITENLNPVSI*KFLI*NI KMKTP/GDUGISREL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 69/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
6774	20675	A	6828	413	114	GGRGRGPGPIPHPPARGPQ*GPGHPAVQVPEPPGLSFPHFRGGFPSSGQCGRGRKERRKPSWTPGSWMAQGRTPAARLEGAVLPG/APGPEAPGTGTINSAPTWPEPP/G/GRQVQDVTAFFPGSARQAR*HRE* LHWKELL
6775	20676	A	6829	479	261	PCFSPFLSNEDCRHAPF/RPV*FF/LVNRGRFHVARAGLEFLT*SGLPASASQAGIAGVSHCAMP/LQVGTFRASIQY
6776	20677	A	6830	492	313	HFITGWPNWKRASAVQGFEDWKLFFPFCFIRKTWGRREHGQSPQAQRTFFQLLLSPKVESK
6777	20678	A	6831	378	1	SNGITCLQSSASFNKIVPSTSLKVCN\VRVDGSRNPSVA/PPPLTPNLFAVAZSISGNGILSTIPITQGRVDEKIKKCYIPFV*ANRHSPPSGVTNINVAHVSLGPFISDDSGVNNKPMQKHQHC SA
6778	20679	A	6832	374	76	QLVEKWTGNVKSITDRVLTKKCELRKEL*ALRTPTGTWNLINDQIMF*KFSGLSFKQVECLVNEKHLYLMPSGRINVSGLTAKT LGYVAASIQRAVTIIQ
6779	20680	A	6833	369	56	LKYLGTSTVENAYDAQNLSPVLSALM*FE/CGMIARSEDRDHPO*QSEIIPS/PANFLFLVEMGFYVGRDQAGLDMTSGNPPACNTGMSHCTRPGRTDVTAILCSDF
6780	20681	A	6834	457	142	DCLALSSRLDLQNDLSSLIQAPFPFGFKFLCLCLPSSMDYICLPFPPANT*FIVE TQFHVQQAQLKLLTSSDLPAASQSAGITQLSHRWPDSSFEGSSSS
6781	20682	A	6835	407	35	TAPATRGVHLKRGKWTYGV*NVPPASIPAYPGVVYQGVGYGADLYGDMQHSDMRGLMVSQHSMPHT/LQQS/SVTVAGACTQPSHTMPLPLPLVY*ELALWRYVAVVATSYLPPAEVMIAPCK
6782	20683	A	6836	1	428	GRTINPPLSLGKSFGLTGLFPENDWPPDVSVPRAPFLARGSPVQSVVREMDQSVQA LLL*MLTFTPHKRSAPRAL/QHSYLHKDRGDPE
6783	20684	A	6837	3	612	FRGSGVFNRRKKLSEHPLNQDVALGTALCPQLPSLPGMGVIEWPKRAACLPNCNQLCPHCCGPQEAQYPL*AGQ*GQHQKPKGA/GPHPPSGPQVPSAPGEAMTAMEGRKLSPAVACNFPQRKNTLPRGPLPRGAPTTT*SLRKP*TPVQAGLAJAEIHHQPCQSQQALALACPDRPHKDRGVKAGGPRGRVQLGGIPP
6784	20685	A	6838	3	412	YRNGFTMLTRIALSS*PR/CDPPASASQSVGITGVNHRVRLFFFGTGTPHPS/MAQAEQGHNLG*LQOPPGKAGTILRTGNFKGGPHTPNFI/CIFFPGKNVSPYPCGWD FGAKAILPPGPPKELBLEGSPPAFGKVF
6785	20686	A	6839	419	26	BETSLRLNSIQCCPLLITQAQVLSFTSGHGRHREHKPTDPSLPACAP/RLTPPPSMCPASHSLPSSQCGPGLTTPPTACARPDTHSPPPSVCPAPLP/CRKVCPPPRSLPTPA*TKPRTQLPSSMYCGRSS
6786	20687	A	6840	365	66	LLEROIGRSYVGPSSKESIFDVPLPHRGIKLVFLCITSSNDTGVHVAVPA*SWH

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						TVVHPRQVGG/AGFELITSCHPSPLT SQTARIAGVSHRARPKFM
6787	20688	A	6841	445	188	GFO*FSCGGLLAGMDTRHVPPRLADFCI F/M*RWGPFAMARLSNS*SAFASQSA GITGMSHCARPATLNSPICGTSLFGLSF FF
6788	20689	A	6842	3	412	PQGSPLQTTVTAPRPRALLMGITMANLQ TRVSTSHLQGPRLTSALTYQMAQVAVAT PPVSVLANVLSARVTLP/LM/VSGI SVVIRQLQAGAGROPSPHGTINSL* VASNLKSLILEVAELFCHVITFEVYQ
6789	20690	A	6843	113	410	NHKCNVPPYNGPRLSEKRLITLTLHYF LNPFLCKSSVLTLLNLKQINLFCCK/YE M/ESHFTQNGVQMDLGLSLHPKQSSYL SLSS*DYRGMPPHLAN
6790	20691	A	6844	2	357	FCPLARTLQSGRFAPV/PNNSGLVRGRRQ EGPHAGFTREHT/SLRAPQPSRENR RTACALRAAHQAGWRITPRAFSPSGC HCPFAEPTSR*EAWGARRKGCCPAPH QPAQDIS
6791	20692	A	6845	392	279	HPFFPCRD/KSLAMLRILINLSWA*VIL LPQPSKVLGLQV
6792	20693	A	6846	3	275	VNLVDKAAAGFERMDNF\ETSSVVGKN LSSSIARVRELYFERKSPSMQQTLLFLSH FRKLP*P*PLATTTLLY*QPSTSRQDP LPAKAR
6793	20694	A	6847	1	454	PEFFETVGHSLPRLCSEASAHQVFL LGSSSPASASQVGVITGHHHAKIIF/ VLFLIVETGFPHVHGAFELITCGPPPL ASIMCILVYLLVFORHLSKOLKQNAS FYFSPGQGLSGFVKCSINCCSSLGLE GHFLPPHSPPLH
6794	20695	A	6848	13	148	GSAMRHTPAG\SLKRLRHRYGLNPEGG GCTEPINCYRTPPMTD
6795	20696	A	6850	204	30	TIFSROVLEIQNLSEKLEVSTVYANNNG S\VLQGTLMASVYHGKILITGVFIKTLY CRL
6796	20697	A	6851	2	429	EVWASGITGRAINAMPTIVIQPNPSSYP CRQFPLQLEAKGFPOLLTEKFGKGLL IYPN/TPILPVKSNERYRLVQDLRIIN EAVVPHPIMPINSYVILQPFPDAQWFPV LDLKDSPFCISP/VDPSQFLFAE
6797	20698	A	6852	3	160	SGWDRHRTQLTIMYSPFLFCRDR/SLP MLPKVLANSWQVILLQPEYVGLG
6798	20699	A	6853	2	243	ACGLLDNATILRVV\PRITLLWGIN KTKKLRDPSIDANSLDLSRVPSDV QKVQYARLKLCSSHSPLKKRSAL
6799	20700	A	6854	24	458	SHAAHAAAGTTRSSHTCEPRDADGKA RCLRGSPHPMPDPSP/PSRTSPGPP PMGDPPPSKAPSPPPVSGPASGVEPT SFPVSEAVMEDVLRPLEQALEDRCRGT RKQVCDDISRRLALQEQWAGGKSLIPC KEBNGS
6800	20701	A	6855	3	183	CCDPVPSASORAGITSVY/Q/WPSLGS LQPPSPFRKRFSLCLSLSSVDRHPPLR PACKVFC
6801	20702	A	6856	2	242	GNEFPYARKLAQRREASTVSSVTQVEVD ENATRCGSGMOMAKDKSLKLTQTQGI



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
6802	20703	A	6857	54	401	RRARDKAL/LVANGKRLWCIEGVC EGERLQKPFMEVLKTHTH/AHTERAH THHTRTHTPRSGMHRNNRLAKNLPK I FFFLSSPPSLFFLI I FFFLSLSLSSL SLSLYKHTPLCLLSLRTSLHRRGALLG GSLIE
6803	20704	A	6858	1374	579	CENFSRSTREPGFLLPH/LFPH/RPA PSCSSPPRQPSQMSVLRKQSPKRA RRARIANPLVLLDALTGELEVQQAOK EWNDFSQPNEEGITALNAICGANYGIV DPLITAGANVNSPDSHGWTPLHCAACN DIVICMALVGHGAATPATTLSDGATAFS KCDVYREGYADCATYLAIVEQSHGLMNS GAVYALWDYSAEFGDELSFRSGESVTVL RRDGPSTDNWMAALHGQBGYVPRNYPG LFPVRVQQRSGV
6804	20705	A	6859	36	269	IALGSDVLTILNPNHESKNEIKRTIPL KIATRI/KYLGINLT/RGKRDLDTEYNT TLIEIEIEDTNKWDIPCSWTGV
6805	20706	A	6860	47	888	TLRALQARPRTGSSCTARTWS/SGA SQHSLRALSNRRLYLSRAKLKASRTSA LLSGFANVAMVEVQLESDEHYPPGLLVA FSACTTVLVANVLPAIMVSTCLPHIERA VSNHMLNSVHQSPIHRLIEVYELAGFP STALGTFPLAEVPLVGNVKKFVIGAPL DTPTPMVPTSRVPGTLAIVATSLSPASN LPSSASAAAPSAKPAQPPQACQGGGA HGGPQQAAMASTAIMPVGLVFPVAFALH FYRSLVAHKTDTRYKQLEELNRLQGELO AV
6806	20707	A	6861	3	391	NKISFFCRDNGLEMLPRVLNSAQVIL /LISTQPPKVLGLQA
6807	20708	A	6862	322	175	GCRCVPPFRASPKIFGRV/RGLDILPRL VSNWDQAI/GPWPFLSLVLQA
6808	20709	A	6863	700	294	VYLRQGLTLPR/L/ESSATLAHSLKL LGLRNPTTSASRVAGTIGACHITRVPI I VFVVISCLLAQAGPKLGSSDPALAS QSAQIAGISHHWPPYYFYWLSSTIPS VLSLHSLILNTILRGSDVTSQDK RSMFAN/VLVPYTSBDDYHLKLVLEEG IGTLNKLVEGSRVQQLKQTYSKFDT NLSHNVALLKQYGLLYCFRKMDKVFPT LRMWQCRSVEGSGF
6809	20710	A	6864	371	77	RSMFAN/VLVPYTSBDDYHLKLVLEEG IGTLNKLVEGSRVQQLKQTYSKFDT NLSHNVALLKQYGLLYCFRKMDKVFPT LRMWQCRSVEGSGF
6810	20711	A	6865	273	34	DYLEPTVYLKLFLLP/CLIEETESHVVA QAILELSSNSPPTSASRSAGITGISHH TOPNFSNNITLLKPYLRLSYALLFA
6811	20712	A	6866	1	190	GAKGMHHTVNLVRY/CCVMRSHTYTW VGLR/FPALKISSCLSLPKCRDRIHEP HLALFCPSF
6812	20713	A	6867	506	293	EKPSNGHKKPYTWISIALFLIARTKQ S\PRCPSAGEWINC/WYTQIMEYYSMLK RNELNSCKET
6813	20714	A	6868	2	116	LFPFCRDR/SLTNLPRLSNSRAQGILL PWPPKLLGLQT
6814	20715	A	6869	10	141	GSAWLFF/FCR/DRGLALLPOLVSNPWL QAILLLWPPRVQLQA
6815	20716	A	6870	2	603	APTFINFPAGKPKRGDTYHLOVRGSA EOIARWIADRTDVNIRVIRPPNYAGPLM

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						LGILLAVIOGLVLRSSNMELFNKTGW APAAALCFVIAAMTSQQWHDHIG/PPYG PKDPHKGHVNYIHGSSQAQFVAETHIVL LFNGGVTLMWLLCEAATSDMDIGKRI MCVAGIGLVVLFSSWMLSTFSSKYHGHP YSFLAS
6816	20717	A	6871	375	1	QGFQGFVPVKFGIAPFAVACNPFPPPSF/ PQGPSPSGQWINDKKNPTFTKTPFLK NSPQKKKIIFLKKFKKNPP/GPNCKPFPK DFKFKRGLPKPKGGPLKXKKKKKKRKN YSLKKIYSPFGHFH F
6817	20718	A	6872	255	23	GRVDPTSTSQAGITGVSHR/GVQARDL GSL/QPLSPGFKRSCLSRSRDYRLV /PFCIFSRDRILPFWPQWSQTHLK
6818	20719	A	6873	5	157	YLLPTSYTHATHHTHTHTYFLMLTWS GLS/SCCYIFSLSGPNTKCNMIF
6819	20720	A	6874	351	132	SPRKSAYGVA/IYLYFLYFLINLSLYS IFYGAPNSFLCEVQEPSLG/SQWEPIS GNHFPSSIKVLAHREVM
6820	20721	A	6875	99	337	AGSPFQKGGKKISRVNRQPTQLEKIFM NCASDKGLVPRIYKLEBSAR/KYQSI PS KVG
6821	20722	A	6876	69	306	YVSHHLSFFF/CFFGGGKALFPCPRIG IKWQFQELLEPSPSGLKQFPLNPPETL EYRVFPFPQKFTFFFTFFFTF
6822	20723	A	6877	335	169	WHDLGLLQIPPPQ/SSDSASASQVACI TGMHHSFNSFYLFCYFKEVFLPTLD
6823	20724	A	6878	2	237	ELGVKVLPHPPYSPLSPDYHFLHNLN NFL\FHMQCARNAPQVFTESQSTDLTA TGINKLISHWOKCVDNCSYLN
6824	20725	A	6879	2	199	RGRVGRQPKRIERLKKLEEGRE/VAP SSSSSSSDFLISEPDISGSEDDDEGE VGEDGKKKKK
6825	20726	A	6880	1	206	FFFFETESCYVAQAGLELLGLGDPFASA SQVVGTTGARHHAQLIF/VFVFLVNGF HHVSQDGFLLTS
6826	20727	A	6881	1	123	WYIHTMEYSALKRKRKLSFATTWNL /RIMLSKTSRRRG
6827	20728	A	6882	15	105	SQLL/WRLRQKRNLRGGGCSFPWLCH CTL
6828	20729	A	6883	223	1	AASTFLPNLKNLSRG/SIRTFSSVTNV RKALTWIASUDIOPFSRRSLTLVARL ECVVRSWPASRRGLCL
6829	20730	A	6884	193	3	QSGQDLPFPCLNFFNF/VFCRDVSMIL PLLSNSWPAVILPFPKVLBLQARAT TSIHVFIF
6830	20731	A	6885	2	355	RLTSSDLFASASQAGVTGMSHRAFR NF/CILPNLSPCNHTPLSLPQIAPTI ILSLWIC/SLDTS/WDYRHMPPIAKV FFFGDGVQ/VRPGWAVVPFAASTSGV EAILFPQPPK
6831	20732	A	6886	1	151	HSVAAQGVQWHDHGLRPGTPTGLKQ/FL PPLKQSSCLSLSSWDHRCATLY
6832	20733	A	6887	314	203	FLFFCGDKVLLCF/RLVSNISWTQVILQP WPPKVLGLQE
6833	20734	A	6888	334	86	QNRSTFKRGN/NGKAWNLNFVIPAWEA EVAAKIAPLHYSGLDRKRLSKGGMKCTS IFCSKSAKDQTLPPVKKISLPTLPSI

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6834	20735	A	6889	345	152	OHARINSVFIVTGTGPHHIGQSGLEIMT/ S/GNMHASASQSRITGVSPHARPSLPY YKCSKKOLCNE
6835	20736	A	6890	2	169	ARECSGAIHTACSLDLMGSSDITFTTSASQ VAGTVGVITMIPRYIFKFFVEMESHCIA
6836	20737	A	6891	361	184	NQSCFSLSSNEHRLMPPHLLANF/SFF DRDS/SLIVLSRLVSNSTQAILPPRIFF FNS
6837	20738	A	6892	3	330	HESAAITGVSHCTQCTFF/CEIGPRFV PQVKGQGHDLSSGEPGPRLLRWPCILTL ONAGNTGTLPHKNTFGDPRGSGFPCG PGGFGTRDLGGFFHLTGKEDTGLDPP
6838	20739	A	6893	2	348	ARAFFTNPFCK/NKGLSMLEPRALNSG AQGILPPWPKKLGRLALPTWPKTGS SG LEGHSSLYPHSLIFPH/CSKCFIKON RLFIILRITENQGLTPLNNAKPAEPVWNE ARTQA
6839	20740	A	6894	340	240	CRD/RSIRMLLTIVLNSWQAILLSWPP KVLGLQA
6840	20741	A	6895	155	1	HLCFWAG/PVAHSCHPGTLGGRGRIITR GOEFETSLIGPGTQDVLKCSRA
6841	20742	A	6896	454	294	PSSNDYRHA/PPHENVPPDFFCRDE/SL PMLPRLVWVFWAQLLLPWTPTKALQALQ
6842	20743	A	6897	49	333	TYICLSFYQSITYLYDKQHDVLETVSHS VSLDPLGLRFSHLSLMDERLILPWLASS MNFF/CRNGLLVLPRLVSNSTWQAILP PMLPVLGLPA
6843	20744	A	6898	434	324	FFFFCRD/RSFAVLPRMLHSWTQAIRP PNLKVLGLQA
6844	20745	A	6899	127	365	LPERRRYVSIQYRYHLFOSILFFYACH ATFNNELM/LGVIAACNPSTLGGRDGR MALGOEFELGLDSIVRLHLCNKIK
6845	20746	A	6900	208	1	FFFFFFFFLVETRPHVA/RAGLELLSAG NPPTSPSQSAKITGIMFVWFSSNLQOF CYAHSFFTCTYSRA
6846	20747	A	6901	1	162	GTSGTRLFTIGKEMQPCPPMAELINK MW/YTMEHYSVLKKEKIFCNLTQLL
6847	20748	A	6902	120	313	DKVL/WRLEQENPLNPGGGCSEPRSHH CTPANATRAKLYLKKKCNFKGTLNYS FRVAVNTNLQMGSQSNYQI
6848	20749	A	6903	340	234	IYFCRER/SILPRLVSTWQAILLPRP PKVLGLQV
6849	20750	A	6904	1	327	GTSGTSRILPWGPGCIRTPSLKQSAHLS LPKCWDONRYRHEPPVYSFANLIKGLFF ELHLSVILWFLLLANPQTQTESKTFPSK /PRLVLNSWPOAVLPMSLRALASQA
6850	20751	A	6905	532	359	RDG/DLVWVPRWSPGFGQSSHHGPK CNDYRCEPLQDFSYSLITVFPSPSREL RR
6851	20752	A	6906	270	3	GGTVVYPRKTKI/WKPAVACNPMLLS GRCGWITRSGLPVSTKNTKISRACCAA VVLATPRAEQENRLKPGDGRDHGHQHG ETPLSLC
6852	20753	A	6907	1	312	GTSNKKNPLTMDDFRG/RTLVSEELIPD VVEIAREVELE/MEHEDVTELLQPHDKT WTDEELLTDEQRVVFLEVGVSVPVEDAV NIVEMTKDKLEYYSILIKY
6853	20754	A	6908	331	61	FRHVGQAG/LOKLTSSDLPAVASQAG

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						ITGMSHHTRPKLITRRKSNRAKLSRQT RLQPPVVBQGLLEQHEVYNVYMAHVSK SSSRGLS
6854	20755	A	6909	419	199	SAVQDGV\SWCDLGL\QPPLSRLLQKPP CLSPFSTWDYKCAPHPATFCIFIRGTV SPFWSWDSQTPGLK
6855	20756	A	6910	341	69	EAHVGLIKARSLRPAWAIQDDPISILK KSTFLAQGGWITRSGDRDLRASQSA QTIVGSHRAG\ITFAFIVERRFHASQG GLDLTL
6856	20757	A	6911	174	356	RTLLWPLRSSILRPMVAHACNPSTIAGQ GGWITRSG\ESRPSPLVNLRLTQANT VKPCLY
6857	20758	A	6912	391	3	SPPPPPPPPPSPPPPPPPQNFPPQASFF FGPPPP/YFPFPPKKSPPNPPPPFFFP PPIGKQFFSPPPPPPPPPPPPPPPPPFF FFFFFFFFFFFPPPPPPPPPPPPPPPPPP LIMCIMLFECKYILNFCRYS
6858	20759	A	6913	43	331	IRDTYFSLSDAPALDMLGTGQVLLAVA SLSGRGASLCVPCVCLCVRIH\IGVQA SGCVVCVC/CVVCVIRVCVCVCHMFA SLLTDLQLCLPTV
6859	20760	A	6914	250	11	TPNIGLFIWPCFEM/EVHYLAQNGLE/ PPGLKPSSSIISLSSWDYRHVMPHAQI CLSVFSLAQKGVPSPSNWLLITIVSITS
6860	20761	A	6915	532	53	SGQLAHQGLLILKESLSEKFSHPFP SAPSSMSHWVYFSTSSVAGAGVC WNLSSLQPPPPQKQPSRLSLTSSNDY TVI\PHILANFLVEMGFLVNGAQLKCL PTSGDI\PALGSQSVGITGVSHTR\PRF LFKIGPLFLFSKMSQDEARI
6861	20762	A	6916	2	373	NHTPVVLIATHEAAGGSEPRRAKIQIA MIVA/NCTPAWVT
6862	20763	A	6917	1	270	GTRQSPRLSLSSSCDHRVSPHBAF/ SPFFYFFFCR/DGFTMLPQVLIWAQV MLLSQPPKLLGLQVGVSHGARPPHCLG VSWVYNKP
6863	20764	A	6918	2	367	RCAPHCPDNRSSFFK/RVKTGLTIFPRQT SNSNPQVILLPWPP/KVLGQA
6864	20765	A	6919	3	354	HEVNI VETAKDLEYSLNVDKTGFKEI DSSFRRSTVSKMPSDITCYREIFCER KQSMLOTSLLSYFKLLQPPQPSA/TT TVISQPSSTRQPPPAKRLCAKGLND FGHWL
6865	20766	A	6920	366	41	SYSGEDAVHIVERTTGILER/TVAVGF HPSERRSVGGMISHSVTCRGIFGR KQC/RQTSLLFYFN/KQPPQPSATIT LI\SQQPSSTRDLPKXRLQLTSSND H
6866	20767	A	6921	3	368	QLIMELHLEPATLILQKLT\TGGASH SHHITAIP\PS\FTRENTLMFIHISPL LLSLNPDITGFFLLKKKPKNHGIRG PSYKRTPEGILLVVAQKTLPPKGLY KIAPLRLFGEDS
6867	20768	A	6922	3	91	FSVLRLV\QNSWFOVCLPWHPKVLGL QV
6868	20769	A	6923	334	91	ERCGKCAHISEIFLSSLDYIVYFV\F FELFFFFFFFFFFFFFFFFFFFFFFFS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
6869	20770	A	6924	375	37	QKFKNTKSKKEIMFNKTKKQVQTF TKAGVCMHHDGSLQPPPRPKSPSCPSL PSSNDYRHAPP/RP/ALFLFLGLWFG LVFLVEIGSCYIAQAGLKLGSDDPTL VQSARIIGPTHIANPTLTITSQCTIRG PG
6870	20771	A	6925	647	1054	CFWKAHQAGETNNIQEGSERPHFCPAD EYTVHSGPAVEDQCPKRRSFAL/SAQAGV QWONLSLQPLPPRFQKFCCLSLPSSN D/LHRHVPACLAQKCFISRDVCHVQOAR LELLTSGDPPASASQAGITGMNHHV
6871	20772	A	6926	3	204	DAWETTGFGMIYDSLDAKKNPEPHR/L ARHGLYEKKTKSRKQKERNRMKKVRG TAKANVGAGKKK
6872	20773	A	6927	1	112	PTRETPRGVASYLVFTTLLTLLPT/LSL IENKILKMA
6873	20774	A	6928	1811	478	DRARSRSRERA\RESSSRLQRDPBLSGR RRI\REIRPGLPESEPRPPPPAALTAD QPPPRRLSESGGGGMS\AGE\ATTTT TTTTLQCAPTEAAAAAQDPAPKSPVSGG APQAAAPAPAAHVAGNPGGDAAPATGT AAAASLATAAGS\EDAEKKVLATKVLGT VKWPHVRNGYGFINKNDIKEDVFWHQTA IKKNRPKYLRSVGDGEVFVDFVBEK GABAAVTFQDPQVTFEGRVADRRYR RGYYRRRGPPRNYAGSESEGGSSBG FDDPATDQSGARNQLRRPOYRPOYRQ RRFPYVYVQCTFDRSRULPHNRIOAG EIGEMKDGVPDGAQLQGFVHRNTPYRPR YRSRGPPRPPAPAVGEAEDKENQOATS GPNQPSVRRGYRRPYNYRRRPPFNAPS QDGKEAK/GEAPTENPAPPTQSSAE
6874	20775	A	6929	324	203	LIFVLVETGFRHVGQDGLDLL/NLWIR PPRPPKVLKENP
6875	20776	A	6930	3	364	HEASLTQTRTMT\HCSRTTQGSTASGR WTRSRHSCAMCSAALMRAAVASRCPSS/ IIPVTPQCLSWP/WKVP/LQCPALIS
6876	20777	A	6931	2	165	GRVGFCSVAQAGLQWHDSSLKPLFP/G SSDCPASASRIVGTSLAFHFLNVP
6877	20778	A	6932	1	370	TELSYSPSNGAISSQNL CFLSGYS/ RSSTQSVAGITGA/R/HITQLIFVFLVE TEFHIV\AKAGLECLTSGDPPASASQSV GLGVSBCANPHEVILKSIIMLGNLVRL MSICHHTESICLFL
6878	20779	A	6933	1	441	ERANTFNPPAPPN/QKKEKKKKKKKK KNPPGPGPPPFYKTPPPFVINGGSPGKK KGKGGKRGKIFPPPGGKKPPQKKG GGGGKKIFFFLFGPGGGNFFKKKGPP FPFPRKKKKIFPTGGGPKKKKKKAPPK KPGGYFPF
6879	20780	A	6934	518	340	PKPENFPB/PSPPKIPPPKKKVFSEKPP GGFNNPPHKKKKYFPFPPPEKLGPPKEFL KRPPPI
6880	20781	A	6935	396	299	VVEVC/GVCVCVCVCVCVCICHSCKSTL HRTGV
6881	20782	A	6936	486	272	PTRAPTRPAPPHADPI,IFCSDR/SLIM LPLVLINSQPMILPLWHPKVLGLQA
6882	20783	A	6937	1	264	YSNLRDRARCLSLSSSSWDYTCSSWDYKC

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						ASLRANF/SNFCREROLAMLKLVNS WAQVILLPQPSKVLRLCLAVSVFFGEKQ GQCS
6883	20784	A	6938	2	407	TGTGCRSVMLTFVFLVVTGPHVHGQAGL ELL/RPPQPKVLGLQA
6884	20785	A	6939	422	65	LKQPPPSFFFFFFFFFFFSP/LP YILYTDASAPCLFKNNTWYIKRIFF SPTFPIPFHEVENVLSLNVNQYCF FF
6885	20786	A	6940	462	209	LSEPNWYRRFPPLPAFALPMLCRDRL DTPLPSLVSS/SMHQAILAQPPIMLGLQ VHSAYKGFCLPVLTFEEVINRPLLLP P
6886	20787	A	6941	491	299	CAEYSPESGPTLALASLAS/SN/QWVYSR ISCKEELLGRTSPSNYNMTVSG
6887	20788	A	6942	429	256	FSHLSLFSSSWDYKHLSSCPANFCTVCT GFHHVGQA/GDPASASQSGVGTGSHH S
6888	20789	A	6943	932	661	FRGTGSYSV/TLREGSGEISAHCNRLPL SSDFFHLSSQVARI TSSQYARLIVFV VEMGFAMLRPRVGLRFLGFKPLHPP/RT P RVGLGLQE
6889	20790	A	6944	381	55	PASLPFCSLISDCCASNQRDSVGVGFSE PGVGYSLVRRFLRSERENIRVGVTRF SRGV/LSPLSLTQKNSLTPCASQVRQ LALLRLAKACTHEPARTVHSLR
6890	20791	A	6945	816	513	FFTFYTFPHEHLLRLLECSRMISAHCK VCLPRSSSY/PASASQVAKITGA/TRHS RLTFCVCLVERRPHLSQAGLELL/NL VIHPSRPPKVLRLQGVTRTA
6891	20792	A	6946	383	234	LTPSLMDNSGLKTSVEEVADVTKIVR ELELKVKEP/NVTDLLQS/YDKT
6892	20793	A	6947	423	60	LNPFPFPPF/YKFPKKGKFFSPPLKFG PPTKFFKRPPPPPPPPPPPPPPPPPP PLNSLVGPPKVEGWVWAQLPRAVGPPL PNP/KGLNKPAGGLNKPFFPSLNGSG EATPPLI PWC
6893	20794	A	6948	1	327	MRLLAALLLLALALYARVDGSKCKC/ SRKRPKI SYSDVKKL/EMKPK/YPHCKE EMVITTTKSVSYRGQEHCLHPKLQSTK RFI KWNAMNKKRVYEEAAGLRRRIG
6894	20795	A	6949	952	796	FFIHFVLEHG/PLLVGQGLELPTSGDP PALASQSGAGITQMSHRAKPSVSS
6895	20796	A	6950	364	6	ITTHKVFILSRATTPKSGLPQRKKIPL FTPIPIFTFGFIWAGGGLVLFVFFV FFFFFFFPPPPPPPPPPPPPPPPPP TPIGFKVLEPKINVFPLIRAVPLDMN HALTIFQM
6896	20797	A	6951	418	266	ISFPFXXXXXFFXXXXPFLFFPPPPFF FFFFFFFFFFFFFFFFFFFFFFFF
6897	20798	A	6952	459	7	PSYLYKPGSPQPNRRHSVP/HIRSNKD PPPPEVMKGGPPTPQRKKYFPBRKKL GGGGP IYPPKKKVFPKKKPGGFKPKPR KKKKIFFSPPEKGGPPPSILNPPHPI FFFFFFFFFFFFFFFFFFFFFFFFLIGKA MLLDMA
6898	20799	A	6953	325	143	LPSSWDYRVPPHSAHFKFCRN/RGLA MLPRLAKPRFSSISILNHPVSSILGA

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6899	20800	A	6954	585	306	TRLAR KTESHSAIRSQCS\GEISAHCNLRPGSS SNSPASASRVAGIKGTHQVQLIFVFLV EMGSHRAGQDGLRSPALVICFPWPKVL GLEAWPALHC
6900	20801	A	6955	2	155	FLVETGFHHAGQAGLELLISGDPFLAK S\DSQDVRITGLHRAMPFLITY
6901	20802	A	6956	3	346	DAWPDWKG\RNWPECANFPTVW/TG FT/HVQAGLELLGLSDVPTSSSLDAGT TGMSHCSRERPEISSRDVHTPGALQET WHITPLASSIRSLRCLDCPINHCPLDK DGVTL
6902	20803	A	6957	1	224	QQRIRSRKRDARKNVGTTIPREGRRITS PRYLFFVTQGETDGV\NGLEAMLLKTR STSPRPSRLHRRRGATSW
6903	20804	A	6958	102	344	GLLKPKSLKLCQCTITPVN\NHCATAANA T
6904	20805	A	6959	3	296	KEEEEEGHGKGGGGG\RRFRPEEEEEPE EEEEEEEEEEEHAFTHVESITQCKLLL CHLSLRVBAGITHL\CFVRAVTRSQRL LTKRRNGSVGHTSE
6905	20806	A	6960	3	172	RLGLPKOMDYKREPF/REGLELLTSSDL PALVSQSDGITKDVGHDTPEQDFTLLGQD F
6906	20807	A	6961	2	224	LALLERLARSGTIIAHCSL\NRSRLRLGL SDPASASSTGTTQMSHCSQPAKLLST CIRNSVAETIKCYLMPCK
6907	20808	A	6962	2	330	KOTLRQQTYYKQILTR\LVADTLAETH ARKEWDITFKVLKXKQPRILVLAKPSF KNEGESFSQPKCTITRVARSQAKGVLIH LEVKDITSTIKMKIRSSSLVEQTHW
6908	20809	A	6963	1242	929	EHGSCSVQAVQWQGHGYLKQPSBAH /DDPPTASSIAGTTZAHYLAQLIFKQFF NSLCCFQWSQVSNRLIGSSDPPASASON AGITGMSHGAWPQLSIYKGN
6909	20810	A	6964	1	378	KFFILQLFLHSFYEHFLFFSFLFFFFFL RPSFAFVAQAGVQWRULGSPQQLPRFK QPSCLSLLSRDYRHAPPQSANF/EFLV ETGFLHVQAGLELPTSQDPPPTASQSA GITGVSHRTRAFY
6910	20811	A	6965	393	43	VSPFFFLKNFYFSFTKTFVGGGSGSPGP POKRFFFTHTNSPFFFPFF/YKSGPRP GFFFTPEPEKGNFFPELRLGPPVFF TRPFPFFFFFPFGRQRTCSFLHFLNVR PLFRFL
6911	20812	A	6966	225	2	TRVCHGVFPGSCNPLLGKLFSSAPAP RGSNGSGPFPFPR/RNSPFFPFSVLLLE NGFHIGQADLELITSSDEP
6912	20813	A	6967	8	341	FVSVPDTHLYLPKIFFFFLHRSLLCLP LECRGTISAHGSLGLPGSSDSSES/STKN TKLPLRGOTCLGPQLGLLRHEKTWTLG GSGSYVPSKGRAMALQGVQONKTCVPH
6913	20814	A	6968	29	362	DYTCHPHSSSELKKKKKKKKKKKKKKK KKKKGGPKKKK/HGQGPFPQGRQKKIF PFKQGFKKPGRGFFEKNFPFGGNLGGP PDPKKNKPGKKNFLGGRGQKNSFLSAN
6914	20815	A	6969	391	17	VFFFFFLKFFFPEDKKLFFPPFLKIF F/SPDNPFFFLGGPSQISPDPKKGFPPK

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						IPPGV/YSPFPFKKGNFPFPPPLNFGPP RVFFKGGPPFPFPPFPFPPFPFPPFLGL RGNAGDCNGYGDVSYK
6915	20816	A	6970	374	268	IMLPRLVLSNWEQVILLPWF/PKVFRLQ VRAPVIG
6916	20817	A	6971	614	315	PFPGDALSPGLECGGAVLAKLQA/CLLG SERSPASASRVAGTCKRPPRPSGFFVF LVEAGLHRVQXGLMLL/MLVIRPSRPP TVLGLQMSHHRLLFTL
6917	20818	A	6972	861	528	PETESRSVTCQVQWCHSGLQ/P/PPG FIKRFFCLSLPSNDYRRTPCCPANFCIP SRDGVLPNMPGWSRTSDLVRLRP/PPC WDKREPLRLAKSRHFNHLLPQGEVEHF K
6918	20819	A	6973	274	119	PPN/VFVLVETNGFLOGGVKLSPTQDPPP PASRRAGITGVSHDPACPKKEYIFKN
6919	20820	A	6974	370	194	KITNFAGLFGYILPYSHYFCKLEKNRR /SLTLRLPLVSNWSAQAFILLMPKVLV LQA
6920	20821	A	6975	2	239	ARGPCSSI/SDOCASGQGVSGVGAPEF G/MOYNLLACLLRLPLEKOSIRAGVSRF SWYSLSRPLFT/RKGNPTPCISQVR
6921	20822	A	6976	361	270	PQWLVPVIPA/LEETVGGSLPFRSSRP AWAR
6922	20823	A	6977	363	48	GPPEKMCYPN/PRPYECNLFGRKRVFAD VLKFKLLRW/ILIDYTVQVDEKSHDBCPY KKGKAGRHGCTKRGQAQGGKRWGAT ARNAFMITSVQSDVRRKGPLAYC
6923	20824	A	6978	9	163	AGYNFLVCC/LPRLLEKCSIRMGVSFRS RYHLSMLPFAKGNSTPTCSMVIR
6924	20825	A	6979	408	212	YETGFCH/AQDG/LELLASDPPASASQ SARITDVSHRAQPHSAFLPWFSSKIFAY GSVNLVFPHS
6925	20826	A	6980	395	254	LIFVFLVETRFHVRVQAGLELLTSSLP SLASG/ITQVSHHSRFPSSAF
6926	20827	A	6981	408	2	KVSEFFPKGPRGKKGAGGFSPPFPFPF LGGGTRNFFYP/IFSQGGKK/KQFPFPF EKKKNPPNPAFWGPPVLVKGWGGRGQP LDPKVSNTMGAPPFLGAKKKTFFSPPP PKKKKPKKKGGGRSRSRTSRTRG
6927	20828	A	6982	2	302	RKHLPH/PVIFVFLQATLRHVQAGL ELLTSSDHRASQSAGITGVSHCSIPA TSFSTPFPVSARMLRGTKMKVPLIGPL PQDRLVAGIYFIYT
6928	20829	A	6983	2	375	RORVGQVGGPVGRTFIPFQAGSDSARI LMLFYCTLHHLGHLFFPFFKNCISGN VLLNPSRPFVILEKKTLPQPPF/HI LSPPHPGAGGGNPTARKIKGLSYRDPK EGHKEGVVAITPTP
6929	20830	A	6984	1	146	PRPANFC/DFLVETRFHAGQAGLKLST SSDLEPLVQSAGITGMSHRA
6930	20831	A	6985	2	95	LTMLPRLCENDTIPACSLNS/SGSSHS LTSTSKVAGTGVHHFHLNF/PLFIIO
6931	20832	A	6986	340	169	VCSSGLSSPLLEQHKNLIFASGDICT /ANGKSGFNQPPFLKTPCCTHRIMST YL
6932	20833	A	6987	346	218	PCLTNF/SIFCRDE/SLTML/PRVLVLS NAQAILLPPRPLLRLQA



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6933	20834	A	6988	345	141	NRKPCPSMTHWIKGSHIDMETYAAIK KDKFMSP\ETITLGEVTRKMTGHRLLS LIRGS
6934	20835	A	6989	154	236	ELTSPSRSVERICSSFIKVLFPVETDLFT LSLSPPFFSVLFFFC/REMGFTMLPTLV NSWPOVILLPWLPKVLRLPT
6935	20836	A	6990	2	156	FLVE/TGFVEVGQVGLLELTSGDLVASA SQSVGLIGVSHRVRCPLFVCTCLV
6936	20837	A	6991	310	96	KNFFFLVKKSP/LNVAQGLKLLGSND PPASVSQSGSITGVSEARFLNPKYKRT DENTSVLKGLNKKKK
6937	20838	A	6992	15	279	NLCFFPSYSLPGLTFFPFRGPHVQGA GLKLLTSGD/LRASPSQARITAMTRHP HPLVCGLLNSTHCDWRGIPHWGPDLP REGFS
6938	20839	A	6993	127	352	KLADTPQSRFVLVCV/LIETKSLCCPG GLQLLASSNPPTSVSQSATITDVRHAE SQVFLNVPKSSKPTNTGL
6939	20840	A	6994	323	119	SSSRDHKGVPPHSAMPCFF/CLRQSLTN LFLVLNWSAQVLLPSPPKPFDLAKK KSSKMWSSLLIT
6940	20841	A	6995	230	1	FFFETESCSVTQAGVWCDLGSLOPLFP GPKQPSCLS/LPNSNDYRHALPCPANFC IFSRDGVSPGWSGWSRLPDLG
6941	20842	A	6996	346	121	EDICTEPFVTDALLIAKIRSPHKCPSVDT WTRKMP\LYTDEKYLKILKILGMSH HSLPVPNHCCLKYLLS
6942	20843	A	6997	2	198	SNVTVAPEEPGTTCWCHAGLTVLVM QSHVDCDGLDVR/NLVICPPNPKKLG IQALNQSPDI
6943	20844	A	6998	183	31	MRLKSSQIQGT/VGHANPSTLDRGE RITQGEQFKT/GNIVRCLYKD
6944	20845	A	6999	3	471	LALSCTTLTAHCNHLGSPLEPTTAP RAAGTTGVHHHAWLIVFFGKDGVAQPG LKLSPK/VIRPQLPKVLGLQA
6945	20846	A	7000	483	239	GNNNLFLFLFFITGSHFVT/RLSCQW VQSGAHSQPSAPRAQVLI/VFVLQTFH YVG/QAGLQLLTSDDPPHSALLKVRD
6946	20847	A	7001	132	353	YAKLTGTFARGPVVPGFTLVAVWWSF AQAGINPFVCIFSNRELRCFSTTL/PL LQIKQVTRGTLCCYMRHL
6947	20848	A	7002	2	399	EDAQEVRLQGRVHSSDKAITPHSQRE FQKQRESAR\SELITES
6948	20849	A	7003	2	135	IFQFLVRNGFHHVQAGLELL/NLMIHP PRPSKVLGLQAYWISTRP
6949	20850	A	7004	2	114	IFQFLVEMGFHHVQAGLELL/NLMIHP PRPSKVLGLQA
6950	20851	A	7005	455	1	ATFFANLMLPSSSQGLKLSHTTLLFL LAPSTLKDHWQROWL/CTCSQHEFR PREADRLAPQVQRNPGQGETPSRKGG EGNNWGGQGLHIYTTTHHTTYVRYTHA NNWNCVVPVLAFAQETEVGGPLEPEVAP ANVTVRPCLKKK
6951	20852	A	7006	371	172	QVILCLSLPGSMDHRTTPHPA/NFLVE TRFQHVDELLELASNDFPASASQSGVIG VSHCARPCYDL
6952	20853	A	7007	486	252	PQVTPFFFFFFFFFFFQALFSTFYLLHF FFFFP2FFPKQFFFP/LSLIKQKQFP

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6953	20854	A	7008	1	113	FFFFCYCLNGSLFVVVITYFFVNE KNFCR/DRSLDTLPRLISNSWPQVTLIP QPPKVLGLQA
6954	20855	A	7009	105	383	SLHRPAHPGLLKPGKGAHISFIHLCRDK GDIAITLPRLVSNWPQVTLIPWST/ MYL RLQA
6955	20856	A	7010	609	348	ESHVTVQAGVQWYDLSLQLPFPFGS\SD SPASASHVAGITGMRRHTQL\IIFVLLVE TSHHVSQTKEFLVDITKFFVIFVSGKR TRIRL
6956	20857	A	7011	382	233	DLEIFRGKTFILHHIFPPFFPFFFC/RRRG LAMLPLK\I\N\SNWPQVILPKCWD
6957	20858	A	7012	359	199	DLTSLPFLPFLPFLPFLPFLPFLPFLPFLP LECSGALPAKCSLGDARARLKLK
6958	20859	A	7014	3	274	CCCCFFPETHSHVTVQAGVQWYDLSLQLP PPPGCKRFSCLS/LPSSNDYTHV/PSSP LLVRNSSICLLSCFEMTELEFDGVLAIY CCVTNDLGA
6959	20860	A	7015	372	54	LPSAWAEERGGPLEPKGLRSQRAEIA/P CTPAWVTEQAYVSNKINTERPFQKLEHV EGLSCTTQKFSND
6960	20861	A	7016	548	158	KFDT/GATLFDGRPAVDEA/DFPSEAV YLTGARYTGEELSDTWQAEHLIEVFLP AQVPDSELDAMESKRIYPVMSDIPALSD LITSHVAGSYDYRRDDAGLWSSADLT YVITRM
6961	20862	A	7018	396	34	QKNEYKPTMQLHLPFAKATIKKILKNG GMHGOGE/METLLHGWCECKL\OPLMKIT MNRFLKEPKVELPDPAPILVLGIQSSCH WESSNPSTGDPALPPLGIQSSQPRKVI KKRYLHTRL
6962	20863	A	7020	2	241	FPGPATAARRRQKEDRYERYDKVLSDKLK EARTRAEFARSLTRLEKSIDDLQDEL/ YAHKLKYQAISEELDHALNDMTSI
6963	20864	A	7021	347	3	NDLSLTHSVAQARVQW/NTSSLRPFP PQPKRFSFSLPSSWDYSLNCKPYHLH FADEEITLTHSQAQLECKSNMYKDIDEN TVRSYKLYKVPQKLESRNRNRTKSSSTE VRS
6964	20865	A	7022	2	160	LREDDRRGRGFHHFGQ\GLELLTSSD/L PTSASQAGITGVTHRAPDWSFCQF
6965	20866	A	7023	3	248	DRVSSVAQSSLELLSSNPHLGFPKCDW YRPNPPLPFPSSRSLFLPSSFLIPCRDRV SMLPKLAGSFWVRPWPWSKYLGQA
6966	20867	A	7024	483	143	PLMLPKFFFFPKAKFWGGVPTGSPPK RVLQKQKQVITFPQKQKQVITFPQKQ KRGPPKELKRAPDFFFFFFFLARDK/ SLTMLPGLVLNWPQAVLPQLPPKALGL QA
6967	20868	A	7025	414	81	PHPLKFFFFPETTFYFNGVFSFSPDPGR KVPPQKSPGGFILLAPKKGSPFPCEPFK IGPPRGIFKRAPPYFFFFFNNRDK/S LTMPLGLVLNWPQAVLPQLPPKALGL A
6968	20869	A	7026	16	218	KPAPRCRNSARENIQNPKHSDTPFLK K/HKINNKKLAGRGTHLWQLLGLRLW EDHLS PQRSRLQ
6969	20870	A	7027	28	272	RFVGVGSPSPGAGYTHLLCAFLSPSEKC

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						YIKKDYRKTCRLRFPYSYHFNKRKSYTLKTMIKV
7002	20903	A	7060	397	129	FWGPHKKNFPLPARGRLGSGFKIA/LPL FFFFFFFSLSLFFFTSGSCSVS\RLKCSG TITAYCSLEFLGSSNPPASFSQAAGTTF TFFLFTG
7003	20904	A	7061	3	351	SCFRLCLPKEAWAMAGAPPPASLPFCS LLSIDCASNQKDS/VKVGSPSTPGAYNL VVVRFLSGSEKRNIRVGVTFRSRRCPSP LSLTRKNSLTPCSSOVROCLALLRLAH GARTH
7004	20905	A	7062	60	324	DDFVSVVQTVGVNCGRGLKPPQPKLSS TSLRSPSSSDWDYGRVPF\NIFCRDRVSL CFPGWPRTPLDLRGSSCPSPKV/KLHTRV TAPGO
7005	20906	A	7063	481	160	RFGAPG/PDDFARMGPRPKGAFTLVHP MPGSAAPPGLLSEF\PHRGPSFAARSP TLRYPGRAPSKGSGEDPARPATGPGPN LIQDGLVIMSLTENVC
7006	20907	A	7064	65	481	CLCPAPRCGAYRGRQASLSCGGLHPVRA SRLCLLPQAWAMAGAPPPASLPSCSLI SDCCASNQKDSVGVGPSEPGVGYSLVVR RFLSRSSEKRNIRVGVTFRSRRCV/LSPLS LTRKGNCLTFCASQVRCCLALAKRLAHGA
7007	20908	A	7065	392	183	GGLG/LIPNPNLSLFSQKKKKQKQKGG SPRGSPPOGLGGGILTPGKGLGSPN FGPAPPFGGKKKSLF
7008	20909	A	7066	538	248	FELRQSCSVVQAGVHGMVLSLQTLHRF F\KFSCHSLSSSDWYKCAPPLAN\FVL LAEMGFHHILAQGLLELPTSNDLPTSA SQNAGITGVSHHT
7009	20910	A	7067	2	127	VTGQAVVHACSPTGLGARAG/MIVNAQQ FRTSLGIMVRPCLYL
7010	20911	A	7068	379	217	KRMFCRNE/GFTTFPRLVLNSMAQTILP PWPVKVLGLQVQTTVPQGSPLSLYKE
7011	20912	A	7069	386	176	KRDKVDKMLKKKNCIHMEYLLAKKET LPFATVWNQLQ\TFILSEISQKQDKYHMI SLICGIMLIYRIE
7012	20913	A	7070	30	408	NSSELGSGVGUGPTEPGTGNLIVCNLLR LWEKCSVNAVGSRRFQ/CTDYDGFPMVG KGNPPTPCASQVRRHPALLRRTLEGLHP CASHEKQVPOLEMKSSVFCIDILTGSC RVEGFPFHGLGSENF
7013	20914	A	7071	310	414	HYVWESFAPALCNIGSLQPPPPGFKRFS CLSLPSSMDYRCPPRLAN\FCSGSLGS WLTAATSASWQAILLSQPPE
7014	20915	A	7072	353	243	IFIFCRV/RGLTILSLRLVNFDQVILL PRPPKVLGLQV
7015	20916	A	7073	1	276	ELWDFPKRPNTLYSLKERRKCVCRHGR RDRNKLTLDIMAFNSFWMKIINPQIQE AOOTPN\QETGRKLALRHITIKLAKTND KKKILKAV
7016	20917	A	7074	362	133	GGGGGGGRYSPOKGTILPITPPSNWGPK GAPPFRGNFFFFFFFS\RDGCLAMLPR LVLDSWAQVMLLPQPLKVLKL
7017	20918	A	7075	3	177	KNSPHHSLPNN\WLYRHMPFCANVEFF CSLAVLPRMVSNSWPGALLSPWPTRMIG LOT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
7037	20938	A	7095	21	428	DKGLTVTQARQWV/HDPSSRQPPSPGLK RFRRLSLPSNWDHRCAPPRVANYFFFR WGSYHVAQAGLELLASNTPTSSASHAG ITALFLRDTLVERFFMQSPCFPPQSGAA TAQIPQGRGTRELFIPLFLANDYLS
7038	20939	A	7096	320	134	LPLVPKITFFPLFLNRDRVLLCPGWSR/ ILSSKQSTLLGLPKWDHREHPPQAVD HTLDPS
7039	20940	A	7097	402	221	DYRHVPFPANP/LVENGFMHVSQAGLE LLGSSDPNPTSQSAGITETSHQAQAYT IFIY
7040	20941	A	7098	427	259	PPPRPKRPSGLSLRRMDYRPPSPCPN FFFFF/CLPVMQGHVAQAQALKLHD
7041	20942	A	7099	422	275	VQWYLLDSLPASSGFKRFSHLLRLTW DYRH/PRPANFCIFSTKDTFI
7042	20943	A	7100	3	404	HASGATWRDPVSTRVWHIPIVPATQEG EMGGSLEPRK/LKAAVSHCTPVNVT
7043	20944	A	7101	539	336	FETSRKSPTEAGVQNRGLGSLQPPPGF KR/DSPALASRVGTGTGAHHHAGLIVF LVEAGVSPHWPGNS
7044	20945	A	7102	408	287	WLILFFIFCRD/RGLTMLPLTVLSNSAQ AILLPQPPKVLGL
7045	20946	A	7103	1074	705	SFLRNSFTLVAQGVNRWGLSLQLPLP WFKQFSCLSLLSSWD/YGRPPPRIANYF FVILVETGFRHYPMPVNSNSQCP/CDL PAWRNWSAGH/TGVSHCAWPKMFLNCC TCTHSPYLGIVSLG
7046	20947	A	7104	227	55	FSQHKINIQFFYGLSPH/MSPFLCRD /RGLAMLRL/VLNSNPHVILPPWPKV LRL
7047	20948	A	7105	479	314	PRLLLIFFFFIERGL/LCSPGWSQTFOLQ RSCCGPLPKSNWGRKRPQCLALKNTLQ
7048	20949	A	7106	37	143	NSFF/CKRRGLTMLSLVNSNSWPQVLT POPPKLEL
7049	20950	A	7107	441	106	GAPSPASLPFCSLSDCCASNQRSDVGV GPSEPVGYSLVVRRFLSRSEKRNIRVG VTRPSRCV/LSLPLSLTRKNSLTFCASQ VRQCLALLRLAHGAHTHPAPTVMHSLV R
7050	20951	A	7108	413	207	CCIQAGPAFFGGPPPPRNGWGVPPPGY /MPSPPVFRVGLLVFRGPPNNWFLPMGL QPDGGLGDPKFKAK
7051	20952	A	7109	92	409	PHLPDGAAGRCRCPPPRGGGCVRAGPOL PPGRGQWGGGLPFPSPKTVGLPOGGAL HFSQAVARQRVSLRGRGRBETLLTS QKGRGGRGTTHSDGPRG
7052	20953	A	7110	408	13	PPWSPGKPPKHAAGNSPPGPPWOTPLS PKKPHNYGGQGGPLMPDPKG/SGPGI PSPKGGKSLNPGQKGIKIGAPSPPPGG PKKKPPSKKKKKKKKKKKVIGKSSQI LLFKVSKILSVNFIHLSSLI
7053	20954	A	7111	290	175	LKKNCR/DRSHMLPLRLVLSNSWPQTILP SQPPKVLGLQI
7054	20955	A	7112	1136	552	ILFKMGCEAGQRCSCEVIPITLGRPRR ADHLRCGVDRQDPTNLKRLYSNTKIG WAWNRVPA/IPA/IRRPATRTFNPDRR WRLPLNLRSHPLHSHGRQSKIP/KKER KKGDRKRGCGQGNWQKQKRRKRGKCE

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						NGMGRIGGRNKKEGRKERKEGRKGNK VWARLGAFPEQGGKGLRRGPSEAVGVSP L
7055	20956	A	7113	570	199	LCLLRQAWLMAGAPPPASLPPOGLISDC CASNQDQSVGVQPSSEGVVYSLVVRFL SRSDENIRVGVTRFSRCV/LSPSLR KENSLLTPCASQVRQCLALLRLVHGATH WPAPTVMHSLMR
7056	20957	A	7114	466	284	RRTGIGWTANKRKAQTQGLTTFPHLLHK QEGGVNGSQKQQRD/VTNSAPFWRLHDQ TANCLG
7057	20958	A	7115	474	224	DSNFEKSTLQKLNLSNISKYRETFPER KSLNQQTSM/LFKLPQSPQPSATITL ISQLPSTRGNPPPAK/RQLAEGSDGC
7058	20959	A	7116	377	111	FXCNFKSFLFFSLSLTRKNVVAHITFFF FFFFLPTPPFFYIFLLIFCFFFLFYIF FFFFFSFFFFFFFFFFF FFFFL
7059	20960	A	7117	417	148	VFPCLANF/NFPVETGSPYVAQAGLELL GSSHPPTLASQSSQITRVSHCSLLYFLM HSNTSISFFSFNALVSLEMPSSQDGI TVLAR
7060	20961	A	7118	2	196	RVPFPDA/NFVFPVQTAFCHVAQAGPK LIASNPASASQSARIANVSYCLEPSL RLRSHLDF
7061	20962	A	7119	2	417	EAGGSLERPNRLHCA/LVAPMNSRCIP AWAT
7062	20963	A	7120	801	450	GPKFLQPPGVIN/RRPQGGGLPRVYK NNYPEDRPIVLPAFFSGGR/GDPGIDK HPLPRKKQKNSPGRGGEPPFPFGPFP GGERKINLTPQRKRVHWQGLAPFPFPS LSAKPKLF
7063	20964	A	7121	3	199	DAWGFAIVQAGVQCCDSSLPSP/R ANFVFLAETGFLHVGQAGLKLTSGLN ALTSQRLRLQ
7064	20965	A	7122	407	164	NVAGLTGAYLDSFGGRDRV/LIMLLRLV LNSWAQAILPPWPKVMQLQACTIEVSS LVAQIASKRLSGVQESDEARITOC
7065	20966	A	7123	33	192	RWDFTMLPRVLGSYSAAH/GPRKMDY KHBP/PCCPGWSWAQRDLPTLASQAGI TSMHLLHQAIPLFLQPIRPSILVP
7066	20967	A	7124	3	399	STPVDWPSRAFTPRGRSAARQGN/TPV GQRM/RMGLSRRSPGQREVSRR/SIS C/ICWQLGKSNVLPQGRSAPALHESR RRGSSPPCPDPLQTLVSPQELSHSAP IHLRSLVTIGDCISTGGAPTCRLA
7067	20968	A	7125	1901	1574	FFEMESCSVAQAGVQVHGRSGSLQPLPG FKQFSCSLSPSSWDYRHLPPHIANFVVF LVETGLHHVGO/SGLELLTGLD/LLPAS ASQAGITGVSHHAWAKNCFLTSLDT
7068	20969	A	7126	408	234	LPSSWDYRSPPPQANFYTFSRD/HGPTM LARLLTSSDPPALASQSARIAGVSHIAQ PVYF
7069	20970	A	7127	88	277	KLSTEYKKRQPEDSFFFL/VEIGFRYV AQAGLELLSSDPPTLASQAGITGVSH HIOPPFKK
7070	20971	A	7128	3	140	ORWNCVPATRKAEAGESLETSSRLOGA MITP/CSPAWATEQDLAS





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7086	20987	A	7144	3	159	HASEKINWYMTREHYA(SQKKNKIMSFPVATWMLREVNILSKLMNENMWSNGR
7087	20988	A	7145	343	115	CEFYPLSCIVFYFPCR/DKGLSLLLRHVSNSWPOVILLPWPCKVSHQAQPFYFRNKQTKIDLSFETAAADLAYYS
7088	20989	A	7146	453	119	RCWKGCGLWISLRTT/WREMLVQPPFNKTWVRCRLKLVKPPPEPATPLPGTHLKKTKAVAQRMCTPLFIVAQHHLLKRLFFSRCVFLAPLKLIA
7089	20990	A	7147	3	105	TIENGREVIS/SSYSSTMANEGLFSLVA RKLGRPL
7090	20991	A	7148	295	23	FANIFSHSAETLQTRRMGPTPNLL/EK NFOPRISHPAKLSPISEGETKSFDPDKM LRNPITTRPALQEFLLKGFMSFPDGMVK LETIIIS
7091	20992	A	7149	1	161	RTRGFFFYLDGVRSLAMP/RIVLNSWPOAILLPWLPKVLGSQTLNVAAYTVFV
7092	20993	A	7150	1	219	DYRCVPPHPAHF/SITPFCQR/SITMFL LSLVLSNMTQAILLPWPKLLGLQACTA MPIDGVELLWVGSCFVKES
7093	20994	A	7151	177	34	ELVSLFSLFSLSLFSPFLSPLPLSLF LPSFNPSF\LPSFLPSFL
7094	20995	A	7152	398	40	MNDRLVLLPHPGNNAVAQSMPTGASN/PGLKQSSHLGLSCSNYRHTPQCPASLLAY VMHYVMYVMYVCRD/RGLCMPLMVLVS NSRFOALLPQPSKIMGPLLGAVAHAYN TSPKGSQR
7095	20996	A	7153	418	179	RNSCTQVNEALNLSGYFFLKLYYDF/ CORQDLAILPRIVNYSWQAILLPWPK VLGLQHEPPCLAVIQPLKGNLKIV
7096	20997	A	7154	767	337	QALLCLGQWS\VAQSWLTAASNSSDPP ACLPSNMDYRHVP PROAEMS FRVSYS P VIKRDPGS PWREMRPCE
7097	20998	A	7155	421	301	HAQLFFCRHW/SPTMLPWLVSNSWAQAI LLEWPKVLGLQV
7098	20999	A	7156	410	269	AGGPTGSGFFFF/CYERGVSLLPRVSD TWSHVILQPOHPKVLGLQA
7099	21000	A	7157	3	237	MQTKA/TMLYHTPTMTVVLGFKRNSR WQARGEIGTLVHCNWCIMQPLMETVW HFLKRLNKLGVVVHACSINYSGG
7100	21001	A	7158	435	211	LFLVEMG\FAVLASLVLTLE/PRDSPTS ASQRARMTGMSHTQPLCLFVSKFHLA EKLSLWQNLRRAGICRLS
7101	21002	A	7159	3	220	SSASQSGGITGVSHARPSEQ/SCSV AQAVVQWQNYSSLITPTPLGKRSRLSL LSSWDY\GALPHPSVAS
7102	21003	A	7160	1	172	FRVIGRTGSGSLCTQVRVFMDDTSRS IMRNVK\SPVRGSDVLTLLLELETLLR R
7103	21004	A	7161	1	180	DAAVPLKAT/ARPTRPDRNK/IDISLDI HGPTSLQKNTNTFRANCIPIVPAIRE ADMF
7104	21005	A	7162	3	108	KKKKTRFKLV/MQYHRFPVNVVTPGK KKGPNANS
7105	21006	A	7163	409	110	GQHGLTQSLPLSAPPARGAVPRNAPPD/ SGLSLSPLLPTAFATTGASANRFSIG PRDGNFLNI PQQOSWFL
7106	21007	A	7164	35	371	YFHLSLLKLKPLASINRFFLTVVVLLR

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						LLFFFLGETEPAPVAQPGR/QGPNLSSL RDHFPSPVKIIFPGLTPPRAOTSGLDPPSP AIFGFFKKKRGSPGPGRAWTGPRGGP P
7107	21008	A	7165	3	382	YTGPAWMSNLVLVLTATSEALVGGSLERS SKLQ/QPPLRHCTPAKAT
7108	21009	A	7166	1	305	TAVVITPTHSVYTEVARNPGACHNGGGL LAKGNSLAKRQI/VOTLAKRHGEELAMV DSLITAGPKLEEA/ASDPAPARVRLRQ ACRRNSVRLCWEHLVSKV
7109	21010	A	7167	383	55	RDLNSVRLMKALALCTPALMGFNSI FYGRVAKLPFPPLSYIQGLSERNNWGD DTTDCSFIFLYIFCTMSIR/QNIQKIVG LAPSEATKQAGGFLGPPPCGKFS
7110	21011	A	7168	465	166	SPQGAQTKGVGFKLAPWGP/PGFPRGK PFFWFKKKLPPQGGPLCSRFPGGLSQK N\SGPWGELFPWQNGPPSPPGKET F FSKKKKKKAVDYDLS
7111	21012	A	7169	2	323	IQQSKTLSEEVSADEVIRRELQTAET EDVTELLHFNSTACCREIFHERKQQMQ QTSLVSHF\RIKLQSQSSALATINQSQ PSTLRQDMPATRLHITGGDLNH
7112	21013	A	7170	3	509	FGTIPDLVLCADLNSLPDSGVVEYLTSGG VETVHDKFKELKYNESLTNPSCHGNGT TKGRITKSPKLASATESGLPTVNTFD FKGLDYTFYSKQIANTGLLAPLDHSH LVNNISGCDHPLIPSDHSLPAQLEL/ YTAFPAFSPQKRPSPQEVVIGLQRTALI HL
7113	21014	A	7171	1121	320	SSCFQTSNHACFVTEFVGGDDMMQLHE DVFPPEQARFYVACVVLGLQFHLKXII YRDLKLDNLLDAAQGLFIADFLCKKRG IGFGDRSTFCGTPEFLADEVLQEAAT RAVDNWLGLVLLYEMLVGECPPFGDTES EVEDCIRLHGRPPTPAFLSVQG/VKFIQ KILQKCEKPLGAGDQNAEIKVQPPFR PTNMQALLARTIQPPFVPTLCGPADLRY FEGETHRAA\DALTPAPHSILITAROQA AFRDFQVSEFLFP
7114	21015	A	7172	355	3	GLFLSLMGRNIFLPTFLPLLPLSLMLGG VCGSP/ITWCCLETDONKRVTDITAKI QKLANFPQIWKMSDPLPCGWSSSLG RKTLVGVILVILGVCLPLCLLPLLVK NIQSANV
7115	21016	A	7173	184	2	EKKVREDDDDDDFMESRSYI PAGVQR NL/LHPLSPSGFKPPSCGLSPRSWHRCA PLHQCI
7116	21017	A	7174	1190	407	SLKRRPARGSRPMSHYTSGQKPYLP NGRASRPRESRMRLQFPALIGRGALVT SSSSLPSPFPTLSWRDEARRASRLKX QNSTPESDYDNTNDMLPGMSSSRKGR QRMVWPGDGLVPTDAEPHVAPSPPTLPS TEDEVIRKTEQITKTIQELLRQAQENKID SYIPCSEIRHVAVTEMAALFPKPKSDM VRTSLRLLTSSAYRLQSECKKTLPGDPG SPTDVQLVTOQ/VIPVCVRPFAKAAQL VTITTKENN
7117	21018	A	7175	3	136	ALHLASLKVFYRYRVLST/LKRLVSNWSW

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7118	21019	A	7176	3	316	POVILLFPPFKVLGLOV GIVKFFPPFFLTKCKRTVTQAGVWVCSLG SLQLPFPFRKQFTCLSPFPVNDYRHLPI CLANFCIFAVETGFFHHVQMGLELLTSG YFPTSAPPDAKITGVHRTQP
7119	21020	A	7177	529	217	LLPRLEYSGWIAHCGLLQSSSQAILG ACVCAN/HEKFAFPVETKSHVTTQAGLK LLASSNPALAGSQSVOLTGVSHCAQATL PFKTVDKGFSFNLSPTPELL
7120	21021	A	7178	3	150	YTICKSKRDKISTYHMT/HLKTHHTHH THHTHTHKPSTTFSYETPTM
7121	21022	A	7179	540	69	ACRGAHVQVGDGSAITYVEDGTACQPTM LSLDHLCLPALAFNFTCTDSGGERICS HHGVTAWSLQGREKLTGRDPLTSPQ ALPIG/CSNKGKCIQPDWTGKDCSHEN PLFTSPPTGETERYKQPSGTNIIIDSIA GAVLVAIVILDETGWGYK
7122	21023	A	7180	452	279	CIDSTYQRIYHLSISLVSYYLSIYRSY LSIYLP IFW/SLYLGPRFLTRDRPOLLS LT
7123	21024	A	7181	501	183	HVRCLAFICALIGFPFGYFSIMPVVT/V DLVGIEHLFPNAYGIIICVNGISALLGPP FAGWIYDITQKYDFSYICGLLYMIGIL FLGTOPCIRIEQSERKTMQGARV
7124	21025	A	7182	446	245	IAVRSIALNGVSSASRYADTVATKLAT F/SLPWRDNDILPSMVFNSPQVIFP SNP PKVLGLQM
7125	21026	A	7183	420	73	DSDDSGQSRLKP/FKRGFTLLDATNFI CDSLEDPKISLTQAWKNLIPFLMDDYEG FKTRVEEVTADVVEIARELELEVEHQLG AVAHAYNPNTLRLRLKPSRLRPQHSK TLSL
7126	21027	A	7184	567	174	FFLRDRVPSLTQAGVWQDSSLOPFPF RLKQSH/PALLSSWD/YRHPCLAKF LIPLORGLAI/FARGVVSNSWSQ/CNL PASVSPSAGITGESHYSQPFLSDSQTK VYKTRSTISSTITEMGCERKO
7127	21028	A	7185	345	59	RNGSSCLAQVIQSLTLPLPLECSGVITA QCSLGLVSGSNPPTSASC/VESHCPAQD GLELMGSSNPFLAGITGMHCAQPLFD LFLYFYKLSVHY
7128	21029	A	7186	1	209	LSVLEIGSHSYTQAGVWVHSSSLQF* MLGLAKSSRSLP/KCWDYRHPWCLPGL LRLKFPDSVGVYA
7129	21030	A	7187	3	225	EKTVSDRGAEZCTESL/NARPCFSALE VDETYPV*EFNARITFTFHADICTLSDKV RHFLKPIALVIINHHIF
7130	21031	A	7188	1	377	RS*RNINGDRDSDHVRGACIETAKRHK YMAADMELFQADINRKKRDIQDYLGRK ISFELMRQPCITPSSGITYDRKDIERHLH RVGHEDFVTRSP/LTHEQLINPLAKMVI DAFISKNGCVEDY
7131	21032	A	7189	1	359	SRATCEVRQQRHG*GIHNSYDWRNTWPF RETKNSVPLSCCIRIVSNNGNSLAHPY DLYARGCRALVGKKLRFPMHVIWAEIA PAAIQLLSMLSACIVMCKRSTDPAYRLI ITVGYTA
7132	21033	A	7190	496	118	QNRKFPFPEPQTS*LGLYPKRYKLYHRD

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						PKTCHFTAALLTTEKPNHHKHLNMDWV 1KKVNYGTGVHACNQSTFLPWFFFRMB HAVAQGVQVIMNLCSLQAAPAWATEXDS QKRKPIDPHKYIVN
7133	21034	A	7192	1337	342	ISEATRTFRESIWQFQSSPREDELRNQL SASGRSHSGPRKSTPEPSCQHRSSHCG CAPVSSAARPOGSPFLSISGALERSQPS VLVYIP*VAAGQPVKACLGASSPPRL* OGLCTGHRTPCKEASWPESSAPPAWHL LESLCLPSERGEKLAQARSQKHLGWKLS KLCPKFKYSMSGPDDSPSVLRDPEAGIT RWAPSGNPEEEVVLQKGLKYLQNTISEVL SVLHLHLIKALQLHSTNPPFFVNARHLIV GOISSALITLNLSQLFLLLRFPFLSQV ERHSPLQKTTGTTETNLVLFQDTPMNP SSILLPSKSYCPALDKASHFYQ
7134	21035	A	7193	469	130	SASMDYRRPFPRESNPFLY*RRGFTILA RMVSVS*PRDPASASQAGCAYSILYQ ERFARLHPACLAAPRYNASDPLSSLHSHV PPGLHLEHHEHLMHCLLPQIGICRPGKLN Y
7135	21036	A	7194	430	149	TVWQFLKQLNLEISCDPVILLGICPRE LKTIVHFKRT*APVALCTVPRKQL KYPSVDEWIKIMWYVHTNDYPSVTKKX LAKHSGSHL
7136	21037	A	7195	257	412	TATSNKEPLKKVCLMWRKDKCWARGFT ACNPSTLGC*GRWIMSRDRDHPG PLISGVVHPCNPSTLGGGRWLA*VQEP ETSLGLSLARPCLY
7137	21038	A	7196	1	124	YGIILFITSEVVFVAGFF*AFYHSSLGK KISKKESVIY
7138	21039	A	7197	2	120	GVAHEVLISPGFQDRLEALVVFIFQI LFAILLVLVFIKKVAKKPTNKVGHF*EP GTEF
7140	21041	A	7199	372	3	VHYVPVQIGSPCCVPHRGLSTIHPGLH SRYTGLGMVAHACNSTLGGQSGKIA*A LEMEISLGNMVRPCLYERTNKQSKPRHM GITTEGLTISLTLTDKYSLIISGFYLPQV LISLHPLGPY
7141	21042	A	7200	396	21	GLKSSKRCOAIACIQDRLPVLVGLKAG FARKLSLSISLQLSLRSPDSKLTIGK IKLTQVNRHAGFEWHEGACTTPSCLQ PAHLTFPLDYHLNQPFIFVLRSDDTGL LFIGKILDRPGP
7142	21043	A	7201	2	148	REPDHHSIANF*KFFVDKGF*TLDELVS SSMPQVVLPDRPRELGLQA
7143	21044	A	7202	1	291	ABGFRMIALVSQAAGTSGYKLSVGVYV QGPLETHMLGLLILSLFSLRGSRTWAF SHS*YKTSDDLPCRNREVEIEFLHYRNL HSHICLSVETKFL
7144	21045	A	7203	262	406	ILARMTSVVNSIKHLILFLK*SSHLSIP SSWNYRCVLPHQANFLFL*F*SFILM PRIVETVILLIQNSPTKIDSSPDDFGKGF YQTLNIVFENIRRGNTSNLHKNRILILI PNLTCTLHD
7145	21046	A	7204	2	247	DTVLSRSGGTALPRSTSLDRDNATIF EQILASLITEPALVKYFDKPECMARIT SAKNIRHMGKPLT*ASDYEISANYG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
7194	21095	A	7253	126	366	INLTFCQQQLDRAIFPPFLKKGLFAP*AEWCKGSGFASLQPKDFRLKKSSSLTLLSTWDYGGMLPCRANGPIFTFWKGG
7195	21096	A	7254	2	213	RPTWATWQNPASTFKKKMSFFPTEFTTVAQAEVQGGNLG*LOSIPPLKRFPSCLKMPEAPKQKCSLIG
7196	21097	A	7255	150	263	EGVSLLEPLACNGALDAHONLRLPTSSDLCAFS*ITTRYKYSYGVCPSHPNMLICSRFTLLSSSSSLGHLTLFLILVCFEKESHSCPGRWAMVLSWLTATFASREQATPAPLSELSR
7197	21098	A	7256	386	93	PPGGLPQSPFSPRAQLKPKSPRGKKRGKPKPGSQSPGFWGFPGPSPFPFKGGGLNMVLGAKN*KGVKKQKKKKKQKPOETKRGNRSIDMKFGGS
7198	21099	A	7257	153	369	KENSRLQYQGLPFSH*PTNSCPGQVQNLTPVILALWEAEVGGSKDQPGQHGKTRLLKIQKFARCGGRL
7199	21100	A	7258	180	3	CSTLI*TRKVLGAHAHYNPNILRGRGGRILA*GQVFTKSLGNVNKICLFLPSHPNCO
7200	21101	A	7259	22	265	QLRAIPDLKLPDLNMGKTLISRLTLGGSTVADICDPSTLRQGGWIA*VQEFKTSLGQWAKPHLVREKKLLQVTKLEYKW
7201	21102	A	7260	326	2	KSAMQICIVDNLKACLEICCHANLHCRPSNAFCFLKVDNVRAPVSPSIPQVSLILKNFSWPGVVAHTCNSNTVRGGGRILA*AOEFETILGNTGRPCLYFLQNNRS
7202	21103	A	7261	1	68	VNLCFTLNLQPGVVAHACNPS*GGRGGRIA*P*ELETCLSNIA*PGVVAHACNPS
7203	21104	A	7262	282	176	GLKKTFFFLVRERVLLCYPGWSAVV*SQLTAN*TPGLKFLSCSLSPSWDRHRVALHVAENIC*CHMPVVPATWEABAGEQLEPRSSVCSSEL
7204	21105	A	7263	588	351	NRTVCLLESISSVNLCIPLHQSPVKLEIFLFFTSNDNFPSTHEITVRPLSPS*AIIFPVCTVTSRMPBATKDPQKK
7205	21106	A	7264	327	2	KIKRELINPFIICLRVISCSPGNAVVTLSNWAQAIRFLCLGMS*WRCAPATHQOVTTFPCRCQIEILHNPVKHQLONTLNYFVFLPCFVLRLHPPSAHNRFLP
7206	21107	A	7265	121	270	AQRAGFELLTSGDLPTSASQSAEITGMSHRAIPSCY*FYVTLHGLTVACA
7207	21108	A	7266	3	227	SSQVSLNNWYREPPCLRFVFLFVESTRSCYVASLELLGSGDEPTVLAS*SA RVIMDHCWPNLSRILLHVR
7208	21109	A	7267	300	1	KMLIANTIMGRSLCGRKSPRVOQTSFVSYPKGLPOPPPSATTLLISQOPSTSKODPPAAK*L*FABGRILAFPSNNVLYQLRYIMCFLEHTGIVHLVN
7209	21110	A	7268	29	344	ASLLALKKKKSGLGAVAHNAINSTSGGRGRIT*AQRFATSLGNQARTCLYKKKKKKKKGKNFTGVGGPQRGAPIPGPWGGKSPAPGKGGPNPFGKGAPTF
7210	21111	A	7269	3	209	LHPLSGPPAPVAAGIPGQASR*GFCRPDPSPDSASVDASLNGPALSLWSGNSRGYGTTPASQIH

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7211	21112	A	7270	86	206	CQPGVVAHAYNPSTWGRGRQIT*GQEF ETSLGNTARPLP
7212	21113	A	7271	45	274	GLFTVAQACDNPSITGG*GSLIA*GQEF KTINNDKSHRWQYLALIEQINNRMLICK NKKELTDICNVTDSFQNRRE
7213	21114	A	7272	1	122	VIVETGYLEVSGTSLKLLTGGDPPALAS QSGEITGLSHRA*SYMH*LVSTGYLRV GQGLKLLTGGDPPALASQSGAGITGISH RA
7214	21115	A	7273	3	242	LLKQLDYRPHPAKFFFFLEFLVKKGFH LVVKGKGTGTGSGGLPG*ASKGVGIPGV SHCPGLIGVFNLTCLKVAISLMDL
7215	21116	A	7274	2	169	LALVAQAGKQWHLQSLPLSPSPFF YLSLPS*DYRHEPSPHSAWFSFSSNR
7216	21117	A	7275	353	76	FAHLGLPQCDYRREPLCAT*KLPLKGR *PSKQVIFSSLTGTHFSNACFSCVMNT IVLLINFWVTGIDGRTSGSSSVKCGNH SIYPMVLL
7217	21118	A	7276	6	87	RRGLTLLPRLGNSNWPQAILLPWPKVL KL*AQTPLGRQSSCLGLPKC
7218	21119	A	7277	1	203	FQVNLCSGWMMLTPVIALGVAHTGN PSTVGGRGQII*S*FYTSLDSGNPPA SASQSGITIA
7219	21120	A	7278	272	51	IFFVFN*CGSHDVQHFNPS*NNLSWS SNMPLTLPWRA*AGK*LEPRSLRAN ATKLDNSGKLLTIA
7220	21121	A	7279	1	131	SRDYRGLPHPTDFFVEMRSHVVAQA GLKLLGLSLPALTS*SRDYRGLPHPT DFVFFVEMRSHVVAQGLKLLGLSLPA LTS
7221	21122	A	7280	411	36	FLECVNHFPPKKKFFFKNTGQVFFPV TFL*KGPALEFFIFPPYGGKFFFLSAK DFPPRVFF*KGPLEFFFFFFFFFFF FFFFFFFFFFFFFFFFFKILFLYKKVHF *SSVHPQPIFF
7222	21123	A	7282	395	181	RKHSTHSDVISVTFNMQSLRLFFIF FILSL*LFRIFFFSFFLVFFFFFFCF FFFFFFFFFFFFFFFF
7223	21124	A	7283	392	2	IKFFGYNN*FNYILKNGLF*QLLI*LIN LFILRQGLIFVUVQCNLVFFFFFFIF EFLFFFFFFFFFLLFFFFFFFFF FFFFFFFFFFFFFFFFFLTQMLFLVN FCDDFKQKQNHILTRGR
7224	21125	A	7284	113	291	VYGVYGVYGVYGVY*SAIKRKRIVA FVVTWMLLETIILSVVSQSWETTHMLS LIN
7225	21126	A	7285	327	44	LKVSFNFSPPKKKVLDPKPPCTLFPPS PF*KTPDPPIPKPKPHKKNNPNSPPQK *GPPQGFKSPDPFFFFFFFPPFP LGSFKLLIR
7226	21127	A	7286	3	215	VILIIIFI*RAFAKKRVLIVBPSNL E*LYDGGYDGLVLTSGLPY
7227	21128	A	7287	367	119	LKKAPAPFFLNPFPWKNIFILSPPEKMG PPROGFKRGP*FFFFFFFFFFFFFFFF FFFFFFFFFPLQYNNYH*ILIIHQ
7228	21129	A	7288	73	259	INKYLN*KKKKKKKKKKKKKKGGP FKKTPRGAQISGVKKKIFDPKGGPKKK QAPGPF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 2009/015,126	Predicted beginning nucleotide location correspond- ing to first amino acid residue of peptide sequence	Predicted end nucle- otide location correspond- ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
7229	21130	A	7289	337	53	LRSFAPFHLPLINNLTDDHVIPLPPSS LCSHYLFNEVIVITLTKITTHLQLGJMA HTCNPNTILGG*GGRSA*AQRSETPSGNM AKPRLYLNF
7230	21131	A	7290	1	96	KHIRDFRAAA*YMHFVDVV*IFLYVSIY **QS
7231	21132	A	7291	288	2	SRVEFKOPFMHCSVTIPGSSYVPTSAS *VAGPHGARHHAC*FLP*FLN*MLLEMG SRHVVQAGL*RVSSSDPPARACQSGGIP GVKPHAQSVSV
7232	21133	A	7292	121	233	YFPFKKKKKKKKKKKKKKKKKKKKKKKK* KGGGRSRKSYLG
7233	21134	A	7293	3	346	NPLNPLNVLIVSPKNSSSLTRKKPCRR RHREKTELRKKRNQHTAARGQRNNHPE TE*ETGQRDRDKQTKQKDTDIQAYTYT DREKDKKRRHQIR*AEAEIRDRTERQR DI
7234	21135	A	7294	46	346	ETGLKRWGDLNNGTIVRAVINLAQADFCV SIPSYHILKKNNTNNCGEGKKLLIVVT AKKSEPGVVIHACNPNILGG*GGRVT*G QMFKTGLGNIVRPGCT
7235	21136	A	7295	254	12	RKDAENINGSAS*IKRVKDLVQSKLKFF QELAKKGLLNPFPFASITLLPKPDNDT SKEDYRPTISANNIDAKILNKILAN
7236	21137	A	7296	258	1	CIGOCVIVAVGRELLCVSRSCGLLHVD EVGGEALGRLLVVPVPTCRFSESFDGLIS TRDAVMGNPKVKAHOK*VLGAFSDGLAL LD
7237	21138	A	7297	191	263	VCSKCEPFIYIMDYAALKRNKIMSIVA RNVQLEVVSELTQKQKTNMNF*VVFG FLLLC
7238	21139	A	7298	2	164	SRVAGITGAHHAQILFVLVETGPHHV GQAAFKLITSNHHAQP*LIHFFYFFK
7239	21140	A	7299	307	8	VMIITPWLPHLSGYIEKSTPYECGFDP SADRVPFSIKFFLVAITFLCLDLKALL LPLP*ALQTFNPLPLVMSLLLIILAL SMAYE*LLKGLDCSE
7240	21141	A	7300	205	317	KSSPACTPSTLG*GGWFA*VQEPETSL DNMVKPOLY
7241	21142	A	7301	140	22	ENFLFLYP*NYFFFFFFFVFVFVF FFFMNINVFY
7242	21143	A	7302	382	151	SHRSBFRPRRSHSVSRPESRGIILVYC SLYPLASGDSANVVS*VAGTTGVCPWAS LLKSGFFFMNDSVLLSCGP
7243	21144	A	7303	318	17	LVPTKRPQVNTYPTATYINYCTKGRKK WAGIGGSCSSQHPGRPSWDPLSLGV* DQPGQHRRTPSLQK*KNWQEPITVPATQ EAEAGWCKPGRQSIQ
7244	21145	A	7304	310	132	QWCDLGAITPANCFYFVRNGVS*CWSS NS*PPDLKLARSLLHPQSVFNPPIISGL FFL
7245	21146	A	7305	338	168	REPPLPAANVFVVRMSHIVROAGPEP PSSDDLPAASQSGAGITGVCHAMP*AT YK
7246	21147	A	7306	276	161	IINAALKNNEFMS*AGTNKLEATITLSE LTQELKVK*KLRKFNITDILLILLIFKI F
7247	21148	A	7307	310	61	ITLVYCNFFYINFNFLKLPDSFVITLS

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3						LRQIYSCTAIVYIIL*APVQ* FLYKMLFIYKMLFYKIKY*NMVFF CGRVDLH*AVPFFFKRWSLTV* SMAQVILLP*PPE* TFLYAFLHI PVNKMSCPVGKDRGMFFSY H
7248	21149	A	7308	257	1	RDGFCITGHTGL*LLTSGDPPASASQSA GITGVSHHARPCILSLTAFFNNMWNWG QQE
7249	21150	A	7309	2	181	FCVFNIMDVKMI*IFLIFVPDVLHG*QK NLLLDTI*KKKSIRIQE**QYKSIKRN YNTVSDEKSGITVAHACNPSTLGQGGGR TA*TEFQTSIDNTVRPCVYY
7250	21151	A	7310	25	340	FVDFSMHILDMLSLYLSIVICITLFLS IIDNIYVNGPHKIIIPYFCIKYIYIY IMFCFWFFETVLLCCFSVFTENDYCSYL HYFLLLGVFGLPHFF*FLYLYMVLFLVF
7251	21152	A	7311	2	193	RTPLGRQSSSHFSLSSWDYRHRVPLHAP AFFFFKGP*SEPLTLASSLHWYFPGGH LQGPAKIIDDPNPSPIIGLKKKSPF
7252	21153	A	7312	1	245	GRPCLIVMCRDSQKGRKGTGLKRAL RMK*GQARMLTVLIPALWELBAGGSP
7253	21154	A	7313	167	2	CHVAQAGVQWYNHSSLQ*PFGLR*FSH LSLPSGWNLSWTPHPANFFIMGSHLP LINK
7254	21155	A	7314	334	152	PHVGQGLLELTLSDPPASAFQSAITG VSHHARPTFYLS*QVGLTVTSFNPQ QRIKH*PHMLGAVILTCNPSTLGQGGW ITGQKFETSLAYMATPRLY
7255	21156	A	7315	2	164	GIPSTWYDNCSTSPQPHF*FFFFFF*KR DLAMLPGGVLSNWPAILQPKGPKVLGL QAWTILYGYGKBMWHKEICKGTHDVL SKLLTTKRFKRL
7256	21157	A	7316	155	9	SNSLVLYLKPSDVIYIPLFVETVSSRA QVGLLEVASSTPI*ASQSVETGVSHH ARPKKV
7257	21158	A	7317	1	293	GGRNALSPPGRGCCSE*GCRCTPANE TQNA
7258	21159	A	7318	262	73	KPKRI PVACDQQTDKRNCSDGYECNN VDFFFFFRVSLCHPGWSAVV*SGDH TIALQSG
7259	21160	A	7319	169	265	FFPFERESRVARQPGVQWRDLSSLKSP PFGKRFPCLSLPSNDYRAQPCPANV FFB*RWGFTTILAKIIVLLS*PCDPPTSA SQSAGITGVSHCAQ*FFPFERESRVA RQPGVQWRDLSSLKSPDPGPKRFPCLSL PSSNDYRAQPCPANVFEF
7260	21161	A	7320	169	260	SPGPLFGLIEPLFSRPFQFWNLFP*TW BYRLALTAPIKFKFLIKTGPH*GIKL RG
7261	21162	A	7321	580	400	KSSGTIKGRASQPFQLVATECCQDCFH FRSQF*YLKQLQPGMWHAYNPSYSG *SRRIT*AEFFSRIGNITKLCCKLNN SLIFKITTENIE
7262	21163	A	7322	130	26	DNWEVLKRSYRPTVAHANPSTLGG* GGSIT*GQKFEIRLGNVVGPCIKNNLTN QLGVGG
7263	21164	A	7323	17	303	GVPIFLKLITGRTISSERESKVPLERK
7264	21165	A	7324	194	8	
7265	21166	A	7325	413	72	

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						ANFRDKRGIPPHKKVIPAEKKL*KGRS PFDGFGKKLTQPRVSAFGHPLQPLPY AFIKSPFBGTHHQDCPFWHLTLISARRQ Q
7266	21167	A	7326	394	177	NVNHTHTTITHTTHTHTHCKSDTQYS SDS*CTTPRCIHDPWPSSSQVTNLAWG LTLAKEVLANNQTEV
7267	21168	A	7327	232	22	SRPFGSKGAPALQSSSCLFSLSDMYR HKPPYLTFNCFIL*SQSFFMLPRLLSNS QPHSNLPKVVLEQV
7268	21169	A	7328	232	3	YHRSSGSLSLQIQLRESKI*APSTPII KEWLSSVAVVYNPTLGGQGGRLT*GQE FETSLGNIAFPCLHENCLKN
7269	21170	A	7329	364	3	PKARRATVRTRVSKAPSNQCLGVNTH VLGHRRPVKNAKTRWSASESQASTCNI TTLGGQGLIT*DREFESSLATWQNPVS VSGNLQKMPFSKQKLYSKFFPIVAYKAFR IWLLCARA
7270	21171	A	7330	177	2	DPHLHKFKARCGGHTL*SQLRLRL*K DQLSLGVGGCFELLWCYCTFAWTERDP SC
7271	21172	A	7331	413	40	RHNLHMTYIVVLDIYTYVFFMYLYI P*CVCKYISCLHMYRPSIMYPCYVYV CMVCVNVTHVIVENAGSCLALSALIENE GHARDSKMTFNPDEKMRLSYKKQLEKL NFMILCPTWKEF
7272	21173	A	7332	147	49	KNYIYPCRRLPMLPRLGNSRAQETLL PQPPM*IGLNSRAQETLLPQPPM
7273	21174	A	7333	148	361	SWLGTVAHAYNPSTLGGREGQT*VQBF ETSQSNIAFPPLYSVLAYAVQPLPFWA MRKLWLPITSRITAL
7274	21175	A	7334	305	2	CPGGPVTRVHR*YVRLSQPDLRVFTSGA MPASAAQAGITGMSHRARPVCIIIFL NIFKVICIFVELTIIPNQNKQNTFLSSTV ASCRILASRPTPIVVVL
7275	21176	A	7335	1415	1164	FFLRQSLLYCPGWSVVAQSLIASSITQ A*AILPPCSWDYSSQHTWLKFFFC*DFG SMLPRLVSGWSAQMVLLQLPKAQAKL
7276	21177	A	7336	1	206	GTRADHLISGPDQPGHETSLSLKIKI RQAMWHPVUMLPFR*IDARESLERMT LALKYVRRIIF
7277	21178	A	7337	65	302	KSLFYFLKLTGTQFHVAVTGL*LLSSD DPASVFSQAGITSMSHTQPKELLKST RNTLESFNEWAKAREWAHRENT
7278	21179	A	7338	208	38	NPVSAKNREYPRGT*FOLGTQARVQWHL GSLQTPFPGLK*FS*LSPRV
7279	21180	A	7339	2	198	ARADHPGSGVREHPGHSGETFPVSTQTK N*AMWVPLVPESCHMDYILFMYETNOMDN KLPKWLTLC
7280	21181	A	7340	2	227	ARGEIMFNAATMQLANISLKLQS* X AKYCMFSLSGAKHVLMMIKVGTGTR DYLGCSTQAVILKNLGTAE
7281	21182	A	7341	3	300	HBGRNTYLTGRDSCTLAASAKACGACP LWGKCDAESKVCRCASDCBERGISTC VDVNCBQTMPEC*AVAL*CTVHLIYVT INNALCLPQLTLEL
7282	21183	A	7342	210	351	RGLTGVAHACNLNTPGG*GRWII*AEFF ETSLRNITKPSLRNPDML



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7303	21204	A	7363	168	2	CFYSTHAILFKELRQKPGAVSHAYNNLST LGRGRLLT*QKFFTSILAW/KPHSC
7304	21205	A	7364	399	62	QPGQYQKHPVLINGSKTKFQWQPPVVP NARRG*A*KNVEPGKVRVQSAQIKALEF NLGPKKKVPPKKKNPWLAKQGLRPEIP AFGKASQKGSPRSRLRPPGFPLPYPAHF
7305	21206	A	7365	289	76	VCDVIRESEQAISRLKCSGIT*AHCNVIS IAGSSNCHASALRVPKSTGVNVSEERGD VDRFRAYGSRGYVCA
7306	21207	A	7366	364	182	QWHDHCNFKLLGSSNPPTLAP*VAGTAGT TCHCAWLT*FLTWKIGFETSLKILVLIG YFWF
7307	21208	A	7367	155	2	ELGTRKBGWEKSATVAHACNPFSSLGGRG RWIT*GPEFPTSMANMKAHFPR
7308	21209	A	7368	342	184	LSLPSSWRDRTTPRQLANFKTFPR*YS LTMLPRLRYFPFYLTTHQTLNSAMTF
7309	21210	A	7369	2	211	AREPKCL*TDWRINKQYIDAVEVTHLAI KLNRLILTHATTWNLENLIGRS*TQKA TCCVIFPMDSIYV
7310	21211	A	7370	190	344	YKRVTVKRIITWIPSTVAHACNPSTLGQO GGRFG*GQFETSIGKILARPCLY
7311	21212	A	7371	24	254	KPQSIGAHASSQHGKRPSEDSHLGSL* DQSQWSELPSLQKKKGLSGRGNCL KSWFLKILGKNVWVLLTPG
7312	21213	A	7372	43	358	DSNLNYSILPHGEADLTQVLLTHRPST AMYFVHYCQSP*ILYGTINT*PPVVRHN PIHIKTPSPCLQASTAINQLSHINCNS KATPHIPLYQQTYPPLTVHST
7313	21214	A	7373	2	288	IHTILAPTSILGLIVVSHLTASLILCL HGIILSLTIIAPLIPNTHSLAPIGPI AILVIAA*QAAVGLALLVISISTTYGLNY VHNIALLOCCN
7314	21215	A	7374	335	1	VQWMDPGLQNPFGVSPFPWLSLBNNL GFKGPPPRPGPFLKF**KPGFSALTRV SLSRPRDSAPLAPPKAGVSRINPRARAP FFFFFVCFCHFFLSGEGKSLAHKGI
7315	21216	A	7375	399	91	RIFFFFPSLRAPPKRPQKPTFFPPPTKPL VFSIPPIFPFPKFLKKNPFSWEVFLFIS FQKDAFFGQGV*KGNNFFFKGPPPLTQ NSQGVPPKKKKKKKKK
7316	21217	A	7376	377	131	YLYTKYFNTILYPTIYNTL*PNMIF NLLFYIFYTYLLNSMILLILINFFYFI LLIITNIIILYLYIYYPIIKNIKT
7317	21218	A	7377	2	156	FHHVV*AGLELLGSSNPPTWAPQSAETT GVSHVQQLPHFLRLKQELLSLGL
7318	21219	A	7378	319	59	DTFMNSQDILYSYQSRIT*W*LYKRO*T KQKSAPEKNGNEVP*THQISTATTLISQO PSTSKQDPPAAK*L*FAEORLLAPFNN VF
7319	21220	A	7379	308	12	FSPTISIN*NYKSNPSPLIYLFQ*PITQL IPTINISTNTPNL*FYLRLLYSTSISLL PISNNVKIK*QPRHTKTPFLPTLIAT TLPLISPPILILL
7320	21221	A	7380	11	169	RRDLAMVPRIFSSSPGLK*SIHLGPFEPH WDYSHPSPWLLFFLFLITRGYFF
7321	21222	A	7381	300	2	KFPFPFGFFFGKGFSL*SEHQKTKQIFF GEFFWGWKKFFLLFFPPQGFPPPPPPPP FPPPPPPPPPPPPPPPPPPPPPPPPPP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
7322	21223	A	7382	163	160	FF*INSLFIQNSFLT PSTNDDEIQRNRSNRPIARR*GLSL LPRLFWAGSNRAHSLNLCGSSNPASAS SKSTMTITGVSHCA*ERLEWAGSNRAH LNLQGSNPASASKSTMTITGVSHCA
7323	21224	A	7383	1	183	VCVVCVVCVVCVCIKMSYSALKKYLWA FVVVWKKLETILSEVSQK*NTTYHMS LIGGS
7324	21225	A	7384	2	196	KIQMNPVVHACYPNTLGGQDSRTAG QRFTQSLGNITARPCLYQQQQQQQRCS LTYDGDKS
7325	21226	A	7385	3	192	RNLSSLQPPPPGLK*WSCLSLPSSWDYR RPFP*CPANCFMLCEFFRTNGVFPSCPGV YTFEPN
7326	21227	A	7386	256	198	TMLSGFLRSAGLMTIS*PHDPPASASQS AGITGVSHRRARPLVFLRDSLYSGTQAG VPMRDLSSLSQSLAEQMRCFP
7327	21228	A	7387	164	311	SRQQKGLSGVAHPNCPNLTGGGRWIN* GQEFETSMASIVKPCCLSLKL
7328	21229	A	7388	3	218	EIMSFAATWMLKANILSTLSHE*IAKY CMLSLSLGAKHWMVPMNIEVGTGDTDPY GCTYPSSTEQGLTYG
7329	21230	A	7389	521	58	SGCOLTLAQGVHWHHLSLQ*LPNL G*FSLHSLPSSWDYKCVTPCPASFLYF LVETGCPCHVAQDGLLELSDNNPPSSASQ SAGITGMSGCAGLRFF*KLRSWRYLVLL AMQVNFQGTSGRGRAYSEADAGQGCCG LCLHRIISQCYALP
7330	21231	A	7390	169	322	APGNFRTN*RRKGFMAQNTLGVSVMNR NGWAWMLTSVIPALWBAAGGSP
7331	21232	A	7391	1	353	GTSPHYGSPFHGQKDVITGKGSQSRPRR VLGSHARKNSLPVHEVKAYLL*KYLSIL RATHILSPDGCWVPITFAQSYIFLSSC GFFLLFFLLLLTSLPSCHELLISFLALF VIPLY
7332	21233	A	7392	372	3	IQAGACCAECIPSGKIRNPNPSIVEGLHS DMSWSLCLFLSGAISVLNFRSLGSSDS PMSA*QAARTAVIRHRTLIFCIPSRDR ETGPHVVGQENLMLLLQLPSGLGFSIS ATLTLMLLV
7333	21234	A	7393	362	176	ASNETSQAY*RLRGSSDSLASAS*EAG YTGKCHQAQ*TFVFLVVRPHEVGQNAI NIRTSIL
7334	21235	A	7394	2	304	ARADCCARNE*GSVGGPS*PGVGYNLL VPRFLRPLEKHSIRVGRTFRRCCLSQL CLARTGNSLTPTCTSWRQCIALLLMLG ALHPLSCTQRPSTHSE
7335	21236	A	7395	256	3	MYAAAYWNKAKITTTESLRHWAGHGSH PYNPSTLGG*GGQIS*AKKFETSLGNW KPHLSKNKQINKQINKQINISWSWCTCL
7336	21237	A	7396	346	2	RDFHYRESHSLITYICLENVKSRLKGR GPIINFTHIQRKNCHGHTRSFGVYVEV GRTEATGPIKRRNGLGAVAHTSNPSNL GGQGGNIT*GQEFKTSLSLPRWLTPVIL LV
7337	21238	A	7397	2	242	RRYSDFPATYTT*NLSSVSGFISLTAV ILITPMI*EA*KKKKKKKKKKRGKGF KKTLGGPKFNRMRSGKNFSLKGGR



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, Y=Valine, W=Tryptophan, X=Tyrosine, Z=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
7338	21239	A	7398	1	289	TKLLGLGYTTLLQASNDPKSPFSTPDGTY GSTFFVTTGFGHGLHVLIGSTILTI*PTR QLIFHFTSKHHFGLBADA*YVHLADARR HSESTTHQCCSL
7339	21240	A	7399	346	40	IIIFTNKIYTKINGKLFTIKILDLYI I*IFFPRK*PTFKQ*KP*IIINIKIYYN NIK*IKYLGFFFFFFFFFFFLFFFFF FFFFFFFFFFF
7340	21241	A	7400	1	334	NSCRRLQMLDLLLPLT*LDQLGYIE KSTRYECGFPHSPARVPFSIKPLVAI TFLDLQIALLLPL*ALQTTNPLPLIV MSLLLIITLALNLAY*LPKGLD*AE
7341	21242	A	7401	2	302	HTINLGERVLAITY*STINLLLTGL TVLHTGLYSVYLMTTQWG*LTPHINIM KP*PTR*DTLVFIHLSPILLSLNPDI TGVVLVLLSYELYLIT
7342	21243	A	7402	57	338	TTHNVIGYTEASTAYESGCDPISPARVP FSIXFFLVATITFLFDLIALLLPL*AE LQTTNPLPLIGMSSLLLIILALSLAY* LQKGLD*AE
7343	21244	A	7403	407	68	QBELVDPLTIVREQCQLENCVKAR*RL *LCDERVSSRSSEEDCSEDLFLAHAR DHCVFLLIYINLKYCELT
7344	21245	A	7404	494	154	SLFIFLYLILFLP*FFFFHYFFFLLSI FSFKLFFFFLLHFFHFFFLFPSPNKK IFFPKIPRFFFLFLE*KKFFFLPKFK LSPGLFFF*SPFFFTTTTTTTTTTTTT F
7345	21246	A	7405	1	400	NPGRFLTSNSSLVYRTREIRPTSGQAF PRK*YHLKKKKKKKKKKKKKKKKKK KKGGPLKKKPRGQK*TGGEKKK*PKR GGKKKPPGKF*KTFFWGGKMGKTPQK KINPLGKKKIFKGRKGTPL
7346	21247	A	7406	2	257	RASLCHPGWSAVV*SLIALALTSNLQF SHIANSLCWDYRHEPFLA*LRFEHRHS GGSICTLNR*ILLSFPILSRYKGLIL Y
7347	21248	A	7407	259	47	YVFFFLFLLEFIRLQSVSFFFFFFFFFF FFFFFFFFFFFFFFFFFK*SFISMFSVV LYLLRQVSIATYTLG
7348	21249	A	7408	3	248	VTFL*CDVEIAVLPLP*ALPTINLALI DMSSLLLIILALRLAY*LRGGLD*AE EIQATREYGRAPPL
7349	21250	A	7409	2	350	ESGMPRRYSYDAYTTNLSVGSFI CTAGLILIMT*EAFASKKVLIVQGF SINLE*LYGCPVPYHTF*EPPVITKSHI RKESNPPLVSSQPHGLADEFKKLGIT TRKN
7350	21251	A	7410	2	232	LDQTYAKIH*TVITGVDLTLPQPLG LGMPPRRYSYDAYTTNLSVGSFI ALTAAILIIMI*EAFAGKF
7351	21252	A	7411	2	321	TSLLAVLLIMTL*LPQNRNRYEKSTPY ECGDPICPGRVFPFSIKFLVAITFLF DLATALLPLP*SLQTTNPLPLAMSSLL LIITLDMNLAY*LPKGLD*AE
7352	21253	A	7412	2	194	STECFLVPTILLCDLDEATALLPLP*AL QTNPLPLVMSLLLIILALNLAY*LPK QKGLD*AD

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
7353	21254	A	7413	1	197	LYTTY*VTKTLLTSLFL*GRYAYPRLR YDQLIHLL*RNFLPLTALLI*HVSIPITISSIPPQT
7354	21255	A	7414	1	185	STPLP*ALQTTNPLPLIVMSSLLLIILA LSLAYE*LQKGLD*AEKKKGAAVLKDP SGGPS
7355	21256	A	7415	347	228	LE*LYGCGPPYMTFEEPVIYKSLRKKE SNPPKLVSSQPHGLHDFFKHKIKYRANK RKGLASVKMDRSP
7356	21257	A	7416	1	296	FAYDHSQINGLYEKSTPYEGGFDPLS RARVPPCKIVFLVAITFTLAADFLEIALLL PLP*ALQTANLPLIGMSSLLLIILALS LAYE*LHKGLD*AE
7357	21258	A	7417	3	202	TCSTI*HVLVNT*LYIDLEIAL*PVP*ALQSTNPLPLISMTSLLLIILALMSAYE *LQTGLD*AE
7358	21259	A	7418	1	321	SNITLALVLTITTS*LPQLSGUGBCTP YECGICRIILNARALCCQIFLKAITFLL FDLRIALLPLP*ALQTTNPLPLIMSSLL LIILIALSLAYE*LQKGLD*AE
7359	21260	A	7419	1	212	RTRGIFRPLRSQSLY*LAANLVILT*I GGQPVSYPTTILGGQVAVLYFTITLILIP TICLIENKILKA
7360	21261	A	7420	2	257	GRVGRVGYSIAFFLQATTVLVDLSA LLLALP*SLQTTNLSLIVSSLLLIIL ALSLAYE*LPGLD*ASYGEMMTTLD A
7361	21262	A	7421	367	269	HCDLKLGGSDPPASAS*VANITGTCHH TKLS
7362	21263	A	7422	2	116	ALQTTNPLPLIVMSSLLLIILALSLAYE *LQKGLD*AE
7363	21264	A	7423	2	336	KPREGREGILPCCSSAMPEGSFPPFOM NLGSFLSFFFLFFFEKGLFLCPPV*S PYGKNLLEPSASRFKQFFCLGPNLNNWD YRLFPFPQNEGVFKKNRVPFVPSLV
7364	21265	A	7424	3	154	LFL*IRTAYPRFRYDQLHLL*ENFLPL TVALLI*HVSIPITISSIPPQT
7365	21266	A	7425	3	154	LFL*IRTAYPRFRYDQLHLL*ENFLPL TLALLI*HVSIPITISSIPPQT
7366	21267	A	7426	1	314	INTLLTLLLIITL*LPQLNGYIN*STP YEGGFDPLSPARVPSIKFPLIAITFLL FDLRIALLPLP*ALQATNPLPLIMDPSL LIILIALSLAYE*LHQGLY
7367	21268	A	7427	1	331	ILINTLTLALLLIITF*LPQLNGYIEK STPYEGGFDPLSPARVPSIKFPLVAIT FLFDLEIALLLPLP*ALQTTNPLPLIVM TSLLLIILALSLAYE*LQKGLD*AD
7368	21269	A	7428	2	373	SDNHITLHLYTTLGLYFTLLQREY FESAPTISDGLYGSTFFVATGTHGHVV IGSFTLFCFIRQLIEFTSKHHGFEEA AA*YHIVDVAGLFLHVSIVYEGSYNHQ IIPSAQKSTPA
7369	21270	A	7429	378	63	PSFFPPFP*NEFFPPRPLFSKGFDPDF FDDPKQKPPKLPDGFSSPPWEKFFF PPPPLILPPRFFFNPPDPFFFEFFFFF FFFFEFFFFFDFLGGC
7370	21271	A	7430	1	109	QTTNPLPLIVMSSLLLIILALSAYE*L QKGLD*AE

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
7387	21288	A	7447	411	110	LTDSLINIVYR*KMSYIS*TN\$A*VYLY IPCIYIYIYIYIYRRIYSIYRC*YIYVG PAHIVLVYSSSYILVYRSHKYGIMGL NILSYIFIYSYFSACS
7388	21289	A	7448	1	380	PTRPQLKKNKNGV\$NGDLCFPGGGQFL IMGFFFFFCILIKGGLNSKMYELSLKLA TYGAKKAEIETETB*KNRRTLL\$RAAQL AIKVTNP\$AMLRIV\$ERDYAMTH\$NFWLN KLNNCHGVAISCKQ
7389	21290	A	7449	200	437	VQSN\$NKNPKRRRL*PGVVAHTCN\$STL GQOARRIS*ACELETGLNNLMR\$PCNYNK FINVLDDVHGVTSPV\$QYVKKVC
7390	21291	A	7450	405	3	PPRPF\$G\$FFFFFYPLK\$FFFFPK\$GNPF\$G FFPIFFPPK\$KFFPK\$NPGGFFLPFL\$PFLG KIFFFL\$PPK\$G\$PR\$GFF*RAPL\$FFFF FFFF\$FFFF\$FFFF\$FFFF\$FFFFLQR\$NFT ARP\$GPL\$RAVPL\$GAL\$PSA
7391	21292	A	7451	2	348	PRVR\$RVR\$YKLT\$KRC\$DLP\$*GH\$SV SLRNT\$T\$DALK\$*D\$D\$SL\$P\$KLE\$GCV NTPN\$NLR\$P\$S\$D\$P\$ASL\$SRAM\$AST RL\$RAMEI\$FVFL\$QNRQDY\$MNP\$GGG\$CN ELK
7392	21293	A	7452	1	168	L\$VH\$G\$HAGL\$KLLT\$SGDR\$A*AYQ\$SAGIT GV\$P\$LG\$PT\$Y\$YF\$R\$AS\$M\$T\$F\$IC\$FAT\$Y
7393	21294	A	7453	184	260	\$SR\$G\$S\$AS\$SR*STLL\$GL\$K\$M\$D\$YRC NPP\$SLAN\$T\$F\$F\$N*1\$N\$F\$W*RL\$EL\$M L\$PL\$V\$N\$S*MQ\$ALL\$R\$LR\$Q\$IH\$PAGT QT\$SL
7394	21295	A	7454	405	64	FFFF\$NFF*KKKI*D\$V\$AK\$IFPK\$IFPFF SGLK1\$P\$GGG\$Q\$N\$D\$Q\$K\$K\$FF*KIK\$F FFLN\$FF*KN1\$F\$F\$VAG\$V\$F\$LL\$N\$FF\$R GAPL\$FFFF\$FFFF\$FFFF\$FFFF\$FFFF\$FFFF FFFF\$FFFF\$FFFF
7395	21296	A	7455	368	2	\$QS\$G\$R\$R\$W\$N\$R\$G\$P\$Q\$H\$IK\$IS\$R\$Y\$P\$AQ V\$H\$ACH\$P\$TL\$G\$G\$R\$W\$IT*G\$B\$F\$K\$S\$THL GL\$P\$Y\$D\$Y\$M\$P\$EP\$LL\$V\$Y\$Q\$CF\$H\$R\$T\$FCN K\$A\$IH\$CF\$K\$P\$Q\$LL\$Y\$N\$K\$T\$S\$Y\$K\$S\$Y\$K\$V\$K\$A AL\$V\$ACK\$P\$TRP
7396	21297	A	7456	2	183	TER\$D\$V\$S\$K\$N\$K\$Y\$Y\$IH\$TH\$E\$TH\$Y\$IC\$V\$HG VLY\$YI*SL\$LL\$Y\$N\$I\$AY\$IL\$Y\$H\$V\$Y\$ILL IF\$KA
7397	21298	A	7457	281	127	Y\$N\$C\$F\$M*RG\$F\$N\$V\$Q\$S\$GL\$K\$V\$LL\$R\$G\$YS P\$AS\$Q\$LAG\$IT\$V\$S\$Q\$CAP\$V\$S
7398	21299	A	7458	2	194	TSV\$K\$Y\$Y\$E\$P\$T\$DL\$K\$G\$ST\$N\$V\$W\$A\$GL H\$GL\$H\$V\$IG\$T\$T\$T\$C\$IL\$R\$Q\$LI\$F\$IFT\$SY\$H H\$F\$G\$S\$K\$A\$G*Y\$N\$H\$V\$E\$P\$A\$R\$L\$F\$Y\$C\$Y* G\$ST\$N\$V\$V\$AT\$G\$H\$GL\$H\$V\$II\$G\$T\$T\$T\$C\$IL\$R Q\$LI\$F\$IFT\$SY\$H\$H\$F\$G\$S\$K\$A\$G
7399	21300	A	7459	22	319	GG\$V\$T\$G\$AY\$H\$R\$IL\$D\$H\$D\$R\$N\$O\$IF\$LA*GG\$SVT G\$AY\$H\$R\$IL\$D\$H\$D\$R\$N\$Q\$IF\$ALL\$IS\$M\$LL\$GL\$Y\$F TLL\$Q\$ASK\$Y\$F\$E\$CP\$FTICD\$G\$Y\$G\$ST\$F\$F\$V\$AT G\$H\$G\$H\$GL\$V\$II\$G\$T\$T\$C\$IL\$R\$Q\$LI\$H\$F\$T\$S R\$H\$H\$F\$GL\$E\$A\$A*Y\$N\$H\$F\$V\$D\$V\$V*L\$F\$LY\$S\$Y **G\$SVT\$G\$AY\$H\$R\$IL\$D\$H\$D\$R\$N\$Q\$IF\$ALL\$IS\$M I\$GL\$Y\$FTLL\$Q\$ASK\$Y\$F\$E\$CP\$FTICD\$G\$Y\$G\$S T\$F\$F\$V\$AT\$G\$H\$G\$H\$V\$II\$G\$T\$T\$C\$IL\$R\$Q\$LI\$H\$F\$T\$S R\$H\$H\$F\$GL\$E\$A\$A
7400	21301	A	7460	1	722	TLL\$GL\$Y\$TLL\$Q\$A*E\$Y\$F\$K\$A\$T\$T\$Y\$D\$G\$Y\$Y

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						GSTFFANTQPHGLHDIIGSAFLTICFIR QLIFHFTSEHHFGFEAAA*YHVSVDAT* LCMYVSIY**GSTFFAATGPHGLHDLIG SAFLTICFIRQLIFHFTSEHHFGFEAAA
7401	21302	A	7461	3	246	LNYSLFFHGRANIGTQVLTHPSTTAMY FVHYQPPP*LLYGTINT*PPVVRNPIK KKKKKKKKKKKKKKKKKKKKGGGG
7402	21303	A	7462	2	155	SRSRAALLPL*ALQTNTPLPLVMSL LIIILALSLAYE*IQRGD*AE
7403	21304	A	7463	1	136	PTRPAPSHLYCKNKKLFFPSTANEAL LADILRCKKKKKKK**VLSASR* GCKLHGMH*NSAVCTVFWLQDMSD* **KVNTQ*KKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKGGNNR*KNIRKLF PSGTANEALILADILRCKKKKKVKK
7404	21305	A	7464	166	192	NIN*MYMHTVCYSDFRKEILLIHTT WMLELDIMVSEISQSQKKYCHILHIEY KLYIHM
7405	21306	A	7465	416	55	LFFFLRLLGYFFLPLNIRVFFFLSTLFFFF VWQFFFFGRFFFFPPQVCFVFFIF*G IFFFFFLFK*KNMFFFFFLMGPPPPFFFF SGAPLFFFFFFFFFFFFFFFFFFFFFLR KANTKKMF
7406	21307	A	7466	295	84	TWGNVTLQLVSCFLCFLLH*GFFCCO CCLFLFLVCLFVCFWFLNLRPSIKCLLP FSLSLGCARIPSSF
7407	21308	A	7467	142	258	POIVARTCNFSTAGGQQGRIP*GREFKT NLANKVHLY
7408	21309	A	7468	3	192	PSRYFESPTTSDGYGSTFFVATGTHG LHVIIIGSTFLTICFIRQLIEHTSKHHF GFEEAA*YHFDVGV*LFVYSIY**GS TFFVATGPHGLHVIIGSTFLTICFIRQL IFHFTSKHHFGFEAAA
7409	21310	A	7469	2	110	GRVGKHHFGFEAAA*YHFDVGV*LFVY VSIY**GS
7410	21311	A	7470	380	8	TPQKKKKLKKAGEGVFPFPPKRTTPPPP PIFIYFIFFFFFIYFFFFFIYQMSF FYSHIMIQRHFLNF*ESFYSCISILQ*L KFFTSFLGLIKL
7411	21312	A	7471	1	107	PTRPHHFGFEAAA*YHFDVGV*LFVY SIY**GS
7412	21313	A	7472	2	360	VNTILALLIMITF*LPQLNGYIEKSTP YEGCLDIPISPARVPFSIKLFLVAITFL LDLEIALLLPL*ALQTNTPLPLAMSSL LVVILATGLAYE*IQRGD*ARWLSEL TOPTNN
7413	21314	A	7473	423	167	VRVHKFLPQVAPHAFFNSTLGGRRGI A*AGEFKTSLGNIVRPPSDTCNPVILGL QA
7414	21315	A	7474	1	73	IKPE*YFLFAYTLRLRVNKLGV
7415	21316	A	7475	131	3	ISWGAEBLITRVPAL*EASGVSRQS IETILANTVAPDAW
7416	21317	A	7476	2	103	PRVSTGTFSSIAHITRDVNG*ITRYLH ANGAK
7417	21318	A	7477	2	325	NTLLALLLIITF*LPQLIGYIEKSTPY RCGFDPISPARVPFSIKFFLVAITFL DLLEIALLLPL*ALQTNTPLPLVMSLL LIIILALSLAYE*IQRGD*TRSDT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						FFFFFFFFFFFFFFFFFFFFFFFFFG GNF*FYK*LLGNRDGVCLPPSYL
7438	21339	A	7498	1	410	PTRPDQLIHL*KNFLPLTALLI*HVS IPITISSIPPT
7439	21340	A	7499	51	478	PQRYTLLMKICITPPGKGRPRVEMLAGG NENTRCLIEERSYKYHSLIKLGLQQQC IPSSLLYKXNMICYLMLCYIYIYIPFY DMYTRQSVLYKLNVMALL*LYLLFL FWK*KYLYFLFM*YKKI FLYLL*YK YIFYLVCVYKNIYTLFCNINILYTY TYVININLY
7440	21341	A	7500	3	110	FTSKHFGFEAAA*YHFPVDEV*LPLYV SIY**GS
7441	21342	A	7501	168	327	APCYKATVIRTY*Y*YKIRYTBQMSRTK NPDINPYICGMILIFLQLSKHKI
7442	21343	A	7502	400	159	NNFSPLRLNCGFFGPKLPFGMFOAGPPG *GFSFFLRSNFLLVFRKY*TFGF*DF FYCPSPNELVGEPPLMGNGKPGPF
7443	21344	A	7503	401	257	TSQKKKKKKKKTKPKKKKNREKPPPKKKR GTRGEPPKTTGGGKKKK*FKKKKKKKKG PP*POLVIRGGRKKKKLWKKKKGAF*K KKKKKKKNPKKKKKKPKTPKKKKKDDG GTF
7444	21345	A	7504	44	344	LLASLANALPPTINILGELSVLVTFS *SNITLLITGLNI*LYTALYSLY*FTTQ WGSITTHLNNIKPSFTRENTLMFIHLS ILLSLNWDITITGSS
7445	21346	A	7505	286	252	IT*FAPHVGGAGLEFLTSDLPASASQSA RITSVQCHAMPVENIFVSL
7446	21347	A	7506	3	213	RELGLKRFPLSLSSMD*NRNPSHPA TFCIFCRDEVLPCCPAGLLILLVWNLKN CCCYEHHRYYCY
7447	21348	A	7507	400	20	SLFQKKVSLLEKSAVOLVMF*DRFSLC HPGNRA*QSGVTTASSLRAR*SSCLTW EYRPSPLPLADFLFW*RRGLPI*PRVVS NS*QGVGLLHQPSKMLFSSSLSPCARPL FFFFNRSTNLRVQS
7448	21349	A	7508	349	227	SDPLTSANP PASASKSPGITGVSEHTRP *PRFLKNVILYSEMEVYN*ASFHVD*G GLELLTL*FTHLGLPLMDYREPPHPA LTKIFGKPYIQ
7449	21350	A	7509	371	21	FLVETGPHVNG*AGLRPLASSNL PASAS QTAGITGMSHCAQPNPGLLNKMTMLAVA TBQWVGYNWFSVPGHITARPBGKRLSDC LISDTNVCVVCVCSGLIFVCFETGCRPA LQPS
7450	21351	A	7510	330	14	DKVCSVTOARVQWHDHKSLLFLSSGLRQ SSHLSLLASWUHHMPQWAF*FY**R LRSHYVAQAGLKLASSNPPTLTQASAG ITGVSHNHWKALFSVTDLKH
7451	21352	A	7511	417	33	APPQGGGPPKRIFGPSRKRGKGGPPPKR FF*KNKPPGEGGKSPPPPKNFFPKKK LGPKKKSGFGWRFADPRAGOGVFNFP FKAQGEKFSRGEINPRAGAKKKGFFL GKKNTKKTKPKKDL
7452	21353	A	7512	81	296	CLRBGASHSAAGLHWDHSSSLHP*NP GLRGSSRLNLLSTMDYRCVPPSLANFES CLLKI TLGSPFPKNL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7453	21354	A	7513	412	279	KKVTGGLGVVAHAYNPSTLGSQGRKIP* AQPETSLGNTGRPCILH
7454	21355	A	7514	74	126	KI*DWVPKGAPLOGPVF*NSITFPEVRN RGPPWPRGPPTVNRG*NRKN*PAPRGSN PPFFFFGNPGPFKLJGWPSS*GSPQNC KKAQAG*APT*KRGPFPQNKV
7455	21356	A	7515	332	20	GEKQVGSYFFGNTERLEFGWTRF*AWIV SNVACHSSISJGVVVFPRQGLAFLPLSPD WQVDFESYTWKIDPQSEETVTLVREYF SWEGAFCHWGKAFNQGKIK
7456	21357	A	7516	1	167	RTKGRFTVLARIVLIS*HCDLPASASQ SGITGVSHCTPRGLSLV*PTAKIST
7457	21358	A	7517	2	223	QRMENSHSYVA*AGLEPFGASDLPA*VA PQAKILLLLGGHKPLTILFRLSSNSW PHVKMPRMPPLKALGLRG
7458	21359	A	7518	151	476	SLGKFAVSFSFSLK*KRALLAVLPRCS NSWP*AVLLPWLPRVGDGMSYHTOPDY HFOARAVAILGLVSTQSHSVTGLFVEN SFRAGHGGPRLQSOHFGRLRWADC
7459	21360	A	7519	3	134	CSFRLGAVAHICNVITLGGRGKRIA*AO EFETCLDNLAAPCLV
7460	21361	A	7520	14	219	APSIHGFPLTYTHTHTHVHYMY*V YINTHIESIKQPLTLQSNKANRIVF KTQFMLTCTFMR
7461	21362	A	7521	134	334	RKHSCLFFNFCCPYLSLETRSHYVASTG LDLLASNPFPALASORAITGMSHHAPP VLTRFKKSLF
7462	21363	A	7522	406	145	FLKTFGSPQGFVF*TPPQGFPPPPFP IFGVPGQGFAPPLFPFFFPQTGIFPPL NPPSPPPQGFPGOFFLPPAPFLKTPP FPF
7463	21364	A	7523	3	382	HPQGEGRRLTSL*NTSLRLKXXXXXXX KRGGPFFKQNPWGAQI*PGKKKQNFLLK GAKQNLGNFGKXPFWGKGLAKPKK N*TFKGKKKFLRGKGGKTKPKPNLLKIF FSGPYLKKIFFPGP
7464	21365	A	7524	319	106	QTRSCSVT*AOQVMDHSSLSQF*TFWLK RSSMLNRWDYKHPEPLCLNFFFFCRDG GLLCHPGWSQSPCLK
7465	21366	A	7525	433	228	MOPYNWEVNSSSOLSSARQRVTHVLT GNFFIK*BRMDLPVLPLVSKSWQVIF PPWPSKVLKLV
7466	21367	A	7526	26	351	CRSLVFSLPKGLRFSVLIHQVFSHPD FFFLIGNTK*RK*TPFIPPA*LEKTPA PFKHWAITCSFSGGDLGRIA*AOEP RTSLANKNPSLEGGKKGKSSCS
7467	21368	A	7527	438	62	QLSKTHAPFGKGFKKZGGPFGPCDVG LAPGKKKANOPTKAPNPKQKQSGGLAS PMGKPP*PPCSMPSDSKGSVPSRGQVA PAPKDYCPV*AAILPSKKKKSKPG*V KRGKPNLYSIYNK
7468	21369	A	7528	3	132	FYYL*RRGFVPLPRVINSWLVLLPW PPKVLN*AMHPIHG
7469	21370	A	7529	2	628	FFFFLGVVNRVLLMGRGGEANSREGRG PQPRGMHQLEVRGRSGQGDOWHTLS PPWGRYRGAPPTFAAPQAFKPFQRLLP N*LPGRSPSCLLPETPALSPLPSAEWGG FKLLTGTSETPGPSPSVGSANQRAQ



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						ATTIVARGHTPCTRGPLDTHAHSSLRHH AHTRPPPRPLAIEHGTHTIAHPHTPGAW VGEPPFGWGRA
7470	21371	A	7530	63	205	GRPTRPRTRGVKLL*QEHEHTKPTGGLPT LIAIDTTLMLPISPPFLIL
7471	21372	A	7531	390	56	KTFPPFNLIAPTEAKSVLLPFLFFPETG SRSSAPGVQVRHQSSIQPH*LGSS CLSLLSN*DYRCAPPC*SPCLSLKCM DYKREPPHPAKGSHMQSYLYLSLYIA
7472	21373	A	7532	543	335	LAAYGGTCLQS*LFSLRWEDHLSFQVQ GCNRLQIQCSPAWATE*DPVFKGEKKE RVLVKVFS
7473	21374	A	7533	3	145	WDRGSLSEPRSPGLKQSCSLSTSNMDH SSEPLATTSMWNP*IPKFLNLK
7474	21375	A	7534	386	106	SNVDTETMET*ECVINDNSDTPYQNLN DTEKVVILAKFTALNACKKSERAQIRH TCVHTHTHTHTHTGSKCLIKYLLLT IQQQNIRIN
7475	21376	A	7535	398	2	SLQPLPPRVKCFSSPSPPRRWDYRGAPP RGKFFFPFGKKEPPPVGGGF*FLPPGV LAPPPPOKGRISGGSPRPRPPFPFKIR ISYFILAKQLKCLFLKKKKKSQAIRKLY HEQKNIPLTKSSVFMESQRA
7476	21377	A	7536	2	344	HSKCVPAVVMVAYIRLYLSISLLHL ENLVHFFHFL*GQNNLPFVAGRL IQRSHE*EMII*VHVQIKREGOIFRK* IFCMIGRG*ITCGQEPETSLVMWKP LY
7477	21378	A	7537	116	224	LHTHTHTHTHTHTHTHTQPNKLP*LPYP CGHIFRRY
7478	21379	A	7538	1	383	WHERTHSRITLLFQGLTLLPLAIA**L LASLANLVLPPTINILGELFVIAITFS* SNITLLLTGLNILVATLYSLYIFTTTQ* GSLTHINNKLPLTRENTLMFIHLSPI LLLSINPDIITGFS
7479	21380	A	7539	31	332	DNYLSSYSSSGSMRELTLASQGRWEP IVDRTPSHRHTHTHTHTHTHTHTV LFRIGPWTAREPRGHICGN*IRNQSP* KNPRTRGKNLRTPEGN
7480	21381	A	7540	199	15	NNVQIK*QFHEHTKPTFPPLTIAITLL LPISPPILIL
7481	21382	A	7541	337	157	AEIVPINSSIGNRVRLH*MESYSVAQAG VQWIDLGSVQPLPGFKRFSCLSSN DSRLYFRCH
7482	21383	A	7542	28	313	RARIGSDQCLSACTQVVENKSLISGDFW WDFRS*SVTRGVVRNHNLS*PPIPG LR*SSGFGLPNCWDYDRDNVWGKKEV TCPTVNLQKQ
7483	21384	A	7543	493	180	GGFRGSMVLRXKGGVGFCLEPPPSR VKQFFCLRFPFRRWGREGSPRSPYFFP *EKPRFFFLGRVVLNPLGGVGVPWPSQ RVGFGGLTPGRASFFFLI
7484	21385	A	7544	403	426	FF*KFTIPTHTLEFFFTFFFTFFFTFF FFFTFFFTFLAPPGGFFFTFYQKFL KFGQDEKFLALPGGGFFFT*GKFPQFF CFLVFFFTFLPLENGVSLYCPGRSRT GLKLSRLLASLRAGITGVSH
7485	21386	A	7545	3	335	RHSDYDPGVST*NTLSSEDSLISLTPA



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US95/15,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						FFFFFPGFIFPPPGISGFFPPFPL*NF YCVDPPIAVILYR
7499	21400	A	7559	386	2	FFFFFPGFIFPPPGISGFFPPFPL*NF FPLRPLFFLGGQADFFPPPKGFFPKIP RGVFFPPPLREKFFFSPPP*IWADPPGF LGGPPLFFFFFFFFFFFFFYRKARTKP ICLMGVSPSHQCI
7500	21401	A	7560	1	396	KICHRILPTETK*EKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK LKIPSGGQPLPGQGEKNPPFLGQBKKP PGVPLKXHLPLGGGHPPPPPKKISPRG EKKNFVGQGGKKQNIPOGKKIPSHKKK
7501	21402	A	7561	1	390	NYVFKFSDKLGAVATCNSTLGG*GL WIT*GEFETSLGNWVPLYLQYQKXK KKKKKKKKKKGGGPFKTLGGAQFGGGGE KKFFFLGGVKKPPRGFLGNPFLGGGK MGAPPPKIKALGEKINP
7502	21403	A	7562	406	182	FVFFFFFXGFFXGKXKXFF*TXHFF FVXXXXXFFFFFFVCFPPFFFFFF FFFFFFFFFFF
7503	21404	A	7563	2	113	FHPTSKHHFGFEAAA*YHFDVW*LEL YVSIY*GS
7504	21405	A	7564	313	97	SPTYPYIRNSAQFSLLAKSFCSPHPT YHDPHLEKSLITCPCQSPS*PIIPPTVC TYINRPPATEEPQNE
7505	21406	A	7565	3	144	DARVAVATGRHGLHVIIGSTFLTICFIR QLFHPTSKHHFGFEAAA*YHFDVW*LEL YVSIY*GSTFLTICFIRQLIFHPT SKHHFGFEAAA
7506	21407	A	7566	1	130	FIRQLIFHPTSKHHFGFEAAA*YHFDV W*LELYVSIY*GS
7507	21408	A	7567	434	1	PDLNKVIFFPHRKKKPPYKCHIVGKHLR NEMYSIQDTNLSLPRRER*RTKTRCIIFF HKIKTSEHSFDIKKH*NYVTLCKVLRK LSTNQRQS*IFLSTNNDTLGRARWLTP ALPALWEARAGGS*GEIETILANKVKP RGRV
7508	21409	A	7568	441	86	NFSPREKGRFVPPPPPLKIFFPPPPPNF FGGGPPSPPPPKKVVFFPKPPRGFFPPP PKKKINFFPPPKQKIGPPPSFF*TPPPPP FFPPPPPPPPPPPPPPPPPPPPPPPP MEVCLY
7509	21410	A	7569	1	155	PTPDRLSLRFAKSGNERTLHKPGVT I*AKAPSKKKVLLVERKSNLE*LYDYG FPYYKIKKPVVIFYNQKKE
7510	21411	A	7570	434	1	SPTRAGKHFFKKNFGRKTPPKKKKKNI FSPDLTKPKFFPPPRG*ILGGGGNCPD PKKGVFPKPPQGVNTPPKKKKKKSPD KKNKGGPPGVFLKGGPPPPPPPPPPPP FFLRQSHLTLRLKCSGA
7511	21412	A	7571	493	196	SSLECS*SLGSI*FLTNMLAVDPDV LY*V*RVLYLVQVAITKCHIVSGLNRR HSFLTAVKARKSKIKVPADLVGGEVSLP SLFS
7512	21413	A	7572	1	239	RGLTILDAIRNICDS*KQVRILIFSEVW KKLVPTLINDFERPNTSVEVTAHVET ARELELEVVDQVTELPQSHDQT
7513	21414	A	7573	391	32	FFPQSPPGVGFPCNLNPNNGFRAGP

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						PPPGYPLVLNKGVPVPGPFELSPDS *VAPASQKIGVSGVSPCPRVMVPPFKK KKLGRVBQRCTMILLVYSKNVPVKPQK KSSIGSL
7514	21415	A	7574	2	383	PRVSTAFSSIAHITRDVNYG*ITIRYLH ANGAKKKKKKKKKKKKKGGALKKKPG GQKNGGGEKKNFFFGGEKKKPGGIFE KKTFFGGGENDHP*QKCKTPGGKKLL RGKGKKPLYPWGEK
7515	21416	A	7575	402	69	KTFPGKSLMKISHPPTYRGFFFP* NFFPLPGPYPTLGGCSHLGP*PKGFPQ KIDPGLFLSPPPKKKIYLFPPRIPLADP GVFLKADPPPPPPPPPPPPPPPPPPPP
7516	21417	A	7576	1	119	LIFHTSTKHFGFSAAN*YHFPVNV* FLYVSIY**GS
7517	21418	A	7577	219	69	NDISANTAIKKFWLKPCTTEGLWNT* LYIHLVEYYATLKVCGDLVVR
7518	21419	A	7578	3	287	HASAQINGVIERSTPYERGPDIPSPRV PFFIKFLLVAITFTLLLELEIALLLPL* ALQTTNPLPLVMPSSLISILALRIAYE *LQKGL*AE
7519	21420	A	7579	10	125	ALQTTNPLPLVNSSLLITIT*ALQTT NLPLVNSSLLITITLTLIAYEGLQKG LN*AE
7520	21421	A	7580	3	299	DARVELLDPOF*VSLPTAARIITITISQ DVLES*ADPTLGLKTDALPRLNQITFT ATRPQVTVQCSSEIGANHSFMPIALEL VPLKIFEGDPVTL
7521	21422	A	7581	3	116	AFASKRTGLGVEEPLTLE*LGQGGPP* HTLKEPVNI
7522	21423	A	7582	398	2	RVPFAPKNSLQITPPLPFFWGSPPKFF TPFPHEVFWGNFKNDFFAPFLRLFP GEKIPLVFFFFFTD*NFVENFFFLSL FFFGFFFFFN*SLF*SPANFV*VTH LFIRMFVFPDFWSPGILW
7523	21424	A	7583	288	9	RGSNLEKNSFPYKVNNGSGSLPFFHL FFSPRGVGPFFFPFETRSRVLAQGVQW HDLSSPPGLK*SSHLISQSSWDY*RAP HPANFVYF
7524	21425	A	7584	1	124	RDGFTMLPRPILLTGLKSSCISLPK* WDYRCEPLHLASC
7525	21426	A	7585	339	76	THPGHNGISVSPKKKIPRGGGPPPLFP PLPRVGGGDSL*PRAGGFN*TKPAPFP SGKKKELPSSKKKKKKKKKGSISTPF SRIS
7526	21427	A	7586	205	87	SISLSLSLSHTHTHTHTHTLHSPRCV PQPIGLVISKWKVKELIT*R
7527	21428	A	7587	353	256	PHPSVTTLVTSQQYQDPPPAKRL*LAEG SDCC
7528	21429	A	7588	159	195	QICRHRVVHINFLMSGSIMITPSPFLF INFL*SYVAQAGLKHLSQSDPPASASQS AERIGMSHNAWPHF*YPVELVHFYINK FVGIELFILTS
7529	21430	A	7589	76	205	RKKPEPEKTCFONITGNFTYCLSTYSHD SD*YVVRT*LCASR
7530	21431	A	7590	218	20	LSLYLASHLWLPKPHLEWAPSKSLRL GTVASPCNPSTLGGRGWVT*QGESST LANMAKPCFY

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7531	21432	A	7591	142	12	QIDYFFYLFY*RGKLTMLRLVSNWHLH IILLPWPPKVLGLQM
7532	21433	A	7592	2	224	QIIEALLITILLGHYFTLLQA*EYSKAP FTISDGIYGTSPVITGFGHGLHGIIGST FLTICYNPOLIFHFTSEKFGGLQAP*Y WLFVVARLFFVASLH*GSLFYPTPSL RVLGSLHHERFDRLNIFCNHRLRTP RHYNLNPHVYLLOPPTNISLYLRT
7533	21434	A	7593	1	323	HAYGNFLVA*LVMTFF*LPVLVDYKHK FTPYEGGFEPKSAARVLFSIKVPLVAIT FLLSDLQSLALLPLP*AVQTTNPLPLVM AALLDITLALSILAYA*LLRGLLE
7534	21435	A	7594	1	104	RACVVCVGVVCLVCLLKNVCLVVCV CVFCAC*KNVCVVCVVCVFCAC
7535	21436	A	7595	383	43	VFISETLCEHVAHQTTTESLGLSTVAR TLNASTLRG*GRMIA*GC*SKTRGRNMD SISHSQTLAQSPHLLGRHPKWCMCVQ AAEAVLKGQVETDASPOIQKIPINSLIN L
7536	21437	A	7596	2	331	WPPTGITPLNPLESPLLANTGGLLA*GUS MT*AHHSIGENNRNQVICALVITILLGL YFTLLRASEYFESPTTISDGVDRSTFFV TGFHGLHVIIGSTLLSWFIRQLICNF TSKHHPGKAVA*YGLNFTKYLGVHPPTN M
7537	21438	A	7597	384	23	LFKTKQYRFLLOPFLKIFFFPLKA*IF LGGPSHYFPFPKGGFPKPSPPWF*IPPP YRKKHFCSTHPKMLAPRPF*KRDPHFF IFFF*+RNGLAMLPRLFSNS*QAQVLLL QSPEVLGL
7538	21439	A	7598	401	189	RVLPCFAGWS*TPGLKCPCLGL*KCWD YRREPPCLIRFYLFVYFLRQGLAMLP VLNSWP*VITLLO*SP
7539	21440	A	7599	81	368	KCVIYFFLSITLGRKYOFFFLERELA FPFQGMGGNGLG*LKPPLR*RDPSCL ALPRGGNGRGA*PSPTNGLGGNGVY SGGGGFETPDLK
7540	21441	A	7600	264	25	AVRHQRLRLFCSHY*NNIVERLGLVAR TGNCPLEDKAAMIT*RHEFETSANMV IFCLDIQSKSFLSMRFSRCLLNL
7541	21442	A	7601	1	196	WPSLVGETNVAISFNQYINWGAIVART YNAGTLAGQSGWIT*QQLSLITLSKVK PSTPTNTR
7542	21443	A	7602	315	82	TCYQVFALFTTAKFKFLCPTLNNWIS RVWYVHTMKHSAIKRAVIAHATMWKL ENILSEIKSQSKATGCMISFI
7543	21444	A	7603	334	118	PKIKTEGSGPPPKGNAGMYK*KKPILVL AAPPHPPPGVFSVFSYFNFPRFFFFF FFFFFFFFFFFFFFFF
7544	21445	A	7604	3	288	DAYTT*NLSSVGSFSLTAVILLIEMI *EASSSSSSPPGGLRPAFPVRPAGL VF*VSVPPDLQCSLAGQLVRFMEELAR LAPHIRWIIQ
7545	21446	A	7605	354	33	EGRARYTRVQRPFRHLGLFFAPQLGX KKKFSFKKKKKKKQNLWGAHVSHNNLS TKGG*GRGSRFT*A*EFTRSQKLGTGN MVKPISNTNPKNERGGABELSQL
7546	21447	A	7606	401	161	YLVSHLLQILPPLALPVVYFFF*DRVLL



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						YQPVAVAHACNFSITLGGDRNIPGGQEF KTTCLSLPGRWAHREFLYLAFCPFYNG IGCLLIIGF
7565	21466	A	7625	271	277	NRGKRTGTSLSLTLEKNPFPGGQFPWANE PE*GLKFWGGVGRKRPFKKKRVFFNSQ GTSFLEFVLKSGPLVLKAPCKEKNIT TQPKKFGFPPGSLKRAPTTTTTTTT LRKSSVTEK
7566	21467	A	7626	2	269	ILGRLSVLVC*FPPKPTTPLLTLGLSLF TGLYSLYLITTTGWSLTHHINILKKLP TFKNTLMPHLYPILLSLNFIDIIKKKK KGGAF
7567	21468	A	7627	397	164	FFPFKVPFKQKPKKPSFPRVF*TFPF PPFFLPFPKKKKFFSP*TWPPGLIF *KPELFTTTTTTTTTTTTT
7568	21469	A	7628	3	324	DGNVSTLYGATGSHGLHDMGSSALLTY WYIRQLLHFTSKHGFGEAA*YHVF DVD*LPLCGSIY**GSPGPKFSGGKG IAPVHGGD
7569	21470	A	7629	2	246	SLGLTTL*KNISVLLTGLKILVTGLYS VYIFATQWGLTHHINKIP*LTRENT LMFTHLCPILLSLNMDISYKQFTS
7570	21471	A	7630	112	290	LISGKGQWTKMLPVLTLTDSFSK*K NFSTLGBQCGRIT*GQRETLGNTVRP HLY
7571	21472	A	7631	248	2	KVFASGRKREPHNYVTHAVGCCRIAT AIWTQWYQGFPALESLRLECSGASAIH CYFGFKGSDSPASPS*LAGTGTTRP
7572	21473	A	7632	383	106	GMQCFKPAIPALEPFPQCFRPGVLN QE*PQNKSPFFFFFKKKKYIYICMVV HAYNPSYSG*GGRIT*AGKFKTSLNNT VRPHLYKK
7573	21474	A	7633	435	133	YACIAGLPKQWDSRHEPGLANPCTFSKN RGFPISDRVVISNWERVPG*PKPFGMG FQTLVQASLGPLLLFLTKGFFFSQHE EQGMDTSSFQHRFFRGK
7574	21475	A	7634	1	209	NAYRIVILCQGLPILLSGKMNPKTKRW LGMVAHACSPSLGG*GGRIA*AGEPGT SLGSLRCPCHCK
7575	21476	A	7635	117	495	STSFDKVLGRHSPLFFSLFETKSCSL TQTGVQWHDPSL*FFFFPK*FSLGLP LSSWDYRHAFFRPASFFVPLVMMFHHV QAGLELLTSQDFPASASQAGITGMSH HALAHLYFSCKS
7576	21477	A	7636	1	241	LEGSSDSPSASQVAGITGCHHQLFP FLAF*LIFNE*FFPGNSFFVPOAGHN GIGG*LNPPPLGKPKSLCLTWGG
7577	21478	A	7637	3	93	EAKAGESLEPGDRGCKSLSCHYTPAWQ QSVTLVSKKETKNTKTSVPPFGVNLILY KVSINILFKEIFYQAPLIL*DNEDSS TLSSALQPGQSKTVSNBTKQKTVS*PG NRV
7578	21479	A	7638	46	228	GIPHQPSKSVFNNVHGFGVAHTRNFN TLEY*GGSIT*GHEFFETSLGNIVRLPPF SLQST
7579	21480	A	7639	1212	1023	KNHSNEWTKRM*YICTMEY*ATERNETM AFAAT*MKLETTILSEVTQEWKTYCMF SLVSGS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
7598	21499	A	7658	1	137	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFLEHIRLLMPVTFSSHR HSSLGDRVRFCLEKKKKKKKKKKKKKK KKKKKKKKKKKKGGGLF*ERKKKKKKKK KKKKKKKKKKGGGLF
7599	21500	A	7659	236	32	LIPLIKFLYF*FIFI*F*FLLTFYFRR LKILFFFFFFFFFFFFFFFF*KNFIK NLIFP*LIYLFYILKFFIYIKTFLFLKI
7600	21501	A	7660	301	65	KAPEKLPNFFVFFVFFVSSFIFFFFFFF FLPFFFFVFFVFFVFFVFFVFFVFFV LAAT*FLRGVET*LAJLTKT
7601	21502	A	7661	70	273	KHSPHKKPASD*NTBLTKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK GPIHRGGEKFFPSFLRRD
7602	21503	A	7662	1	353	ILIINTLLALLLIITFGLPOLSGCLQR STPYEGGSDPISPARGRFSLKGLQAMT FLL*ELEIAL*PLP*ALQTNLPLIDM GCLLLNIILCLSLAY*LP*GLDCRYH SQRIOQ
7603	21504	A	7663	1	131	FIQILPHFTHSKHGFPRAAA*YHWPVD VA*LFLYVSIY**GS
7604	21505	A	7664	2	192	PLSQSLY*LLAADLLLT*IGGQPVSYF FTIIGQVSVLYFTTILILPTISLIEN KILWAY
7605	21506	A	7665	356	2	TPFFLSSPGGSGSPTPARPKNPPPWG GGGLF*SRKGLF*PKNFWGGYIPFFLF *KKPFFPPGQSPVTSKDVVPPLLM PPRPHVRLGLPKKSPSSRWETQVK TKKRAA
7606	21507	A	7666	312	2	GFFFFFFFFFFF*DRVLLLRLEKNG VISAH
7607	21508	A	7667	1	233	PWLSNAEPDSANSCLEVOIMIQDD SFPTYHYDFMYCVIY*RLSLAVSPGLV SNWPAQILQPPQSLGLQE
7608	21509	A	7668	174	295	IFFLPFCGHSVLAVLRLVLSNWTQAIL PPLPP*ILGLQA
7609	21510	A	7669	183	330	NKFKLYWSPVAMHACNPRTHRGWIT* CEPFETTLAMVMVXPCLY
7610	21511	A	7670	3	319	TSNTLLALLLIITF*LPQLNGYIBST PYSGDFDISPARVVPYIKFFLVAITFL LFDLEIALLLPL*AVQTNLPLIVSS LLLIILPLALAY*LQGLD
7611	21512	A	7671	1	313	ARGRRRRRRRRRRRRRRRRRRGGGGP TQTDCKGGRNT*RGRETYRESE*DRRP FLPTYRVNLQRFVGLRLKGGADKTFCL ILTLARDYVWPDYRUGADEM
7612	21513	A	7672	3	91	TRRRERDR*RRRRRRREIFREKNSQ S
7613	21514	A	7673	1	115	DELANLFI*KAGFFVPLRLVLSNLQV ILLWPPLRH
7614	21515	A	7674	3	232	TRRRRRRRRRRRRRRRRRRRRRRR HYRE*DRRRRRRRRRRRRRRRRRRR AVALSAPAVGRQTRERISR
7615	21516	A	7675	1	234	RRRRRRRRRRRRRRRRRRRRRRRR REIERERERLQRRRRRRRRRRRRRR ALERG*KPQCGFWKRRVKEPLGLKLL
7616	21517	A	7676	1	262	RRRRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRRRRRRRR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
7633	21534	A	7693	370	151	WVAEVRGSL GKKYSVASDGRKLPWPQGFXTADPFFFF FFLK*RCGFTMLFRLVLNPNWQQILPFPQ PPKVLQLQVLRHHIWL
7634	21535	A	7694	3	373	WPGYTLNQAYAKIHFTLIFTGAILNLTFFF QHPLGLSGMPARYSDYFDAYTTNLLSS AGSPISITAVILLIFNI*EAFASGRKVL IVPEPQSAGITGVSHCARAYLFDIR DGLSLCWPGWT
7635	21536	A	7695	406	394	KFF*KKFLFPPTTFLRACLFTFFLP XGFLTKYIAQGIKTPPKKCKPTSSSLKV LPSDPYFFFPIDPPPIFFFTFFFTFFFTFF FFFTFFFTFFFTFFFTFFFTFFFTFF ECNRL*W*FTYFFFKESPHCI
7636	21537	A	7696	2	334	ILINNTFLALALLITTFWPOLGYIKK STPYECGDFPISPARVFPSSIKFFLAAT FLFDLEIALLLPL*ALQTTNPLIVM ASLLLIILSLSLAYE*LQKGLD*AE
7637	21538	A	7697	2	95	IALTIYIILTTAPILLNLSSTTLL SRT*NKLT*LTIIYIILTTAPILLNLS STTLLLSRT
7638	21539	A	7698	423	326	RQCLTMLPRLVNS*SQVILLNPWLKVL GSQA
7639	21540	A	7699	400	32	FKRYTESYFFSPNQIQFFFFFFPHR*NFY VOVKQPPPKKFFFLITPTPERFTFFFL *KKNIFFP*YFFPLNPL*PPLP FFFTFFFTFFFTFFFTFFFTFFFTFF FFSNSFFPY
7640	21541	A	7700	125	407	FINTSSTFVVKPTTCWQKHTPTARTD LCITIFFFFLEKNFLVQVQGGQGLIG *LKILLRG*KQFSCFTLGRWNTGGIP PPKNFLKKFF
7641	21542	A	7701	50	225	PWNVVRMSCWLGKVAHVCFNFTLGGGR RIA*ACEFETS*VTQ*DPVSVLKRRKN FK
7642	21543	A	7702	2	146	ETALLPLP*ALQTTNPLIVMSSLLI IILSLSLAYE*LQKGLD*AE
7643	21544	A	7703	1	93	ILIINTLALLLLINTGSLPQPKGYIKK STP*ECGDFPISPARVFPSSIKFLIAT FLFDLEIALLLPL*ALQTTNPLIVM ASLLLIILSLSLAYE*LQKGLD*ALL LMTWGLPQPKGYIKKSTP
7644	21545	A	7704	2	112	GRVGRHHGFEAAA*YHGFVDVG*LFLY VSI*GS
7645	21546	A	7705	1	325	TAGQFLPKSLILLSYNPAITFLGYPKI LKTYYMKTCTWMEIALPIVQVWTKQ SKLWYIOTIKYYSVLK*NELSYENTSK KLCILLRERSQYKKPPVFLIPTM
7646	21547	A	7706	2	169	SRSRAGTIAIT*TNLPCFLMT*PTLLVL TILELAGALIQAYVFLVUUSLYLHDS
7647	21548	A	7707	263	346	MLINVPGLHFGVNTYSKESPSVQGGV QWNLFSMOPPTGFK*FSCLEA*ASDN LSPHEQYRLALSFLKLT
7648	21549	A	7708	343	163	PKFF**RCGFFHVGQAGKLLRSQNP SASONGKTGVNPLAWQNNISIPWAP
7649	21550	A	7709	459	144	FWPGASSHAFDPTLGGRGRI*AHEF KTSIGNIVRPSIDTCNPKVLGLLA
7650	21551	A	7710	2	83	NFLPLTALLIYVSIPITISSIPPT



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						LIPAFALRILNIAKLYLIPKPNIIYLLPNCYINI
7669	21570	A	7729	2	303	AAASTNMLFFFLGRILVVENLGHVGLI FTFKKLWNQAGRRGSHL*FQHFGRQWE DHLRSRVQDHPQHSKTPSSLIQKNKMSI ESNLINLHKLFPSTGRM
7670	21571	A	7730	67	65	SICSYCFSSVFFVKSLFSAHQASLGG CVSCOS*AFQRLVFLPKLYFLY*WGLTM LSRLVLNTWFOVHILWPPKVLGL*APC GNEA
7671	21572	A	7731	354	238	QSILSDVAVMLD*QAEVFIWNRLLTY VHEAKKIGLVK
7672	21573	A	7732	33	186	RGALAVLSRLILTPGLKSSCLDLPKON DYRKEPPRPQGF*LVNLVLSF
7673	21574	A	7733	1	181	VNAGACSSIGGVFFLQHKKCHGRDYEP RGITTLERSYVRETTTHLVNSKSK*PLRA QINL
7674	21575	A	7734	336	80	HLKEPSPGVFPVPPFNLEFGPGSPKFF FKJAFSPILSFFFGKI FKIPRFRGENFA P*NTGKNS*KDRFPSPPPKKKGFPPFF F
7675	21576	A	7735	2	163	TPVSTGTPVPTLT*VPSPIIFPVSKKA GCLHLCINFCTELRLNLSLTIRS
7676	21577	A	7736	87	258	KAPSVCLFSALLMLLRMSARTSVCTVRP LSPS*AVISPVCTYTSRWPEATEDSQK
7677	21578	A	7737	1	103	LDKSGITMILQPSKLEPRLKAVLSIREH MLKNSRP*RDLYDSAAFKARTKARSKC RDKRAHVGEFF
7678	21579	A	7738	193	300	GSLEPPPPFFFFFLKKGFPNIVTRGSPN PPLEMGGPTPPPKGNVYGGGPP*FHPF GGVGPPIKGGGLGPPRVTVQKPLFPFK KKKKGKGGKPPSPPLGGVKKKGVNP KGGGSKPKFPPPPPPGGKKKPLKKK KKKK
7679	21580	A	7739	150	17	GRVAQVWMLHATPAL*KABAGRSLEPR SWTPDNGTWHLPSTK
7680	21581	A	7740	1	358	SPPPPPPPPPPPPKPKKLENPPPPK NPQKQNPDPKTKKSPTTPKKKPKIGT PPOTPKKINS*KKKNNPPENKGLNYP NKPNIHPAPPKPKKREKPLVETIKKKG PSPKKKK
7681	21582	A	7741	235	147	P*FFLGDEISLCCPGSLTFGLEQASCP GLPRRWNYKCEPPHVKIIF
7682	21583	A	7742	131	12	AASTYQ*FKIQGALIRINIFIVIEFPL KILQIGPVFTL
7683	21584	A	7743	1	184	NGYWCFCNHWGKESKTLNRSGTVAH TCNPTSGGGGRIT*AGSKSLGDKV RHLV
7684	21585	A	7744	347	202	SIFVETGGHYVD*AYLELLAGSGSPASA SQSPGISVSLCTOPWQFE
7685	21586	A	7745	138	263	KKRKYIHFKTN*MTAALFIRVPEKK QSKCHSADEWINKF*YIKICLSIHQND LNIASTF
7686	21587	A	7746	358	169	AAVAERTONTKTELDLGLNKKIYI WPGVVAHVCPNITIGROGMIT*GQIE TSLPTTR
7687	21588	A	7747	78	346	AIQMLRNQVKIKLPKSPVEIIPKIVPQ FOVOKIKSQNNFLLPQESQIFATSTG



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
7707	21608	A	7767	346	90	SQSRITGLSHHAQLSSLSLVVENVEN TPSSSFFSFPFFFSFIPFRFFFSNR DRVLVCYLGS*TPELK*SSQGLPKCW DFROGPCLTSTAFYISITVNFSPNCY S
7708	21609	A	7768	278	87	AASGVPSEFSPSAGYLLVCRLLRSLEK CSIRVGV*FSRCHLSPLSLTRKGNLSLT PCASRVK
7709	21610	A	7769	5	272	AVTHPINESCVLWIGKSCCLLY*LFEEK KKKKKKKKKKKKKKKKKKKKKKKKKK VARKINLFLCIQKVDAGGCTLWGGPPI FFFFL
7710	21611	A	7770	198	33	QRPOSRCRAWLGMVAHAYNFGTILGG* DRTT*GQBFKTSLGNVVRPLYKQGF A*WLMFVPTITITWKKVRLLEPGLRPS WATWRKP
7711	21612	A	7771	97	410	ILCVYLHFGVTHFPVHL*YHFLPLPLA LLI*YHVSIPITISSIPPYT
7712	21613	A	7772	5	415	VVRVTSYHSG*AAAYAT*YTLSEAGSFF PLTRELLI*FMKRBAFT*KR*VLIIEHP SINLD*LYGCTPYHITFDPVYVLSKRR RRDSHPKLASRLPHVLDFFKKKKGR RF
7714	21615	A	7774	398	122	SPPPPPSSPSFFFLPPSSSFFLFFLFF FFFFFFFFFFFCCRD*VSLC CPA*SQTPGLK*YSYHGLPKFVWYHEP PCLAYFL
7715	21616	A	7775	1	336	FNFLILITTESRSVSANCKYLSLPGSS NSSASASRVAGSRGAHETWLFPTTFF F*KKKGAPPQGGGFLTLKKKNPPPRAP QRGGINGTFRPQNGGGKFFPWGKKKF
7716	21617	A	7776	1456	1232	FAIESHCVTQAGVQWNLASLQSPSTEF K*FSLCLGLPSSMDYCVPHLPAFYIFS RDRVSPCWPGWSKTPDLK
7717	21618	A	7777	400	2	NTEFPYGPPIISLGM*P*EMETTYIPKP CTOMFLEVLFTIAKK*KKPRS*LING* ILVYPLMEYYSATKRFDMHTQVDAI GNILSERRQM*KTHIVYSIHRASCTAE VRIKVSYGRAATWIKSILIA
7718	21619	A	7778	360	218	PYLANT*NL*RWHLMLPRPDSNSWQ VILSLWPFRVLG*QRGGRVQGRGARGW MSKCRGGDCLCWAGA
7719	21620	A	7779	1	372	FEVRSVAHAGVQWHDHRRGFEPFLGSSD DRVSASCI SRITGASHCIQ*LA*LLTK VL*VSAPCLSVNLRSLTLLKSDTLFSG RGNLNLGSLQTTISPSRHFQLLCTFR SLFPLVIVHKK
7720	21621	A	7780	372	219	ATSLLSYFKKLQPPQSSATTTISQ* SSTRQDL*PAKRLKLTGSDDP
7721	21622	A	7781	358	145	IKNIHDSWEDVKLTITRV*KELIPLT DNEGLKTSM*EVTAENVVLEARELEEV EPKDVILVQPHDTINR
7722	21623	A	7782	317	146	GRVDCKPFRFOMLVLRLGMVAHVCP STLGGRGWIP*GQFKASVSRMPRHL Y
7723	21624	A	7783	13	186	DRVSITQTSWAHPPTAS*VANTGMH HTWLVFFVEMGFHVGVQVGRPLLS WK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
7724	21625	A	7784	339	221	KMDLMLARLVRNSWLGQSSYLSL*NCW DYGSEPLCPAL
7725	21626	A	7785	355	3	FGNSGRVDLFFFFFLDRVSLCCPCS A VINLEVHISALQOPOTGLKPSHLSLLS SWDYRRVPPHS*GLF*GK*YSITQLR FLVHLSGLRSLPKPVASTVIRTRQS GLGLK
7726	21627	A	7786	1	201	QQFSHVFRLLQFQFSQEPSPSHIQG VCTRNTKVSQAN*CVVPVIANREASTGE SLSPGRRESTRP
7727	21628	A	7787	270	1	RPRRLHVFQVLMGLPKCGPLHMTLTLP YTLTTPSPTRSLGPPPECK*SFHLSFPSS WDYREMPORLANFCRGRILLCYPDWSS PGLKQS
7728	21629	A	7788	229	2	DGWRLINAAQIGTVAHAYNISNLGGRGR RIT*GQEPKTSITNMKEPCLYSDHEVRS LRPARPTWRNPDISTNTNM
7729	21630	A	7789	118	263	CSKGYTWPDAAVHTCNSTLGGQDGI A *AQEFKTSLGNIARPPISVF
7730	21631	A	7790	246	359	TFIFSETSHSVTQGV*WHDHSLQF* PPWAQVILSC
7731	21632	A	7791	70	102	AA*SRLTATSLSRVQAIPLPQPPEQLGG QGGRIIS
7732	21633	A	7792	7	312	FIDFQRLHNSYSCDKGVFDSEIYSIC IVLICK*RFPLNQKKKKKKKPKGLI* KKKKKQKQKQFPWLPNPSTYNSLFL PKSFLWLTCKDPPPLTLT
7733	21634	A	7793	1	341	IKPS*YLLFAVPTLRVNVNKLGGVALL LSILILAIYPIHLSKRRSLI*PRPLRS LY*LLAADLLILT*IGGQPARVPTTIIG QVASVLYPTTILILIPTISLSENKVLW A
7734	21635	A	7794	1	143	YGSTFFVATGFGHLMVIGSTPLTICFI ROLIFHFTSKHFHGFEMAA*YHFDV V *LFLYVSIY*GSTFFVATGFGHLMV IGSTPLTICFIROLIFHFTSKHFHGFEM A
7735	21636	A	7795	2	257	KWAIIEPTKNSLIPYIATITLLNL YFYLRLIYSTITLLPISNVKI*KQFE HTKPTPFLPTLIALTTLPLPISFILII L
7736	21637	A	7796	22	326	RDASDCSQNLVPLVAVK*MVPLITKK KKKKKKKKKKKKKKKKKKKKKKKK AKIIPKKKLIIPFLQKQKKLWGFKK KPLWGGKKRNPDKKI
7737	21638	A	7797	506	281	RGAN*NRSGCGKPKHRSRERSRERS RERERERERERESPRPPKQRQRERET IQ TILSLTVSLAPPPTCVF
7738	21639	A	7798	435	336	MRSNIHFTSHHTHTHTHTHT*TLKQH TFSK
7739	21640	A	7799	411	106	RNPPLPFSPLQGGFPPIYWGPPRF PPPL*KTPIGLKIGADPKKKPPPPG EKMVSF*PPPPPPPPFLRRPFLPS GGPWGHPGPPPPPPGV
7740	21641	A	7800	2	296	FVPSSTANWCFFLWSVF*TGGSNYFF VHR SYSQGVLDLIRLANTISNLSFI*RG GLAMLPRLVLETRAQTLHWSWPPKVLG QVWATVPSPFOLKN



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
						PPSHIYIDRNKH*MRHSEKTLFLWGSGE VRDAAPWVSHIPTAL
7758	21659	A	7818	190	292	NSHLFFPWRVFFMS*CTYMLVLEGSEK KTYSHA
7759	21660	A	7819	498	139	RKAATPAPAAAEPPDLPQAF*PPEFED TQDARGRRGREDPQNSP*THNDRQPS RALCSTRMRHLWIGPAFFLMTSLSVSG AVIPRNGGPGVSSGPCLLQLLQCGAGS STIRKIPS
7760	21661	A	7820	489	330	ELGFLRWVQAGLELLS*SNPPASASLFT SMDYRHRDHTGRHPGIYDSKMACIF
7761	21662	A	7821	490	260	FFLXNNXFFPFFFXPKKPFXXKXKXFF FFXKXFFXFFFFFXFFFFFFFFFF FFFFFFFFFFFFFFFFFFFLY
7762	21663	A	7822	493	482	VGQAGLKRLLSGDLPSASQSAVITGVS HRARPIMYFRVQ*AKGSHV*RWY
7763	21664	A	7823	456	121	ASFFPIQYKLGGLATPPQEGGCG*GIFI KMGYKRRPGGPHGSGKRPTQ*KKSYFI NVLVLFLRLDKGLAIPILVSNKQAQVIL PPWPPKVLGLQTRVTPGQNLKKNFF
7764	21665	A	7824	294	457	LCIGFVILISYPMNEMNYCEPVTVAHT CNP*TLG*GRGITRSGRDRDHPQHG
7765	21666	A	7825	26	235	SVWYNSQKRNKVTFSW*IDQKRCIH LWNYSAIKENVLLNATTTWIMLNTIK LSKRSQTLKSNL
7766	21667	A	7826	30	303	SYVSVVFPGSSGPTLSTFWHQTPRTYL NSVASAINLTKQCPH*PEKKKKKKKKKK KKKKKKKKKKKKKGAFKKKG*KTPK KTGGF
7767	21668	A	7827	464	21	REPPHPAPADILLHFWPLEL*ELLVYV LNTRCVVICDDTPRKLTCQMPRLILLQT EPL*VLFNLSFGSLSSKS*NLVNFEC KGTDSRSFSLFVAVFCLFL*RMGLANLH RLVLNCFQVILPPPFPKLLGLQVEATT HEFHGTE
7768	21669	A	7828	372	205	FFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFIKKFFI
7769	21670	A	7829	463	313	DIYPERRNSKINSFPAITWMLKLAITLK* LGRKPNIVCTHL
7770	21671	A	7830	449	266	VQMRFLHVGGGL*LLPSGDFRASVQ SMITGVSHHAQRSIFPKKRNDCDRPD NNECT
7771	21672	A	7831	480	148	LELALSHQAAEPHPRMYGYFKVLKER DFYPRITYPAKIILRHSGRMKTFPPDKOT IAPHFINTRPVIGRMKKVHQSEITKGC** AINNHLKVKKKKSLGW
7772	21673	A	7832	23	131	QEGNSKGYHLNMQEERIKLERKKNL EGEIIHFYKMKASEALQTLSTDTKID KHGKQ*FL
7773	21674	A	7833	16	339	NTDTLGLSMFPCRDGLAMPLFINLGL KRSCDPLFNCWYRHGPPYLASVLLK *TILLSLLPYHMKHCVFNVLCTNFCG GVCPMGLLCLRVGYLSLKHTE
7774	21675	A	7834	355	70	KKTPEGFSGVFLGPFYKGLPFFFFFFFF FFFFFFFFFFFFFFFFFLQFFLLCQGL S*STKTPVHSKYILSPFPHCLIFCPFIL LCSTPCNGAHY
7775	21676	A	7835	494	282	PENGNIQGGACSEPR**HCTPAWAKER

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SEQ ID NO. of nucleotide sequence	SEQ ID NO. of peptide sequence	Method	SEQ ID NO. in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DSVSNAKTIQNKKNIZN*HSISTAKARN IIIS*YKSELKKKM
7776	21677	A	7836	305	183	LVIVTCLTVRPLSPS*AIISPVTICTYTF RWPEVTESQKK
7777	21678	A	7837	179	191	LGRKRYLFYLNGLKCLYIKCVQCVNCI YIGVYIGMCVYICIIYILMAS*NQVTSF LSFYVELLNRY*IPVKVITVLENLRMG LP
7778	21679	A	7838	466	343	LGRLRQBNHLPERRGCGSEPRSRCTPA WETEKDAYS KINK*TKN
7779	21680	A	7839	451	89	LRIVTR*SGVICLEKQAWAMGAPPPASL PPCSLISDCCASNQRDSVGVGPSQPGGG YNLLVRRFLSLSEKRSIRVGVNRPFSRCH LSPLSLTRKGNLSLTPCASRVQCLALLR LAHGARTH
7780	21681	A	7840	442	164	AHTNQFSQCIKRSVTPDLMBEYIKGAHA AI*ENPVYEKKPKKVKKNRNCPKMSL AQKKHQA*KKASSLPAQEQAAES
7781	21682	A	7841	494	359	IQMLPRLVLNS*EQVILLWPPKVLGLQ A
7782	21683	A	7842	577	224	ITFFFNKIFLERPGLNIGDIWVSTPP LQG*TNPPPPQSQSVGLKAPP PPGLIL VFLSRQGFPLQGRVGFHPPPGDPPPPR FKKIWSHPGGGSPPKKKKKKIEAVLIG AFRLR
7783	21684	A	7843	404	56	HTLSTNVCSYLNLDFFSLRGRGLIMLP RLANSWQRIILLPQPP*LGLLRLRLQ ENLLSPQVQGGQGNETPS
7784	21685	A	7844	1	323	TNVLALLLIITFF*LCQIGYINNSTP YBGGFDPISARVP*CIKFLPBAITFL FDLEIALLLPLP*ALQTTNLPILAMASL LLIIILALSLEYE*LOKSLD*AE
7785	21686	A	7845	419	159	FLFFFPXFXXYVLSGGYI*YNCNLESS* QYFFFFVMAFRIFLFTFLHFYINMF* CTYFYLSC*FEYICSHIIHYFIYHL ENF
7786	21687	A	7846	475	124	FFFFFPQPPORGGPPPPPNIFFFFTRI FFFGVFFFFFPQKNFFFP*KTGQVFFF PFF**KIFFFFGVFFFPVFFFLSPPP SSSFFFFFPFFFPFFFPFFFPFFFPFF FFLKRQGA
7787	21688	A	7847	6	189	LIDTVSPSVALAGVQWCHSSSQP*PPS LKRSSRLALPRFWDYRCAPLCAHSPNS NHKK
7788	21689	A	7848	20	249	KNFIVELTCSNTVATFYVGFQDKCIL PTQLFFL*ETGHSVVARLECSGVIMA HCSLDLIGSWRPANFLNPL
7789	21690	A	7849	101	398	LFQKKKKKKKKKKKQSEKLEKKKPGSEK NKGGEKKKI*FPLKGGKKKNPRGNPKKKT FPFGGKKGRKPKKKKSPERKKK*RGK GGKKSLLCWVEKNLG
7790	21691	A	7850	87	226	GSLSPINLVPLPILHLL*KNFLPLTLLAL LI*YVSIPITISSIPPOT
7791	21692	A	7851	2	440	GATIRRLH*FFPLSGYTLHOTYAKRHF TIIFIGVNLITFLPQHFLCLSGMPRRYS YDAYTT*NISSVGSFISLTAIVLITL MS*EAFASKRKVLLVREPSIDLERLYGC DPYVHTFEEPVYIISRPRKRESNPAKLV



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7808	21709	A	7868	52	187	S LDPN*RRCLTKLPRLVLSNWAQVILPPW PPKLLGLQV
7809	21710	A	7869	33	373	AGVQWRDLGLLQPPFPQFKRFSCLSLPS GWDYRHAPPHLANFVVLVEMGFHHVQGA GLKLP*GDPPPLAYQSAGITGMSHKAR PGISVHFLLKLSFDPFKIIFRPGASTMP S
7810	21711	A	7870	100	119	VFVRIVFPGGLLFSPCSPHLCQPRHLK AEF*FFVRTGSMPLRLVSNWAQVILPP WPFVVL*LQA
7811	21712	A	7871	471	446	LINLPRVLVLSNWAQVILPPQPPKVLGL* AYI
7812	21713	A	7872	449	33	FSFFFFFLGKKDLFFSPRGQGGQANSA FFDPNPNFGKGSAPPPLPKSV*NPAP TGVFFFCGGGA
7813	21714	A	7873	334	41	PCPSLFFFFFFLRQSLTLMRRLCSGVIS AHCNLCPLSPSWDYK*HCPYLATGAPGLL SQNELSYVTL*LQESRPLCIPVDFMTFL PSLCFQSPNSTTL
7814	21715	A	7874	342	716	STGIFLFCVF*DGUSTLAQAGVQWPDLG SLQSPPPRLK*FSCLSLASSWDCHRVPP LLANYLYE**RGFTVLAMMVSPS*PCD PPTSASQSAGLTGVSHCAHGPMPFLNWP LKSCPSKSGRAV
7815	21716	A	7875	454	215	FPFARCH*FP*TLVHANEKSHHYSLI SSTQGHCHGCRPGQPLPRKTRDLCSLVY LLTFPILLSYDPAKSLSANVTQR
7816	21717	A	7876	492	176	PCGGRGAGGWNWFFPHLEASASRAAN ALQPHTRSSQAPAGPTGPRQ*GAQLHQQ LLCSISHQALAAPQGRQDLQPMPEP SPRPPLPWAQ
7817	21718	A	7877	281	439	TNSIDL*HMAVFLFFSLFFAFLSPSL SPSLFFFAFL*VPSPSLFQRQL
7818	21719	A	7878	507	338	LLRLRL*EGHLSFGGRGCSKPRLHCIF HWATE*EPFSKTINK*N*S*MINMKIN
7819	21720	A	7879	55	298	PPCLANFLKFFL*QRSLPMLSRFNSW PQAVLPRLPPKRNQLYLVGCCQCLNP QHLCSSQHTFKILFDIKHGRFLRH
7820	21721	A	7880	145	292	YFGGQIYIFICRDRISLC*PVLLTSLV SNSWPEAILPSQPPKVLGLQA
7821	21722	A	7881	3	203	LSLLPRLECSGTTTAH*SFKLLGSRDSP TSAS*IAKTGMHHAQLRFFFFVPGGV CVCVCGGVV
7822	21723	A	7882	324	211	RWHLAVIPIPL*EAKMGSLARSIRPV WVHNETPLF
7823	21724	A	7883	2	124	QHFGRRLQVHRLGL/HYQRGHGHTPS LLK*INVIYMT
7824	21725	A	7884	367	141	KCDYHREPPRLAQGLEFLNFCFELVT EPPCPALAY*NFL*RNLSLATLPRLV SNPQAILPRNPFPALGLQE
7825	21726	A	7885	471	215	RGMCVSHFLICGARYNSAARESLIKE FTCTERKHTHTRAHTHARHTHTHT HTHTHTRV*NSRSQPCRVHACSAYLIG G
7826	21727	A	7886	462	204	RHSS*GLDPCWDYHREPPHLCISSP* RKSDISLSDGLGTCKHWWPQVKSRA SVGRDCPSGHFTLAGFGQLGA

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7827	21728	A	7887	409	152	PVFLALERPNODFLRPGVLDQF*QNNKISFFFFFKKKKKYIYICMVVHAYNPSYSGG*GGRT* AQKPKTSLNNTVRPHLYK K
7828	21729	A	7888	1	152	GVHVCCDCKCICVCLCVGVHGLCLVCVSK*VHMCHEGRTIFGNLSWEGD
7829	21730	A	7889	101	399	ELINIVFFFFPLPLPFLFFWGGDFKKQ LNDPFLTNSMKNKHTTQKNPMGC*KKAITNPQKKRRKRSFSP*TKAQPTQKNG QNSQSGKAVGALTAH
7830	21731	A	7890	478	142	KPSKKKKGVNINPKKIAFFSKPKPVF KKKKLLKNDFPKAKKQFFFKTPTPLRPR EK*FPGPPKKKKRPPGLFQKN*KGPFW PREKKRVKKKKKVKSHYDNNHMPISVH
7831	21732	A	7891	497	320	PPWKFEEFFWSP*LHKYTPPVVCVVCV VCVCVCVDFRFFKPAFSPQSHFGNLIS FLL
7832	21733	A	7892	217	23	IPPFKRFF*EMGSHAVT*ARVYQWNNHSLQPKTCGLKGFSHLTLPSNWDRCRVS SSARRQSH
7833	21734	A	7893	652	470	SSSSSSSSSSSSSSSSSSSSSSSQPERK TRSAPQVEGKPNFCSLEAPPGLSLFS CLNP* RSMDDGPPP*PHATKTRAGDGL LCATHERARHCTPGLRPLFLAL
7834	21735	A	7894	25	178	GLLFFWDDGLVILHKLVSNNFVSSDSP ISASQSWDYRCDDPPCAPCLFW SP*FFWDDGLVILHKLVSNNFVSSDSP ISASQSWDYRCDDPPCAPCLFW
7835	21736	A	7895	104	451	ILSPNTTWAEADIMLSRTSQQTDRYC MILLVESKNVNLPGMNAEAYNPSTLGG *GERIS*GQEFETSLANTARHYFYKRNFKIKSKPKKIKVRKSKQKNVRMLLEARNKGRYG
7836	21737	A	7896	510	335	SCIVSLHRSWDLWHVFFFLANF*IFRKGVLPCCPGWQIYTFQLQIPFLSITPVAFSG
7837	21738	A	7897	37	260	AGNSQNGGGACSEPRWRHCTPA*ATERESVSINKQTKFLCSVPYFESTHFCNTEATGAWGEKVALGHAASH
7838	21739	A	7898	35	466	THTCGGIRKRLNKRKNQK*SQQKPSAPKEPEVIGNKKTNNKPKKKKTPQIQPTKCFRANPLRVTLFFVTQNKTPTRGRKTQCKVXLFPFNPCLGNKQTLPLRGLQKKKKKIPFFYSHPEPLAQKKATFWNG LGFT
7839	21740	A	7899	494	149	PARLLSLHSYEVKSVLPKEEGLLNFPVQSVTAHTPTSCIGLEKI*LLD
7840	21741	A	7900	494	114	GABGGPLSKKKKGNLPOYHTQWPSLSLYLNPFLSNHNTLTLCNHTHTHTHTHTHNH*LSRVGLFVLKPGQYQANGRWSP*YNIKE*PRKTRVMPVTPQLRNDGEMLTFWCSSRNSFMHVLGKL
7841	21742	A	7901	19	454	VWNSSVSIHTHTHTHTHTHTHTSTRSWVGWHMIPVLSTQRAENGRLGSGSLRIQRAMIVPLHSSLGNAARPCV*HTGSCCVSQR*VQVHNNHSSLYPOTGPQSSSLSLLSR*DYRHVPVPHAPSCVCRVVCVCVCVCVCYQDRGLTFH



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7857	21758	A	7917	445	2	FFFFFFFFFFFFFFFFLSYP*LIHYAEGIG ASPCYIMLGNFSSPPCGTISIAFGNPF YRLYFISHASADAWDPREFLDYRRGIN
7858	21759	A	7918	2	407	PPPPQVYFNWRTIFFGSGLLHIFFPQK RFCFYRTITNYIKTLFIKKRNIFSLHI IMVPPRSY*TPPLPFFFFFFFFLFFFY FFFFFFFFFFFFFFFFF
7859	21760	A	7919	107	11	YWHIYTLTCYSALKKKKLLFDITLI NLKIDMLSKISQHRKIH*FKI
7860	21761	A	7920	1	70	FFFF*AAKSCSRTIKCSITLACQNFELP GLSDPPTSAT*VAGTGVCHHTOLRFIF IV*LSGRILLQDQVQKNNISSV
7861	21762	A	7921	123	260	GTCARKEFGAVAHAYKLSLGG*GKIT *GQELBLSLVNMVKPL
7862	21763	A	7922	184	399	LHLNRVLKKKKGGLPLYSRPAKVN PALQRLDGLLIGSLRLSNLIGFGKAPHS WGG*AFFAATGLGLHLVIIIGSTFLTIGF IRQLIHFPTSKHHFGPKADD*YWHFADV A*LLFLYDSY*GGRILSNLIGFGKAPH SWGKTGNDNPPDMKSS
7863	21764	A	7923	2	407	GRVGNI*EATASRKLVLIVEPSINLE* LYGCPPHPLHTSNKKPPHTKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK NFGGKKKPPFFWGGKKKKGLPKKKNL FWGKKIOPTPQKKKIDGSKKF
7864	21765	A	7924	1	398	PRPPPLPSSRSRAPPPFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFVAALFPKKKKNFFFF*FPRG *GFYFPPLFYFCGGGGVFFFFFFAGN NIFFIPPKKNGIFKTLRGGGG
7865	21766	A	7925	2	335	NLTFPQHPLGLSGMPERYSDYPAVTT *NILSSVGSFISLAGILIFMI*EAF SKRKVLIVEEPSINLE*LYGCPPPYHTF EEPSIKKKKKKKKKKKKKKKKKKKKK
7866	21767	A	7926	1	328	RTGRTEGSENSPLRQNSPCHLSHPTL KKKKKKKKKKKKKKKKKKKKKKKKKKKK GAKI*PGPKKNLFFKGLKCTPLGNFS KKFPFGGKKKKKKPKQKKTLKCKKCF
7867	21768	A	7927	27	226	LSR*HM*NKSHIYSFRKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK GHPKSI FVL
7868	21769	A	7928	398	2	GGGGGGGGRGRB**NHKKGRDPPIPK KKPFPARKNRGGGRBPPQKKKLPQ KKPGRGPRAPQKKKCTPPPPKKGPPD KNPKKAPPFFFFFFFFFFFFFFFFFFFF FFLGLIARTTTTINDMKHR
7869	21770	A	7929	3	156	HASAHASAPFV*SVMTAVLLLSLPV LAAGVTILLADRIILNTTFDDPA
7870	21771	A	7930	405	249	ASAHASAPFV*SVLTAVLLLSLPV AAGTILLTDRIILNTTFDDPA
7871	21772	A	7931	921	699	DHPQHSBITSLQKNTITSCQGAH* QVLRLRLREDCLSPGSCSSEL*SHICT LACETE*DLVFQKKKKF
7872	21773	A	7932	423	259	HDLGSLQPLPGFR*SSYLCLPSSWDYR CRPLRPAQRGILMAATSRILTRSKGN
7873	21774	A	7933	395	35	PRVKRFSCLWLPKGGPRPRAPWPGTFC FFC*NGSPFLPGGSITLAPNYSPPPAP



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						QNGLVQALRPPGPPPTFFPLTPPTKAPWS WPFPGGKKKKLSPKGHSERHLWHKYIR LLSQHGGM
7874	21775	A	7934	1	118	NF*IFCRDWGLALSPQLSNSWPQVITLP PQPPKVLGLQA
7875	21776	A	7935	322	383	KKKGLTKITLCLFVKNTFKRTKQAPD RKKRVPIFLSYKRPVFKIYKKLPPFCRK KIKKKIPPGPTFSCLSLPSWSYDHRP PPCPMPVFCIYNNKNSDPA*PG
7876	21777	A	7936	3	131	GTHRVQGVLLTITGDPFASASQSAGI AGLSHRSQPLTKSL
7877	21778	A	7937	334	146	HPQGLNT*NRKVSSCAHSSRLSLPFW WDCRQSPPCPVIMPLKRGINHALYSPSR KLHLFL
7878	21779	A	7938	2	371	SEPGAGYNLLVGRF*SPSEKCTQVQVT RFSROCLSPSLITGKONSLTPCASRVQ CLALLNLVQGVLPGLCTHCLALPSBN PVPQMRMQKSPITFCIADAGSCRPLFLF GHLGSSPQSKL
7879	21780	A	7939	2	95	RLNLGGGGCCP*SCHCTPAWVTRNSI SKK
7880	21781	A	7940	1	191	ETRPSQTPGLK*FSLSLPDKSDYRCEP PCLAVILSTIQNSMPSNI PAASYSS*F GLYSSRW
7881	21782	A	7941	127	383	SKDCVRIVLRAQAKAGSYRTVMRCRP AVANTCNHSTLGSRRGRIA*GHEFKTSL GNITVILPLYKNNKKKKRGARLKS PNLT P
7882	21783	A	7942	235	3	YHLLFGYFCFFLRKKPFPPOLSLFSKK KKKKLARHGVAFLGRMR*EDRLRPGV QGCNELWNCCTPANATBQNP
7883	21784	A	7943	3	225	EHGSLYPTTGLKQSSYLSLLSR*DYR* AAPCPANFFIFNFL*REDLIMLLRLVSN SNTQAVLLPPKVLGLLV
7884	21785	A	7944	2	232	TLLPDNLSTTYPNKKKKKKKKKKKKK KRGGPFKKKKF*TRGGKKNFFFRAPKI PFGGRVLKGGGKKPGSEPTN
7885	21786	A	7945	394	41	WCRWLETWAGGSGGAVPPPPFFPHSS WDLALQSGGASSPFSQAVAHACNPSTL QGQGWIT*VQBFETSLANMKPLFSK KQPVTAVAHPAKAHRAWCTPTTHMTQH VLHVL
7886	21787	A	7946	405	100	FFFSFRFSSSLFLFLSSFFFFFFFFFFFF FFPFFSTGLFVNSPTH*SLPVPRIFFF SYLAQTSVETMLQTB
7887	21788	A	7947	391	212	KKQIMPAMR*HLTPVRWITKSKAKC WQCBENGTLAHSNWKCKGTBETGKLAG F
7888	21789	A	7948	106	301	LQLPITQLVNHSTYFMKIRYRLGVVAH TYNPSTLGGQGRRIA*GVQFKTSLSNTA RQKKKKKK
7889	21790	A	7949	342	208	GLGAGTHTYNTSTLQD*GWITSQGF TSLANMVEHVVQTCQF
7890	21791	A	7950	391	21	RQGFWILPRLISNS*PKGSAHSLPCKW BYRSEPPSLATYVTLRHPFCS TLLGQ GRSKFIMKWSRLKGLLAKVSSLRSSYC SSLRLTGLLEILLSPLLPFLETGSSGSVQ AGVQPLCPGLK

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7910	21811	A	7970	399	212	TGVQNSNHSLSQSQTPQLKRLFLLLLS IMDYGCMPPYLS*KN*FCTKGGSCYVAE ADVNL
7911	21812	A	7971	584	424	RPRRENKLNPGGGGCEPSRYCTPAWV TE*NSVSNRMKTNQNPFFSCKQFD
7912	21813	A	7972	105	1	PSNPQLSHL*NGILGRVWMLTPVPLNW EAEGRS
7913	21814	A	7973	363	28	SSSLGCHPOLNPHITLKLRFVTVYA*NK LCDKIEKKLFFTALHNKFLKKLGRV KILPRNK*TKKGPNEP*NILCLWIERI NINKVPYPSKVMYRSNTLPEVAVFSQ
7914	21815	A	7974	404	250	FFFFN*RG*FTMLPRVLNSNTALHP ALASOSAGITGMSHHAQPLSLIF
7915	21816	A	7975	2	60	FSCLGLPFCWDYKHAPHLANFCRDGVL NY*POVHLPLQLKVLGL*ACTTTPG
7916	21817	A	7976	325	81	KTHSLLFQGFLLQPLLPSPHPHAPP TPHLIFLLLLFCF*FFK*ROKQGLTL PKLLSNSYSQVTLPPPKVLSGFGA
7917	21818	A	7977	406	282	QWRDLGSLQPPTP*PK*FVSLSPNSNE TKAGRSREPGGG
7918	21819	A	7978	382	221	DCITISASYLQGNFFFLGDKVLCPHGN SAVA*S*LTVTSKRWHVYSSEISLY
7919	21820	A	7979	423	29	FLW*RGFTSLPRPLVSNFAAQCLLPNL PKVLGLQA
7920	21821	A	7980	3	238	SLAFFVETGSHFVA*AGLELLSSNSPA LASQASITGVSHHTQPE*GYSHM*PQY PYOLRENSDTLLSNWLFNPF
7921	21822	A	7981	324	128	NLSVSPYTFELSLNGYEVVHHDV*TL IFVWVVVSLFLCFLNFPLVCMVVFVFC CCFLSVFCI
7922	21823	A	7982	1	86	NLTMLPRVLVSNFAQAICLSNPKVLGL *AQAICLSNPKVLGL
7923	21824	A	7983	1	137	RPAHFCTFFVETEFCHVAQAGLELLGSG DPPTSASQAGITGMSH*D*PANFCIFF VETEFCHVAQAGLELLGSGDPPTSASQ AGTTGMSH
7924	21825	A	7984	2	277	PRVRSQVRVYQYV*NLQTHVFFDSNLI GIYLTDLPHVWNNMVKVFAVSVFVIA KY*NPCLTRQCNKLNPIHAMEYVVTIK KNEDGRA
7925	21826	A	7985	211	42	GPQKWRPGPGENLGFFFFFCCRRDGL TMLPRALNS*VHAILPPQPRKVPVGNV
7926	21827	A	7986	409	183	LLRLK*SSHSLPKNWYRCEPPCPATF FKRQILKESFPGHNTCCHLFNSLEVLK NGRTCTNFPHTLAVLKNM
7927	21828	A	7987	2	194	RFFSTQSLRLQPPPPQLK*SSHLSLQSS WYHARVPLCANFLFWFLQGQFAFL LKLKFLK
7928	21829	A	7988	483	209	SSPSLGNFCIPSSGGVSPNKNQFQPD LVINPPGPPSLVFFFFFDEGLSKMLLR LTINF*AQVILLPQLPE*LGQADRQVP LYPAEVE
7929	21830	A	7989	164	29	KFWFWLGTVAHACNPSTLGSQGRRI*A OELEPSLIGNEGRPLYK
7930	21831	A	7990	3	474	PTRAPLRAPEFTTVSEEFSEKHIFGFEA AA*YHIFVDVV*LFLLVSVIY*GSPPPP PKILIKKNGAETKFFF
7931	21832	A	7991	469	323	VETGLHHVAQDGLLPTSGSPASASQN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
7932	21833	A	7992	469	13	IGITGVSHHA*PDPFTLEOF KGDTVSSSDSSPSCGFLFPVGAS*LLCL FTQALAMVGARRPFSNLPCLSLSDCCAS NERGVSVMGSPSKPG VQVSLLYCRLWRPL EKRTIKVGVTRFSRCLSQLPLARKGNS LTPCVFVWRHCFGSHSVGCTHCPAPAVR QAPVK
7933	21834	A	7993	15	439	TASGRPSITKFFLVATITLLFDELTALL LPLP*ALQTNTNLLFVSSSLMILITALL SLAYS*LGKGLD*TEPNKKKKKKKKKGE KKKKKKKKTKTKGGGLKKKLGGAFLN GGKNHFFFFFFWGEEKTPGGFLGENFLG GGK
7934	21835	A	7994	392	186	YFYIINNFFFFFFKKIFT*YIFFFLLKKFL *YSPKKVFLFF*IFFFPSSSLFLFF SSSSPSFFFFFFF
7935	21836	A	7995	11	386	TWEVEVAVS*DEATLQPGQGE*NAISK KMTGRMFLVVSFTIASSWRQLKCS*TG E*MKSLWYIHIIEYLTIKENKVLSEHV SRL/LIDTGRERSKTEYTYLNPITYNL RIAKLSGCGGSHL
7936	21837	A	7996	3	186	DSFCF*RQSCSITQAGVQMGDRGSL*PQ SPGLKRSSCFSLPKDWDHDEPLAPAGV AVLN
7937	21838	A	7997	316	649	RDSHSPFTEHSRSVAQAGVQWHDGSLQ ALSSGFPPSCLSLSPSHWDYRHPPCPA NFLYFLVEMGFQHVQCNGLDLITS*STR LGLPKGLITGVSHNHKPAQGGFHHVG
7938	21839	A	7998	468	336	BRGPTNCLARKVSL*PSMPPASASQASG TITGVNHHRIRHRSLL
7939	21840	A	7999	464	283	TLCGGITRPTNIMKGNLLYSKSYGLANSL LPKNPRRNIGNV*PNTVALQPSHVDI
7940	21841	A	8000	46	487	RQGRSLQKFLFFVQVLCFAHRGGVYRG RQAGLSGGLHPRVRSQPLCLPT*VSAN MAAPHASLLPCLSLSDCCASSEQSGSVG VGSPKPGAGYNLLVCHLLRLEKRSIRV GVSQFSRCHLSNLP LARKGNSRT*PCTFR VRRCLAL
7941	21842	A	8001	295	1	TQPWGTHRKLEPKKKKKNSGDREWRKLC NSVTILNATIMYTSSEMLRPGTVTHQNP KTSGG*GGEIA*QEFKASLGNIA*SWL YKILKLSPLWQT
7942	21843	A	8002	144	317	EEFYLRNV*RPQFVAYACFPSTLGURG GRIT*AQSFRTDLGNIARPCVYLRRKKK RS
7943	21844	A	8003	69	291	HCVNTMIFITVIKYFYLNQNNMSRYNYS HFMKKTVDQSD*MTG*RIQAVAHACNP STLGGRIA*QGEFKTSL
7944	21845	A	8004	3	176	IVAHSSITPGLKQFS*PSLSPSS*VYVNM LPLRANY*FFGINRVSLSCQGS*ATLAS LLGSSSSPAGACQAKSTOTCYHANLII DFLVQTGSRCLAKNGHELCSCL
7945	21846	A	8005	419	178	NPPPKKLLSSSSSSPLPHLNWGTGGFF PPPPP*NPPPENF*GAPKKKKLSPRA EKLVPFKGPPPPFFFFF
7946	21847	A	8006	429	225	QPLPPRFK*FFCLSLPR*GHRHRPDPH FNFFFF*YFLRMSFVLAQAGVQCHDLS IYLANEFWLLDF

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7947	21848	A	8007	756	224	PPHHQPHVPPPLHFPSTPSDAPPKISHA AAPNSNPPQAHAPPADPAHSPSPSPPP RGATPPFPFPPPSFLAAGRAPHFPREP LLPSSSSPPPPPIGEPPGSPPLLICT RPEK*N*GPPKKNNFPPPPKNNMFL*K GPPPPFPFPPFFFLRQSFLLVAQAGVHK RLHLKKSN
7948	21849	A	8008	170	559	SSHLSPQSSWDYKSGVAHTCTNSHLGG ODGRLT*AOQPTSLGNIVRCHFYPKCY FINKLPFYSPFINTNPKKKKKGGAVLK NQSLRPRAGKVLVFLWQHLLQPRGRPK NGTGKPGGLENLAPR
7949	21850	A	8009	1	662	ETRR*RSWYMPVLELSHYGAGESLQF *KMMVD*APIAPLHSTLGDENLTPDLKK KNGETVANTSPLSTAKPAKLPKAKKD QLMRDLFLPKTKPKQMSGLDARSRW LKIWRRHGIMPLKNIGPTEDVQASAG GVEENMSTDIETPAKHDRPTEDVQVS ARGGVEENTSDIEISEAKHDDHLLVDEL SESLVCLIEDPMITGSGWKPCLS
7950	21851	A	8010	377	2	NFFFFPPPPFGFFFGFFGFFKFF*IF PPFFPRMPFF*FFLGVLPLFKK*IFFF PPIRRCFFPKFFFLPLLLFFFP*FFFF FFFYVDFPFSFILNIFFFVYPSLEFT VLILSLIYHEADP
7951	21852	A	8011	1	363	PTRPLP*RGCTMLRLILNSWQVIC PDRPPKVLGIQT
7952	21853	A	8012	278	39	FXXXPFLSPXPLIFPFFFFFFFFNFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FH*DQ*FSNFDFTPTTLISNLI
7953	21854	A	8013	79	412	MNECILGKGGKGGFFECENLGLC*FL KVP*DSDIWLGAVAHAYNPSTLEGQGER ST*AQEFKTRLGNMTRPCLYQKHTKKK TKKKPHPGLGWGAWGPTYLGGVGTKIT
7954	21855	A	8014	277	19	FGNTHNPLIGRSVTVQAGGQWCHSSSL *POTPVLKQSSHLSPSSWEIEAASQV RITALQPGRQSKTLPNGSGPVLRAARR SI
7955	21856	A	8015	1	130	ARIVSIS*PCDLFASASQSGITGISHH TQLAHNTLKASPTLF
7956	21857	A	8016	4	417	RLMPFLNPLFF*RGPTTYVAQVGLKL LGSNDSPASTSTLITVSHCTQPHLL KSSHSFFPLKTLDSMTCNSWQVHLPL TACRALLPCPLPSACFPSLQVPSVETC CVPATLTITLPLLRAPKSHVTLCLPLF
7957	21858	A	8017	388	158	CVTWASNCINWTCFPLS*INSHCHREY VLJ*GEIYNVCISLYLCIYMCVCIYISV CVCVCYIVH*TPYLIHKCLI
7958	21859	A	8018	154	382	GIERPGVAINECNSTLGG*GKWIG*AO EFKTSRGNMWPKQIYLKKKKKGGAVLK DPSLRPRAGKVIYVFWGLI
7959	21860	A	8019	396	237	FFFFFFW*GFTMLRLVNSNAQVVIH LWPPKALGLQVRTWVGLRLANF
7960	21861	A	8020	412	168	GNLGSPLPGNCRKHPFLF*KKK*SL AVLPKLVSNEWP*MLPPWPPKI*GVQA RAPPPQILKKKSSSHFYNSHNSL
7961	21862	A	8021	1	124	TRFLHVSQAGL*LLTSGDLFASASQSD YIIFSPAKIIFL

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7962	21863	A	8022	3	200	HLSPYVFFPKDRVALCHPGNSAVVQ*PI VTSI PMSSC*KLTSVVRNRPSVILTR* PVSTKNTKN
7963	21864	A	8023	3	132	FLFFPQ*FMRIQLAMLPMLGNNSA*V ILLPQPPFWLGLQA
7964	21865	A	8024	3	187	VQAGLEPPTSGDLPASASQSABITRMS HRAQK*DFIGSFSSEFS
7965	21866	A	8025	405	231	SDRWIKKRGYLHHTTY*ALKRSLTLTH ATTWNLNLLSLISQSPKHRYVYVPL T
7966	21867	A	8026	175	382	GKRIPPPYPPQREGGTPPQTGFLPFFP LKKK*PGGLGGARFSPLLGGVGRKNST LKKGGAINLKGPSPGLPGGKRWAPQKK KKKGAWMLMPVIFALWEAEAGRS
7967	21868	A	8027	83	374	GEQVWMLMAENFSLGQCGRITWDRE FETSLANIFPPISTKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKSGSGVS*K KNPSFRAGKIFF
7968	21869	A	8028	382	148	SPHCSLDLVGLRQSSSHLSLPS*DRCV PPRLAIFSPAFLPFWAETTTTTRATMLP RLVLNS*AAAILLOPLVLRLL
7969	21870	A	8029	88	208	SGSV*ENNPFLSHAWWQSIIIPATQAEV GRLLSPRSSRSA
7970	21871	A	8030	1	283	NKSRIRKALQVTEKQKELBMMLMNLQ PNGSHAMIQMMKILMGKMKLKE*DK ESDKDRKDEREDRDRTDEPTPERRTS RDSDDDERDRDKNRKDKKDSKDDSE ADEDTDQDDYDPMDAHKADEDDDED EVAQMTKKKKKKKKKKKKKK*KKDRK DEREDRDEDEPTPERRTSRDSDDE DRDEGKDEKDKKDDSKDDADEDTDQ DYDPMDAHKADEDDDEREDVAE
7971	21872	A	8031	2	139	LQTLPLPLTA*LLASLANLALPPTINL LGELSQAQFAVIGWYLLY
7972	21873	A	8032	80	324	YLHFYFFVR*KLMGLDTAHTYNFSTLG DPERRIA*A*EPKTSLGNMVKPCIYKKK KKKKKKKKKKKKKKKKKKKKKKKK
7973	21874	A	8033	299	158	GNOPGASAHFCNPSTLVGGGRIT*QAE FKASLGNMVKHYLYQRHGN
7974	21875	A	8034	416	60	AQWLTSIITPL*BAEVGGFFEPRLSLPA WATE
7975	21876	A	8035	398	271	FYPL*DEVSILLPRLVNSNTPAILPPWP PKVPLRHEPFPFA
7976	21877	A	8036	385	151	FLYFL*RLGTLTLPLQVSNISSSDPPT* ABESAGITGVSNDAIRICILTRLPONS SH*NVWRGLGCTQSSALIPG
7977	21878	A	8037	3	406	PASAS*VAGITCTHHAQLLVFLVFLVETG FLVFFPMAVFLVFKTKNGVPGQQLVFFA APPALGGDPPGQGGATPSVKGVLVGLGT RGGAPAPKKLGAKKPSHLLGGGAGNLP KPRGQKGPYPYFYFLARDFFLG
7978	21879	A	8038	428	20	LANO*WKPPSPNWTIKSPKKKKGGPGQ GPPPLTPPLWAPKARKLGSPLWR*NP LFPQKPKKFPFGGPGPPYSPLPQKLSPK NGVTPGVGSHKKKFPSPPLGQK*TP FPQKKPKRLKRGMTLHGSTFQSL
7979	21880	A	8039	3	194	QNKISQVWVYTPVILATWEAGGSEVSP GRQLN*AKTAPLHYSQDRYLKASVDS



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7999	21900	A	8059	1	279	VLLYHPGNSAVVQSWLMQ*TPSNADINR IARGPKRSSHPSSLSSWDHRHVTPCLAN FFLL*TWGLAMISRLLLPLRLKRVLLD *APSPGSL
8000	21901	A	8060	408	315	SLTMLPRIVFNS*QAALLPWPPKVLGL QV
8001	21902	A	8061	198	2	RIQHVRSNCHREVEGNAQNLTPSTLGG RGRMIS*AOEPETRLGNTVRPCFYKHLK SOPGMVRI
8002	21903	A	8062	3	294	GLSPTAHPITATPQPLPSGLSVCKRLFL WANCEQCQPHLIRPCPCPRIGPECALYT TSCLLQLKLRKRGF*KIKKKKKKKKKKK KKKIF*WGGGKK
8003	21904	A	8063	197	184	IRDPLFFF*GRVSLCCPGNSAAQSRILT AL*PGRLLKRTFFYL*IRRSWDKHAPLP APP*LPWVTLITPTSTHVSAVCSLLY VKSBOCKQ
8004	21905	A	8064	3	373	TSGSLAKRPADCSAOPPTTSSLGCGSP VRVCITVRPCTHARANTHTHTHTHTH SNHG*APGALYIQELQRGVSHVPEKEK SDPETA*TKGG*HVINPHGRQSGSQBE HRICVGRCCSG
8005	21906	A	8065	532	106	ENKPLHNSINKYTGKLLRDKALLYCPG WEAVMS*LPVANSNAPAILLCQPLS TDWYGRVPPQLKVLPSKKKKKPTNLLR PKQTRNQDIYKRGKVGFLCSYCPALL LLL SLLL LLLL PSFSTRDSAGAGCCSS LP
8006	21907	A	8066	411	130	PHAQLIFLER*SLTVFPRVSNWQPAI LPFPKPKVLGPOARWVPSFKVLLESIL RIPTSVIFFPLNLCSNKLASIKKGCASA AFLPNQRFPAN
8007	21908	A	8067	3	32	DAWADANGSLTDEWVERINYLHAMOYYS SFEKKREL*YVRTCMLNEDTWVSLIROS QRDDYCMIPHI*GRTRGVH
8008	21909	A	8068	410	116	STFNQITWPGTVAHTYNPNTLEGQAGRI T*GQELETSLGNITRPNFLFCQACPGQ GLSTRVMGSLHYFVLPRLPLKCLDNR KSPFTHPVLPCYE
8009	21910	A	8069	158	289	DLCSLRLNIVRPLQLYKK*KISQVRKKKK KKKKKKKKKKKKKKKKKKKK
8010	21911	A	8070	388	1	ATFPFCLPKPVLQCPKPKGAPQKPF GGFFPSISGPKPPDPANDSLSKGRV PSQSPIMWVGA*RPFPPLWVG*CI KIFLPPPPPKPTPALSDFFFEAEFRS CMPGNNAVMSRLSATS
8011	21912	A	8071	15	336	KLDKRYDRIGSPGTHASGYILKPLVAE ASYELILSLAFFFERRGLALLPRLGGS GVIVAHCTLLKLGSGGPASAS*VAGTA GMNHHGHEPGLFEKQNSGPIF
8012	21913	A	8072	396	274	PHLITWESSL*QGLAMLSRLVSNISFO VILSPWPKVVVL
8013	21914	A	8073	189	54	NKPLGPGMVVQACNPTLGGQGWIP*A PEFKISLGNLAKPCFY
8014	21915	A	8074	3	257	HAFVILFETRSCLSRIESSGAMIAYCR LGLGSGDPLTASQVAGTGM*DDAWL ROVSNWPOVILRSLPHMLFQPSLET TLPATWEAGAGGLEPKSLRV*CVFTAT
8015	21916	A	8075	1	119	



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8016	21917	A	8076	232	266	VNSRTTAAAA LPYCSGQWCLGLFI IQGVQWHDHSGSLP RLPGLNQSCLSLPKQVDYGREP*YLA* YQARYHGSLARQNVFNIRPGIMVHARS STLGG
8017	21918	A	8077	390	143	LGGLVFCPPAKKGFFFNPINLGTTRFF PVPFF*KPAPENIFGPKKKAIPSPFEG VKDPLKRPPEFFFFFF*FF*FRLIV
8018	21919	A	8078	424	144	LKNTFFTEL*NRDVELCCFRLVNFN AQRILLPWPVKY*GIQA
8019	21920	A	8079	182	45	VHKAGWVAHAYNKE*TLRGKGM*TGGE FETSLASLDNMVKPLRC
8020	21921	A	8080	405	163	YFLEBMGFPHADQAGLELLTTGDPPKGM SHCTVNLNINVLNLIQHPHINIQNNV*PH ISGPVKLTBENHNHNMSTQKHSP
8021	21922	A	8081	39	240	QSKTVSKKKRRTIFCRYRVS*SPGFKQS SHLGLPKGNVYRREFPHASTFSQSFV KDHFCSGVSS
8022	21923	A	8082	2	263	DCCVSSE*GSVGVGLSEPGAGYNLIVR LLRPLEKRSIRVGSRSFRYYLSMLPLA RKGNSTPT*CTSQVRQCPTLLGLHPLCD KPO
8023	21924	A	8083	1	248	SVGVGPSEPGA*YNLLVCCLLRFLQHS IRGGVQSQFSKYRQSWPLARKGNSPT* ASCGMRGALLMLTLGLHPLSNKQP
8024	21925	A	8084	3	255	HLSPSSMDYKRMPPHLNFFFFFLGKK GVLP*GQTLRL*NNKPE*PEKAGV KGVTHRPK*NGKRPEDDTQGPFL
8025	21926	A	8085	409	145	LRGPYKKNFSTQAPGRKIGSTFKAPFF FFFF*GQSLQCPGLSTGVLIHCSLE LLTSSDPASSASRVAGTIGACHCS*VLQ TPTF
8026	21927	A	8086	199	26	GFPPFPNKTEIF*RPEDPLNFFPLVEMN LTSRLSLSNPWAQAVLPEWPKALGPQ A
8027	21928	A	8087	222	3	SVGITGVSHRVLMYFTLKGLGRGHSIC NNSALGRRGGIT*AEFETSLGSVARI HLYKKYKNYPVAVRL
8028	21929	A	8088	415	197	TILCFYHNNVSFSSNPFLS*IFIF*D RVSFCHPGWAVVQSMITVFFILCATVK YFTCOQYIIMIFALNS
8029	21930	A	8089	297	71	FIFPENKNRPEVVAHNCNLTGRGGRIT *GQFPEKLSLNIARPHLYKTKQNLISK YIYILGFQTLQIOLDIANY
8030	21931	A	8090	185	415	PFGLKQSPHLTLSS*DYKHTFPFCRVNF FFFLGGGFPPFKAGFNLCN*RNFLASPS KACMGNIANLGP IFRFFKK
8031	21932	A	8091	2	125	EKQASKKRKE*KK*KKRKKRKKRKKR KKRKKRKKRKEP
8032	21933	A	8092	8	412	KQFGITL*VCLDLSYSSSLSHNSQSLC VAPLPCEIFPHKPLCACHFFFPQSNV LALLPKREYRGKVGNGNLLGL*NNNP SGTSKIASPARKLPHHTHARFPNWIKT DFFYIAQTGF*LRPSRNPSTLEV
8033	21934	A	8093	249	143	NIFAAITNMRLTETILSEVTQ*KRQON FSLICGS
8034	21935	A	8094	3	280	PERNDYRHEFPGPASPT*LLLVFN* R KGLVVGQRQLLASSSLPAPASLSAGI

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						IRMSHCTPAWVTVRRCY* INK* INKDYT IRONLKKM
8035	21936	A	8095	404	16	OMGFCLEFLPSSKEVFPPPIFFPYRESF FLFHFFLDPRQY*LYFIKKNIPLPSFF IFLFLRVSPY\FFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF LSKACICISSHGG
8036	21937	A	8096	358	200	KSYPISSLIFPSHYFLFLKHLIATVY CFLIDCTLFPSPYCPQCLFVLLSGRFP RSL*TFH*RLVPSFPIPNVOKLF*LSL ICPCCIYLYTLYTFYFETVFCSCCLGWS MMA*FNGMKIRLI
8037	21938	A	8097	2	132	KEEKLERKE*KKKKKKKKKKKKKKKK EGGRKEGKEGKNSS
8038	21939	A	8098	48	331	PGTWHACLGEDILKWTQKGRAGASH RTSWIEPLETVFLFLAGRLESFGKTY SRLGAVAHICIASTLGGGRQIT*GQEF DTSLADFCST
8039	21940	A	8099	7	373	NGRLRGRFAMLARLVNLF*PRDPTT*AS QSAGITGMSHHARPTIESFIHYCWCKM E*PLCKILLYFLIFIKKQKLGWNCHG SLLQPT*PTGLQRSLFTLPPSGWDYRGR PCPNLI*LLI
8040	21941	A	8100	116	432	YLRNLPFGRAFSPALLIMCSAL*ESH TVAAQGVQWENLQSLQPLPPIKGFESCL SLPSSNIFAPLSYFPFNSSPTNISPSLI GPQITDPLFKKKIKVSNVVE
8041	21942	A	8101	361	138	FNLIGRKKKNFGGLKEGSESRPPNPGPQ FFFFFFFFFFFFFFSG*RWGLTNLPLRVLNS WAQVILLPWPFPKSLGLEV
8042	21943	A	8102	1	199	PIRPPVFLMENEFYHIGTALIELTSGN LPASASOSAGITGVSDR*LA*YLFPFHE LFCYPALLLI
8043	21944	A	8103	412	46	KGSGPPPPPPPKIRKKGPPNPDPFFFF SPFFFRGF*GSPPPPK*KVLLVGLPKPK PPFFPLGWNPPPPPVGGSPPOSLOFFF FKCVPGWVFFFLPFFFFFFFSPFLFFS ETESHIIAQA
8044	21945	A	8104	192	2	EELELFFFIKYLLPRNQKVKRRL*RL GPVMAICTPSPLGGQRENITRSGVQDOP GQDGETP
8045	21946	A	8105	373	183	GGPF*FYILLFLDNFFPFLSFPFSQD FFFLSSFFFFFFFLFLNYVVF
8046	21947	A	8106	373	281	SKFTAPPPFFFTN*RLSLTMLPRVSN SNAQVILLPQPKVLR*ATQRKGFHQ EQI
8047	21948	A	8107	3	114	FLIFVHIGPNYVAQGLLELSSDDPAL ASQCAGITGMWHARPYVLI*TLNIPLP YDPEILFLGILYR*NKTYVHTKACT*FF ITPLEVLAKTWKPK*PSVLGLQA
8048	21949	A	8108	416	243	PGVFPPPPF*NPPELIIWAPKKKKYFP PPPLNLFVFKGPPFFFFFFFVFVF L
8049	21950	A	8109	2	211	SVIQAGVQWVHSILQFRLPGLEQSSCL L**CWDCKGEPNHLAIVTTSKHTESCSL LCIPTATPLGLVT
8050	21951	A	8110	172	28	HVVCFTISFFGPFYFL*ROGLTKSPRLVP

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8051	21952	A	8111	2	225	NSWV*VILLWPFPKRVGLQQA QKSAKNFYHLSTYLSITYSTYPTSHYS IYLSITYLSSTYK*VILEQKNSIKKG CL*CTIQTNCL*QLKE*VIRLIPKL*YK IKLPTCNVHLNWFLLCNISWYLYKLAM *RKLVCFA*FVYVNSNKLITIKRIGH
8052	21953	A	8112	392	221	PPFKRESPPDKVMPFPDIFGGGKTKK TLAN*FPPKKEFPVFFKKEDFF*N VGNFTPK*AVCF*NFVFKKKGAPK KXSSFTDIF
8053	21954	A	8113	369	112	IFFSITYYXHPFPFPDPLFTFPPLFP FPLKKKKFFFPFPKXKFFFPKXKFF FFFPFFFPFFFPFPFPFPFLAF*HVS SF
8054	21955	A	8114	418	248	KYLLPTPGY*NLTLNGSPFPFFFPF* D RVSPCCPRLP*TPRLTQSSCLSLRSWD HRCMPLRLVTF*FTFKLSHQSLRLITY TLAGTTLG
8055	21956	A	8115	229	78	SPKGAAPFFFPF*RNWNSPKLVNS RQAVLPDWPVKVGLHRRGWIT
8056	21957	A	8116	356	66	PLFPFFYIGNFKKFFFPFYFFFPFP PKHYSHKIDFFFIKFFPSSSFFPFP FALSSFFFPFFFPFFFPFFFA*FVPE FLYKIPNLYPQL
8057	21958	A	8117	212	81	RRLSHCSMLPSSSNPPASAS*VAGTSG TQGLVWVHGGSPRE
8058	21959	A	8118	367	2	GVFFFPSPAKGVFFHFPFFGLPFPFP PPFPFPPLMFYTWG*KK*FSPRQY FFFF*GGPHEFFFPFFFPFFFPFF FFFYAEGIGVSPCYDMLQYNFSSFPQST ISPRVRPRV
8059	21960	A	8119	38	215	FFKSAFHHTRLFNFFFLSKTGSHVA QAGVELLG*SSPTSAFBIIGITGLFIS FKN
8060	21961	A	8120	266	2	PQIFLPIFTRSHSTQGVQVQCHSSD QPONPOLKQSSLS*DYRHTLTAPG*FC FL*RCGLAMFNLVLSWPQAVLKHPC CGMC
8061	21962	A	8121	3	332	DAWADAMGHVPPCANFVFLV*TFGLH QAGLKLPTLSDPPASASQSVTFPLET ESHSPAWETERDSVSQKKKROGRFKGS NFTSAGLQRFIFPMOPPKLISAGV
8062	21963	A	8122	378	66	LFIFLPFIREVFPCLIG*NNAPFGVLYN GPPFFPFLLETVPJHAGQAGLKLQSSD LVPSASQSVGTGSHWQKLRIFIN SFPFPFCNMLVPLAGP
8063	21964	A	8123	2	316	ISMLLALLRLTITFRLPQINGVMEPTP YKCGNPISPGRAPLFKHTVNDITLL FDVQIALLLPL*ALQTTNPLIVMPSL LIJITILAIRIDYERLQNSD
8064	21965	A	8124	331	14	ITSILITITTF*LPQINGYI*KSTPPEC GPDPIPARVPFSIKFFIVAITFLLPDL ETALLPLP*ALQTTNPLIGMSSLLLY ITLALSAYE*LQKGLD*AE
8065	21966	A	8125	2	228	ITITTF*LPQINGYIERSTPYEGFDPIS PARVPFSIKFFIVAITFLLPDL PLP*ALQTTNPLIVMSSL
8066	21967	A	8126	451	200	KA*WNRFAINVTKYTCSEKRVKPTF



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						LPSLPPRALPRSGASSGPDGGAQQPGR RRKWAFLQGI RADARGCAVTSPEPYRL PGAGAAARRR
8083	21984	A	8143	166	368	ENILWAMVVLDCHPSTLGG*GGRIT*G QSFKNLANIERPHLFFFFFFKRDLSLA PRASGQGLP
8084	21985	A	8144	1700	621	DERDHSVLQQPACLTACGEPILSHSESG SKIGSERESGEGHSHPEAPPFVSFVGR RS*GQDS*GPGPGNQDTRGELSHAAEN WTPDPAALAAVAGGTSLEPRGGGIG*RCR SHTARSGARVGSANAHARGSGSFSHSG SHGCLRNQSPRLGACALCGSAWVSGL* GSGLTSPRRRRERLRMPGVAAGRPR*GN PRRGGRQKHGIPASGLPGRCWLGTONST LQPRTRAPEELFVPSSESGSTPEKMLVS FHGSSLNNEATPKYSQQREAGNRWQGS LSLERMPPWTSHPLGTPPLMPVAVARCC ILPGLWPLISPPSGSASPVSGPGCLSL WPNAPKKDDFFVRQGDTSWRSVS
8085	21986	A	8145	390	38	HTTFNLYYFYYYYFSLFYFYYYYF FFFFFYFIFLFIYSLLVGVWVVLGL GLAALLAKLFLVNSLCRRYRG*SLLYY AWL*FTIFPLRYTYQARFQLSFILY GKWPG
8086	21987	A	8146	20	187	KLTTSTGRNPRGRTRNPF*VF*RDGDL MLRLVNSNMLPLVNLPLWDPKILGLQN
8087	21988	A	8147	417	64	VRPRVRPRVRPRIRKKKKKKKKKKKKK KKKKKKWGGG*DFWGGEGKPPPLQKNDP LLFWGFFLKSTFFFCGGLFWGGFFFFF PPPNFLGVGGKKKTRLLCGPFSAFFGG EKN
8088	21989	A	8148	351	187	RLGTFYLSNLRFYLSITHGPDPYIGRL TSQNLPLLLLDLT*LEKLLPKKSQTYN
8089	21990	A	8149	465	60	PDHFWNPKKNSQFFWAKKKKKIFLGP *KMWAKGVVFWGRKQFQRGGKKG*KG GQLFYFVLSSQVLGGQNHGPPGKAGFGE NFFFFGQGLGWAISRMLRTPLEFLAGGGE DPKKNFPPPKIKTLGAGVKK
8090	21991	A	8150	1	175	WYRHRVFPYLANVFFVIFGRGRVSLCCP VGGPTTELKSSCLGFP*GMDYRREPPH LA
8091	21992	A	8151	59	35	RNNSRPRRPGKFLTSGDLPASASGSAV ITDVSHUWPETFFR*RA
8092	21993	A	8152	269	159	ARVEVSKKYYIYTHHTHTHTHTHTHT HYTTKKLDS*LFQVCKEKFQRIVVQ
8093	21994	A	8153	1	256	EGGPPRRFFFFFFFFFFF*TLKI RFIWRKQKTEINPKDGLIJDISOVLISQ ITNHFHRRYFCNFTCIQBRDINQSLFL F
8094	21995	A	8154	252	41	LIIPLVICIVFIVLQFKFISVISLNKGL PRNEHFFI*RWGLTMLPRVNSNSKAQV ILPWPMPKVLGLQV
8095	21996	A	8155	21	443	HELSLI*FISTLAETNRPFDLVGGESE LVSGFSIEYAGGFALFIYGETNIIII NLTLTTLFLGTTYDALSPELYITYFVTK TLTLTCLVL*IRIYAPRFRYDQLHLL* KNFLPLTILALLI*YVSIPTISSLIPQT
8096	21997	A	8156	2	205	LLHLMHFNLEIQKQ*TRNLEKRSISR

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						HVIINLSKAKHKG*ILKAVREKMLIMYK KPLVKLQVSN
8097	21998	A	8157	2	205	LLHLMKIFNLEIQKQ*TRINLGRSISR HVIINLSKAKHKG*ILKAVREKMLIMYK KPLVKLQVSN
8098	21999	A	8158	2	222	VYTWGITGARVFFGEF*LPVNIPIRHLK FYNEPIRDANESASASTENPQSSIIHPQ DEQNGDIRTKVTLEH
8099	22000	A	8159	1	297	GTHVQGSCELELLTSGDPLASTS*SAGI TGMSHHAPLNCSTYGDSTFSLKCPETV ACWMEBGMKRLMENBQGREAHQKLESV INFYIKDSMTKKYK
8100	22001	A	8160	138	437	NEYDHSITYKERDFVVCVFFPFPSKKS LTVGTQGGPSYLEPPFLGNKEFSCLTFL GSDNGGATIRLG*FVFFRCKGVSPCG PGWS*TPDLRKTTPSA
8101	22002	A	8161	330	148	QQSKT*PFFFFFKKKKYIYICMVVHAY NPSYSGG*GGRIT*AKQFKTINNTVRP HLYKK
8102	22003	A	8162	391	253	RPAPADF*FFFFYRLGLAVLPRVNW PQATILPQPLRVLGLQI
8103	22004	A	8163	131	3	HKVSLCYPG*SALMQS*LTVASNSWAQA ILQP*PPE*LGLQA
8104	22005	A	8164	97	440	NKGSILCPGGRPGALSHPTARSGSPGP TPQKIGNNGGPPPTPVNLEFFEKRGFT VQGGGLKLR*RSPPPSAPPQNGITGGS RRPGTQKKFLKTLGSETKMAKLITY LK
8105	22006	A	8165	541	295	FSQQKKKFTSTNLSHORESTYICKRNE SHSVIRLLEGSQAIMHNCSLKDPSSSDP EASVS*SAGIIGVSOHLANTYFKKIF
8106	22007	A	8166	440	259	FPQKFFFFFFVKGFRHV*AGFRLLD SSDPPLAFQSVETIGMSPSARPMFGVF HSLR
8107	22008	A	8167	23	405	FRICHLRLVHLNVYFIPSTDNHLLSTS AMFLYNDVWIAQNVSGPFLGIIRTF FFFLKGEFFAPQVGGQGNLG*LNPP PGLKGFSGLTPGGGNSGGGPNNKPNFW IFKKGGSSTLWPRII
8108	22009	A	8168	23	388	PYFSCALPRHHPPTNLGPHLNGAPWG QPSVAHHTLFFFFFLKRDFCFVPRVEK LWLEESSINPPLGLKLEFSCLTLMTGN NOGPPPPVIFCP*KKGGVYPWPGGGE TPALKETPOL
8109	22010	A	8169	612	498	NTHSISFSHHRHMTHTTIANPTTYI REP*DNVQ
8110	22011	A	8170	2	288	VNLTFPQHFLCLSGMPARYSDYDAYT T*NLSSVGSFISLTAVILLIEMI*SAF ASRRKVLIVREPSINLE*LYIKKKKKKK KKKKKKKKKK
8111	22012	A	8171	381	101	OKSLQPSNITATILESVQVIFLGSPPHL ORWEMRLTKNLRGLGAVAHACNPSTLGG MGWIA*AOELETSGDP*PPSNRLQFTG EHNNDNKLI
8112	22013	A	8172	136	360	TKKIFGLK*TKKIFGLLKKKKKKKK KKKKKKKKKKGGGAFKKKFFPRGGGX IFFFFGAPKNGGGVLTGGGKPGVT KK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						IYRIHTYIDIVTHI*YIHTYIDTHMWVCVYIYIYRCMGVRET
8132	22033	A	8192	41	416	ICRVKIASRPLELTHSLSLVELS*FCLTAQ*RNDFLALKHLTAVLYNLILHSSGFWSLLKSHFTFLAL*YYL**F1*SN*RRDLAVLPRLVSNMPOVILPPQPPKVLDIRYPPSLALILFFN
8133	22034	A	8193	2	183	KRLSTWKKVVESEGFQGNVGVPSVAHA CVSSSLGQQGKIA*GQEPETILSNIVRPHLY
8134	22035	A	8194	2	465	AGVCWHDGLGSLQSPPGPK*FSSLSPSSWDYRSAPPCPADFCIFRDNWAGWGVCGFHRVARAGLELLTSGDPASAFSGAGIAGMSHRTQGGQDNFASWRGGPQMSPPSCCLFLQNTFTSLKPSNVAPYPHASALGGGEYGGPPSPQHLE
8135	22036	A	8195	397	149	LICLTDLPTRFLSLADVFTVENTKRVKDLIKLGUVVARTCNLNTLGG*GGRIA*AHBFETSLGNTVRAVIVOCPSVILSR
8136	22037	A	8196	355	95	KKIMPTLCLKIPS*YRCBETQLSLQSSCDHRMPPHPTNPF*QRLHSLMLRSLVINSRPQAVLPHGPPKVLGLQAPATAPGLISLF
8137	22038	A	8197	382	112	KTFGKKGSPPSPPPPPFFFKFSFAPSPRGKKAELKSGRLGCLCPKPKDPPPGSG*TDGKPPPPGQPIFFFLKGVCLFSRGSKTFI
8138	22039	A	8198	32	361	ASRIGFILQEFLEVRWTTNPSAGADGYNFKLQKGTKEKTSQVAGAGQ*CHRNLLP*P*TSCLKSSCLSLSSWDYRMYFVLGKQVTLILGKRLSVYPRDVVSLC
8139	22040	A	8199	1	314	INTLLALLLIITF*LPQLSGYIEKSTPYECGFDPISPARVPFSIKFFLAATFLLFDLKNALLPLP*ALQTNLPLGLMPSLLITLILALSAYE*LQGLY
8140	22041	A	8200	3	109	FTSKHHFGFEAA*YMHFVDVV*LFLYVSIY**GS
8141	22042	A	8201	3	216	DAWAARVGRHRTLRILF*IFVEIGSLCVSQAGLEILDSSDPSSASQAGIRGMSHGAQOEHLFHRPIGKIK
8142	22043	A	8202	1	267	RIHTGKPYKCEGTFGFGKPSLT*THKFFVYCRVAVLLKHCYSHLYPH*IIVNGSEADGRMCLLCITFFHPLABEGQSNVKNRKYNP
8143	22044	A	8203	422	92	PLVVALPPKIGQAPITPSSSPSPPPPLFFPQPPVEFPFPPFPPFPPFPPFPPKPKKFFPSPDPKGIFFP*TPDPFPPFPPFPPFPPFPPFPPFLLIYVLFILC
8144	22045	A	8204	445	260	VCSDDLFTWADGSPPLPLKPPDPNPFEGAPKKKNFFPPPA*NFFLKGPPLFFFFFF
8145	22046	A	8205	103	248	PGGVVALACNPFSSLGQ*GQWIA*AEFKTSLSNVNRPISAKKKGQPF
8146	22047	A	8206	407	197	QLIFKFL*EQASHYVACAGLELLGSGNPASTSQSVKVTGMSHGAWLIAPT*RTSTIHYNSLVLLLP
8147	22048	A	8207	1	142	SCSVAQARV*FRLGLQDPPFRFTFFSCPAWETVRLHLRKKKKKN



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8148	22049	A	8208	2	370	PEVFDYFN*FKNL*LHKTCTQ*L*AALF VITKTWNQGCPLTGTENINKLEYIHTMDY LAIKINELANHKMM*RLKCIILSERS* SRKATYYMISIIIRHPRGKTIIEIVQNS CQGLGERQGL
8149	22050	A	8209	363	108	KKPRVACLSPGVGVRERRRR*KEERE RERSRERSREBEL*KLGLADLCIKVG* R EPTFKRKYVKRYAKILEVSGRKKYGVV
8150	22051	A	8210	386	254	LRFQGGVCSERELCKOTPAVTR*DSVS EFGKKKKRGPENS/LATNF*ALCNDLY LRCSMLKQQRQRKRKERTVRFQQLHNN LTLGFV*LIVQRE*RRQGNFVAKYMLY TFS*PGSFRLRKCVHVFVGYEACS PL FPLIHNQLHKAAC
8151	22052	A	8211	3	131	AHLFIAMFTYFKPTVITYCSKKIKPK MLLLDSAPSYPRALMIMYKGMNVFMH DNLTFILWPMDDQ*VIFTS*SYILRN*FC TIAAIDSDSSDSGGQSNLKI*KGFTTL DAIRKNICDS*KL
8152	22053	A	8212	86	286	WSINECTVLSVQLFHRKPTISPKNTSYNS GVMAYTNMLSTLGSQDQILT*GQEFETS LANMVESCLY
8153	22054	A	8213	393	344	SFFPSLPSKMGFKINVPSPGYFLFFLNK GRVFGQGFKILNSNFPPLASQGGGI SGISFWPRALVTP*WNLGN*RTIVSP NYGLK
8154	22055	A	8214	3	313	QGLVLHSHGLQD*PFGRLRSSCSFLP CSWEHRCPTPHLANLILCVCVCVET GSHFVAQAGLELIGSSDPLLSISQKSD YKV*AIIPRAKQNYMLFY
8155	22056	A	8215	165	348	RPCPLFPEDLLTFSRGPGTMAHACNLS TLGGQGGGIA*GQEFETLGNIVRPHLY FYLKK
8156	22057	A	8216	379	218	VFLVEIGFLHVQAGLELPTSGDPPASA SVSAGITGVSQKRF*YNVFIFQKSSLL NALPICSLTMLGNLFSMPHTPKFFTC
8157	22058	A	8217	32	276	RYLPITAAFLTAKI*KQPKSSLDLKNI KRLWCYITMEYYSALKVILTVTTWNNL VGFIPGDIHIQKAKYCNISLIGI
8158	22059	A	8218	171	2	EGVFGRLGLFFFLDRWNLCLEWSTVVQ SRLGATSAS*IQAILFPQPEELGLPLP
8159	22060	A	8219	530	73	TRPFGVSNRSYLNQVYFFPSTLITGGL MRLTIHFFFLVYENFVPRVW*L LLYFYSSSIDLLTAKQPCLENGDSH AC*THATLLFPYSI*YLGLPSFHLFFV CFSFYFL*R*GLTNPMPLVLSSWPQVIL PDQPKVILGLQA
8160	22061	A	8220	350	135	FFFFSOTGVQONRVQ*EDHNSLQ*PPG LRQSSCLTLPKCMGYRCKPLCLASHIYF KDKVYTSPTVHTQY
8161	22062	A	8221	185	331	PGWVAHAYNPNTLQGGKLT*ADEPET SLGNINSVPKKRRKKRKNM
8162	22063	A	8222	73	232	YCSFKFTILCLSNLGVARTCNPSTVE GGGGRIT*GWETTSLSNIVRSCLY
8163	22064	A	8223	418	211	AMPSLLTYLTFICRKKKTFPYWGFT MTS*LVINSNTQVILPPWPAKVLVLR LALFYSLLVLPSP
8164	22065	A	8224	227	33	ESHSTTQAGVQVNDHDSGLQPPPGMSLY

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						CH*CLRFSWSPAEKPCWCSLRPMELERWSGASDA?
8165	22066	A	8225	244	287	TDSPTSAFRSAGITISIRHTLPKSTF*IFCRAGGLAWLPRVLVNSWPQVILPSQPPKALGSQA
8166	22067	A	8226	53	235	NKWKQGVVARTCNPTTLGG*GEWIT*GQEEFTSDANWAKIPPTVWFAFCFEETDNKSHTK
8167	22068	A	8227	275	25	GVNLNRPKPKCI*QNSPMLPGVVLNSWIPAILLPQRPKVLGLQAWITLLYKWWYCKEMHKEICBETHDVLSSKLITTRAFKRHL
8168	22069	A	8228	386	211	QLKLPLPLKNKLRPP**KFFFTFFFRQGLTILPRLVSSSWHQMIFFPQPPVEVLGQA
8169	22070	A	8229	1	117	VFILFFY*DGLAWL,PRLATNSWAQAAILPSAPKVGQLQA
8170	22071	A	8230	356	26	WRVGSQQP*PPGLKQSFCSLPSSSWDERCAPPHPINYFQICDRVYKRNANWNTSPNPLVILSQSAGITSLKPCGSEISTVIFISHQLLLVRQVPMMLVLQKTKCI
8171	22072	A	8231	3	188	FPRLRPA*IFPFIYFFFLKRVFLCHPGWTQLLDPNWTQAAQLKQSHLSLLSSLNFRGSA
8172	22073	A	8232	2	253	KLDYINGUTINLAQKCLFCLFGSIFFQR*GLTLLRLPNSWFOALLP*PLTVLGLQATMLGSQVPPVDELCTLCRCFPGLS
8173	22074	A	8233	373	65	PEKAGSCLLALFOLQNGHPPWASTLPAAITDPLGLATVNNVSOPLKSHHTHTHTHTHTHTCTCTRTLLVFL*EALTTTPLLRSICKHRESACSLSLTWPLCC
8174	22075	A	8234	390	46	RVFKPG*NPPVLKAPAPPLFFGGV*GRSPKKKNPQGGGGPPGFHPFFLTPFFPIFLRRPPPPFFRGLGPPPPPPFKTPFFFFVWVGKGLPLQKKKKFFQGISITRSVILHK
8175	22076	A	8235	387	216	QKLGVLVPPGRVIFPPFFFFCC*GGGLTMLPRLVNSWPLAILLPQPKVLGLQV
8176	22077	A	8236	1	201	EFFFTIPQCFPQFILLSF*REGLAVLERLVLPNPQAILPPQPELLGLQAHPTTLGPVIFYSYCVRA
8177	22078	A	8237	399	229	SVGGGLTMLPSWSQTPGLK*SSHLSLICKWDYRPPPHLAHPSLIMQLYCHTSLS
8178	22079	A	8238	192	335	SHLPLSSSHSYFPA*EQGFANLPRVLVNSWAVCLPQSPKVLGLA
8179	22080	A	8239	442	254	GRDVLVLCFGKSSQTLGLKSSCLGLPKHNDYRHEPPHPARNIKCVKAPTLFYFYPALVQINLP*QLQGTSCVACMC
8180	22081	A	8240	381	180	VLKDFCSHRGPTMLPRLVNSSLK*SSHLGLPCNDM*RCRPNWPSLCLLSTFNPPTLICNIHK
8181	22082	A	8241	388	260	NAIPFYITKCCNPSTLGG*GG*TT*GQEFENCLANMVKPCLY
8182	22083	A	8242	1	145	GPFTLVRLVINS*PLDPALASQAGAITGVSHCAQLIYVQRSLQLLW
8183	22084	A	8243	1	173	GLTVSQAGVQWCDHSSL*SQTLGLKCSSLSLSPSSNDYCKCKPQHQADRFFLMEFFQM

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
8184	22085	A	8244	202	327	TLFTRIFRF*RGGLAVLPRVLVNSWPFQV ILLWPPRVVLGLHV
8185	22086	A	8245	42	289	KEKRSTILFFIFCRDGLVLMPLRLDINS WPKTIFPPWPPK*LAQAHTTI PRGGGS IILICIRVDKRRKKQYAKSNPEGET
8186	22087	A	8246	592	485	NIVSQAGVQWHLNLSQLPLPLGLKNTFSC LSLLSS*DYKHVPPCANFICISVETRFPC HYGAGLELLASHNPPAPASQSTIGTGV SPCTRPRVTVLLMLANQPS*BAETLV NLATNQSDADSLAPGLSGHCF
8187	22088	A	8247	307	12	MCSPVFSFKQKNPLFLNFFKKRFLFFP GGRQGGHGFPLAPLGLNKFVLPLPFP NGDTGKGPPARGNFFFFFGQIFSRDFV SPC*PGMSLIPDDR
8188	22089	A	8248	392	237	HYGQASLAPLTSGLDLPASAPQSAVTVG SHRANFTVLI*SFSS*KFNNV
8189	22090	A	8249	153	386	FFPQWPKPSLLEPPPPMLRGFPFPPPTIL GGQD*KRPPPPPPNFCFFKNGVSPSLWS GW*TSNLSNPLSPSPKRVGIT
8190	22091	A	8250	387	166	IEITLDAIKNIDHSWEEKISTITRVWVK N*IPTMDNPSGFKTSLSEVTDVMOIA RELEVEPBEHVIELLHDIS
8191	22092	A	8251	405	266	LFAIVKR*NHPKCLLYARINKGMWHISI GWNILSLISKQMKFSYFLLTMMLEVIN LSELSHSQKVT*YMWPLA*GHLEKLNL PLKQGTPLPSSSP
8192	22093	A	8252	379	201	PGANVACNPSLGGRSGLA*AGLETS LSNMTKPPCSTPQCLVNLQNLNLYP YTP
8193	22094	A	8253	78	311	LDLYFHTRRKKGLK*IFVFI*SLSQKD LKVGTPGACAHYTPRIMGMKGLQAG KRIT*AGSEFETSLDNIVTKCL
8194	22095	A	8254	303	81	TPCAENFKLRFRFHITLSLQKNNLYIS FLYF*SHSLTILPRVSNWSPQAILLP LPPKVPGLQVSATLGL
8195	22096	A	8255	2	376	NGYNLVCHLRLPLEKSSIRVGV*FSG CPPSPPLARKGYSLTPCASQVRQCLAL LMLTLGLLHPLSCPHCPTSPSVNVPVQ LEMQKSPVFCVSHAGSCRLELFLGHLG TQSSLDSEFFKKVI
8196	22097	A	8256	70	356	LITAYNLTYDLSWRHFFVYLRKITTLH WVCSITYCWW*FVYSWNNRIDSIGK KRTNHYDQLIFNKGAKSTELRKNSLENK WQDKISTYKK
8197	22098	A	8257	403	85	PFQWPPVFTIPPLNKSPTPPGQPEF PGCFPSWCKNPRLLKSKPSGWMGRGP LPPSRGV*AGNPLGDORGRVWAKEVP LPSCCLHKAFFPPKKKARKIK
8198	22099	A	8258	249	2	YCSGDLZSYRPGVSKGHEFSFRDRIIM PMGANCVAYNLS*TLGGDGLWIA*AF GTSIAXIVKPHLYTHHHTHTMY
8199	22100	A	8259	2	189	IQCVCTKSHFCHPGMSAVQSWLTAAS TS*A*VDFSHLSLINSMD*RVTPRLVN LILFDS
8200	22101	A	8260	453	128	PPFFFFLIETVSHDVP*AGLELSSSH LASAFQSAETGVSHAQFSSVNLHS S
8201	22102	A	8261	420	79	KNP*PPFFFFLIETVSHDVP*AGLELL

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						SSSHFLASAFQSARTTGVSHIAQPSVSVLIIHSS
8202	22103	A	8262	1	262	NSRTERLGWSQSHFCHCKMEAHFVVGSGVQVCDLGLSLRPLPPGK*FSCPIILSGWDYSQCRP CRTCSLTFMHSRSPSQSEKKWTC
8203	22104	A	8263	321	100	SATKNYLLSRQSPGK*KNGLGAVAHAYNSSTRQLGGQIA*A*EFETS*GNMRRP HCYFKYKLNLRHSYSPR
8204	22105	A	8264	145	275	KPRDYSEFF*KKRDLAMFLPLASNSWTHAILPPWPKVLRIGQ
8205	22106	A	8265	73	351	SLCYRSPKRCRPFKGGHFKSKSYLQDAQWARTLLSTLTAQNKSAHHKLTCD*GAVAHACNPS TPQGRGRRIA*VQSEIETSQGN TGRPHLYKK
8206	22107	A	8266	382	232	LVEITGFCHVQAGLKLITSDPPASASQ SAGITGVSHCAWL*T*YS*DFQ
8207	22108	A	8267	397	130	IGQAGLKLITSDGLPFSASQTAGITGMS HRAMP TFLSLAR*NASFQVGHFSPKYQV GTLAKSLKCHQVRSDTLSPILCCR LIYE TLGKF
8208	22109	A	8268	309	97	DTWYRIRKRDHCTITETRIQSVRPLSPR *ATTSRVTCYTSR*PEANBEPQKITR HCDFLFLWTLDTQLTL
8209	22110	A	8269	2	224	DSSGIGSPTRPFRPKKQKLFCDPITVSLGICLYDQRQ*SVFQRDLCHSIMPITALEFIVLWKT*HFLMDE
8210	22111	A	8270	374	2	TSKSSARKDPFPHSHLAKGFFFLFMFF FF*NKICKDGLTMLPRVNLNWA BOLL LPRSPKVUGIQLATQRASILLCNPTY AGIFQHUVVNVKLLMKQCFPCAAPT K TQNFPRV
8211	22112	A	8271	1	379	PTSASQVACTTGTTHHIVLFFFGLFEX KGVFFSPSGOF*TPKPKPPPGFGKRGG KKGGGPPFPARGMGSGVFFPFPKPPFV LIGGGILFKGR TLD*PKRAPFPFPFSLF LPKHTSPFWIKNDP
8212	22113	A	8272	80	401	AWGMEFCILLYSCQYLSDLHFSKAF FFKREPPPAQVKQGPNL S*WNPWLG G*RGFSGLTPKGGNYGPPPPPLIFLFF LRRNGFFPWGMSKTDLRKDFC
8213	22114	A	8273	405	95	PPKRFWSSRGFPQRKRLGSPTPPKK KDFIYSYLSKSLKKS*INRFSAAHICN PSTLGGQGRIT*GQRFKLSLNTGRPH LKRTINVKLKKIKKNG
8214	22115	A	8274	167	52	DKBQFCWVHICNPSTLGG*GGWITRF LNMVGLRLY
8215	22116	A	8275	276	23	KYVSSRPCTVANSCKSPDLQGGWLA* VRKYKTLILGNMWMKLLFYKKLT*QNVK CIFKKYCATRSRYVTKEQKDRKKGTKE
8216	22117	A	8276	1	114	FTMLARMVVIS*PRDPPASASQSGTTG VSHHARPGLS
8217	22118	A	8277	2	87	TMILRIETNS*AAVITLWPPPAVILQZG
8218	22119	A	8278	357	347	SEGLATYQLEAFVCDLARGFCGRSL WPLITWNRGGVFLVQVQEVCCRLALG SLSPDFVL LPEGGGPTASQAGIIGVR DRAQFNCVFEIGSYSTVQAGVQ*INHGS L*P*P

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						GCCSEI*GANHSFMEIVLELILPLKIFETGPVFTL
8236	22137	A	8296	1	199	YLYIYLSILLSIYLSIYLSIYLSIYLSIYLA T*LAI*KEIYYEYVLVMTASIFPHILPS PSWRPRKVMV
8237	22138	A	8297	1	318	PIRPFPIRLSRPIKIQIALMKFSLCPEY LQ*ADYLE*SLWIRPDVAIPHACMLSL GG*GGRIA*AGRFPSISGNIVFPCLYCI IKNKIKKKKPLQIHAFTLCFID
8238	22139	A	8298	416	304	GPLHVQAGLKLISGHLPA*ASQNVGI TGMSHHARL
8239	22140	A	8299	352	31	EMILKAAREKK*IPYNEPLCLTVDPLV ETLQARREWYDIFKVLKKKNTKNTNPFY KIEYLVLKLSFKYEKVTKLKLDL*Q*LRD FINTRHANRNTSRRKKRPIIKHK
8240	22141	A	8300	382	266	RWDVFMVLKPLVSN*QAAILHVLGFLPCW DYRREPPHLA
8241	22142	A	8301	2	273	PI/TFPSSASDALSSGGPYHSECCFTY TTYKIPQRIMIDYETNSQCSKPGIV*V VHTHTTGGRGSGQLLEGSEWNNWGD PQRTSQV
8242	22143	A	8302	77	430	GMGLSMRHTHFQYLAHIHPCVHVTHTH THIHTHTHTHTLCH*HTIRKSVRYGTE HAQDPFSIFSEYTFWCACTHTHTHTH THTHTSVVVTHTKVCRETCLSFYFPRSG TISUAQELKRCLENTKELGVWCTLSLL SVANTVFFSYKQVNAARGGLFFSLSQA E
8243	22144	A	8303	137	396	SSVTDNNYLKPVVHMAIRC*LFQCLFS KKKKKKKKKKKKKKGGPLKKKICLRRG GGIFFFFGAPKISPRGV*KKKKKKKKK KKKKGGPLKKKKFNFGGGNFFFFWG PKNIAGARLKKPGGKNFRSP
8244	22145	A	8304	329	144	NGPFFFFFF*DGVSLLCCFWDAVARSR LTFVFFTLNCSVVGHSELQHWQDYL KLKTF
8245	22146	A	8305	404	157	RTYNPSTLRRSGQIT*QGDFTSLGDR VGPHLRKRERNYSLVBCFYRIKCYPE SHKQAMMLQLKPDFTLHFQHIATN
8246	22147	A	8306	394	294	SLCFLTPRDFNLGALIKNFYSPTPGMV SCVLSKGPFFFFFFFKDGVLLSCPH*G QNPFFVFALEWSGTPELK*SSHGLPRAN DPTFBPQMAVELLY*RSFPVLLDGL ICIFHSFSPBSLLP
8247	22148	A	8307	280	2	VDSHSVTFPSIVITVMLDSIQVVKQLEN IKSMFQIVARACNPSALGRDG*AOEFD SSPNTAKPCLQPKKTKQKTNKVGST LETRSNRL
8248	22149	A	8308	136	330	MSYQKSVNKKYSNNACRFPTTWARHSG SCLRLYNFSTLVGSGGKIP*TOEFETSL SNIAREFLY
8249	22150	A	8309	3	118	IFVVLVOMGPHHVQASLEL*PQVHP PQPKVLGLDA
8250	22151	A	8310	2	366	TRVDPRVRVSTHRLNLCFGSSHASTSA S*VAGTTSACHHARLIFSFFFFLGPSE KTGFNFPAQGGFELGIREPPPPFGPD GFGGGGGTFRPRRWKFKDIDIPPLVSN RGDQEPFF









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						LEETKQDKLNKSLKKEAMLRQSCSEEL KSDLNKNEELKQRTIELTRACQKQVEL E*ELAFYKIDAKFEPINITYPSEYADIDK APDESPYIGKRY
8295	22196	A	8355	231	158	PFIFLYLQSNDIARGLERGLPEKSVIG ATDSCGDLMLFMK*ESVAPMIFSGSRP LSKPPALSLMWK
8296	22197	A	8356	2	164	TRGVSRQKQKQGWKDVSVVYVGA HACNPNTLQCGRWIT*QGFETMLP
8297	22198	A	8357	23	291	CTHTRAQAARHTSHLPFYFLYTPNPFEE TGSH*TVQACLRLPASDEFPASFSQAG ITTMSSHAWPTSCILKVKMALCSINCSA ACFLY
8298	22199	A	8358	1	307	FFFFTEESCSFAQGWQWCDLGSQPPF PGFKQFCSCLSLSSNDYRHPVRLANFC IFSRDGFHVGQAGLQLTSKNDPT*AS QSAGITGVSPRAQCPAF
8299	22200	A	8359	75	266	FUKTESNLPITVLEAGSNTRKAE*VSG ERHGLCLQDGLALLPLRGNNAVSSHPRGQ NMHRKAC
8300	22201	A	8360	1	295	NTNVFCVILLFRDRVSLQCSVRSTVASS *LIVNMNLSFPSS*AYRHVSSHLDFFFF FKIQRLILPLRLSNFWQELLLMLPQG LGLQPRPQVLVGN
8301	22202	A	8361	376	293	MGFRHVSQAGLKLLTSGDLPASASQASR ITGAGHHAQPDF*HSGDSWQAPPSPRDQ G
8302	22203	A	8362	375	142	QREFLRLPNDVGEYRATVTELPVSES WNTQKDL*QKGRVSTYCRHTYGVGES FSVQRGEHVQGRGLQCELEI
8303	22204	A	8363	36	363	QLSFNPLTGKKVLRVFIGQPLFLLG GGVRFAGAHSGAQTVMHNLSSHAKRP SCLSLFSCDHRHLPHFANFCIFWT*I PPCRSGWVOTPELKQFTHLGLPKR
8304	22205	A	8364	455	235	GAQARAPRGGITFFFF*RGFCMLFRP VSKFWG*VVPPLPMPKRVGLD SWAPPP DFIFFSFFVKKRVCLW
8305	22206	A	8365	432	175	STDQVSVANGPS*PGGYNLLVCRNLRP LKKCSIRMGV*FSRYCLSNLPLDKGN SLTPCASRVRRCTVMLRLMLRGLHPLSD KP
8306	22207	A	8366	383	83	RLIVFICYFSKK*GLELLPRLVSNFWP QVILVWPPFKVLGL*ALKKMLMDMVTHA YNPFTLGGQGTBIT
8307	22208	A	8367	27	304	FPGFTLTKKSSN*CHLRPCLPSIGKVR THTLGNLSIRGYGERCSLPHCLWBSIC LPVQSN*ALHKVQMHIPFQAI*SRGI LPTDTGKH
8308	22209	A	8368	165	204	QNIPIAVSFFFFFLKRVSCFPG*PAGG QSLFIALTKPQ*GILIPYPCPNWLRG PPPNLTNFF*FLNLRPLGPNLHYVD KTSPLLYLFFFF
8309	22210	A	8369	400	201	KERPLPFLRLIGSFPGTMPFFPSKGEVK NSNFSKY*PPPIINPADRVCFEGLEVIT KFFQVRPPFP
8310	22211	A	8370	21	408	LIPSTYVVCVRCECVCCVCVNI*GYA CNTLLIACNLLQDVPFSPPTKDKLPSG FLTLVGKK

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8311	22212	A	8371	1	94	NTLGHEN* LNSGFGGCSEPRSCHCTPTW ATR
8312		A	8372	546	972	PTHSLVGR* PSPCLGLALEKTLQVMHFL KDSVNLKGSNLLVGLNLTSPQIQATLS PPLQPKTKTYEEDPKSKPKKEKNVEVN MKENILRYAEQQNEEEKNENSKSLEEEE KFDPNERYLHLAAKLDDAKEQAATPKLE KK
8313	22214	A	8373	502	178	QHFWRLEKQLSFPALGG* QPGPKKGNPF PQKKAKNLLG*NDQPVVPTTQKGGGGES L*PGRTKSPPTCTSGWKKKQNPVLKCKKN PQKTNCIPLCIYHIFLINRKTINTV
8314	22215	A	8374	362	112	YRMSVNFQVRAKRVSQRINTFPNFF* D RVLLCRPG* STVVQSQLTVASTSWAKAI LLFPQPRQAKYFLRLVKCSSSEKGERIE
8315	22216	A	8375	411	21	VLGYPTLVSPSPQLNTRVLLFSGSKK VISSSNRNPRGVVANGG* FDKPLIAGAR ASSKYKAKGNCPVRVRGVAMNPNVHFPG GGITLQRIGKPSAIRTYPAGRGKVLIAV RRSGRLRGANTVQEKEN
8316	22217	A	8376	450	108	ASGGRGPKK* LRSRFPVDSGAQGSFPG LRTESLETFCGSPQGVVLEFPFRPRLQ WNRFPGHRRRQHRPRAKRSRQQPFES SH*QRSGESRPAPVPRPCPLPWKKGVLE E
8317	22218	A	8377	25	306	EQQFPFVAVHQSQPGGAPPEASPSHPS SEKQPVPFPFRAPLVQPKP* LSPPHHP AAGLIAVHALAGGPGTVCRGLGPAARA VSVRVPAARC
8318	22219	A	8378	376	149	PAHCSLLIFGPRSSCLSLFCNWFORA PPRVGNFFFFF*EMESCYYVAMLP SLVLV T SWALAILPVLPPKPLGLQA
8319	22220	A	8379	98	374	SVFFPVGTYEGDAAPTGGGLPALGR* G AAGGHVQGHGPHGPHRGHAAPKPSAQGGP GHSRECLFPGGGAAGGERFPFRAGGQS WMEAFSMT
8320	22221	A	8380	2	807	RFQCCVRAPRACAVSGVFKLNSVF* SGR SAPHPFTHS* VRSWSKWLKTSQTSRTR RRSEKVRVSYQAWTSSPPASASARP A*RTSSHSYSSSTCSCLWNPSSWSTOP SQTFTVRNSSLTSLCLITRKHAMNPQVL PCTPVRPSCASVTITTSFLL* QALASR VT* IAPFRGSTTTPSPFRL* NLP* LSR GPQK* KSGSWSSSSA* TRVVRTAPLI TSSLLSRSSCKAQTG* ASCRPVRVP I P AGSSLGASAPGSRCHN
8321	22222	A	8381	104	327	CIAPPEMLGKYEVGKQSGVLSLKLK LNTHTHTHTHTHTHTHTHTHTHTALYLIRE GRKK* CYCMRKT DSTCVS
8322	22223	A	8382	400	270	KPKLEVRASGVQVNLSPITPAEFKAG G*LEPRSLRHFMVCN
8323	22224	A	8383	178	588	ADLISGAPGPPGGSQDNANSEHSRACA PAAPGP* WLOPWLC* WTQSPLEARGS* NPGVSHSSRIPGIPGAAGTSRPSGALPP PQAGHGSSSGELHVARGCAQGRPLWSHR PGCQLLELVTAADSHRCASRGAAW
8324	22225	A	8384	423	78	QGGLELABITGVTVESPEEPQRLLS* GG TVPTCLASLHRTL* TVHGSASSFLAQG

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						DMEPLGDRLGQTEOLH*GGDRASLQDI CFLLPVLISLLCPRLSDLRHRVGVTFGT ED
8325	22226	A	8385	434	176	FADDSRPFDFLLLV*CAMALLIRQQLLEG HFIVNMRLMQDYPIIDVQGLQKAKELQ DSK*PGGKRPWFGRASRPCAVALPOTHR NL
8326	22227	A	8386	2	305	RLWEDPFGN/PPGIR*PGCGGGGHTI REEQACQWPRGSGWRHPQAGPLQLGQ WRGKGAQQGARRSPQGSLESPPTLSAA PPAIHICSVGGVRLHCY
8327	22228	A	8387	331	91	EMRSHSVQAGVQWRDYGS/LTRFGLS FNWNNDWVGL*GDPSPPMLLPSS*ARP GGGWGPGGGHVSKAAGRLQGPP
8328	22229	A	8388	2	250	IRVRLWSQLFRRLRWEDLLSTGGGSCSE P*SCHCTVTWAFLESCLRCAHVYVVTL LTALLGSLPCANPRQTVAVSLPQAQIV
8329	22230	A	8389	388	176	YWDSQ*CMPSFAVP/VESACICAIHGNFS KSVNSVLAQVCDGSSHKVYPTHDGRCHIR EAFD/YKIDICDDDA
8330	22231	A	8390	445	330	PPRFPTFPCSLSLRSSWDYR*PPFRPNDF LSLSYVLHET
8331	22232	A	8391	559	142	LRTLPVTLGKSLASVSPSPVVGNGWIT NRSPSAKRGSGPNRGPHASCCARITH SLRSPAGVNLTPQRPILLIPETCHPS ESAVARTDISKARWMLHSRSPWPI*DET SQAEREGIRCYIGHPAT
8332	22233	A	8392	104	400	YYETPKKERTSYVYHLRFPFFTSPPFFPE TKPNSVNGPBGKGPILG*LKPWLLG*KH FCLTLPSGNTRHVLPPVNGPFFTFPFF KKCKVFFFWAPRGV
8333	22234	A	8393	408	169	DQVWIKDWNIGSLRPR*KSPQITLITTP TAVKIGIPAMIQHSQVKAAPETWVR PSLDNPKVTLKXMTSPAPVTLRS
8334	22235	A	8394	1	269	YCCPLPSSKALTQENSPSYSSPFLVNPFG LSLHPGSGGGKMINERGRKLGPSAGPLL LFLHFAZAGRQPPDNADSEADLQQVRH KLQGP
8335	22236	A	8395	2	204	KDCRVNKRVERVLRFHQAGKPIGCDAS TSLPADAPNWSNAALCCPGLSCVNCWQ GESRTCVGEGH
8336	22237	A	8396	3	285	KVTVKDRKELRKRINLEEWILEBQITRL YDCQRELPALBIDVDELMESSDARA ARVKELLVDYCKPTFAFISGLLDKIRGM QKLSTPQKK
8337	22238	A	8397	1	192	ETGPHHAGDGLLELLTSGDCPSIASQSA RITGVSHCTRAQLLTBQYFYNQNLPS APFYKRAP
8338	22239	A	8398	8	241	LNPFLYAFIDPRFQACTSMMLCCGQSR SGTSHSIRGEKSASYSGHSGQPGPNMG KGGEQMLEKSIYPYQETLVVD
8339	22240	A	8399	2	240	SCINPFLYAFLEPRFRQACTSMMLCCGQ RSAGTLHSSRGKKSASYSGHSGQPGPN MGKGGEQMLEKSIYPYQETLVVD
8340	22241	A	8400	10	272	CNWQNYLVVRCAQDCRDYFAERLYRS MGAGTDDEETLIRIIVTRAEVDLGKPK KPHQKYQKSLSDNVRSDTCGDPRKLLVA LLH



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8358	22259	A	8419	711	296	NVANS DGLIASLWKEYGRADARWYFDP TIVSVEILTVALDGSIALFLIYATVKKK YYRHFLQITLVCVELYGCWMTFLPEWLT RSPNLNTSNWLYCWLILFFFNGLVWVLLP GLLLWQSWLELKKMHQKSTSSVKKFP FTVSSLCNGLIAAQLLFYVNAKPPHRQK KQ
8359	22260	A	8420	3	97	GGGIADLAMSIAFNFGSLTDLILLLLGT CAYIPSLAPNLLDRNKTOLLGI FWKCAT IVERKSPYVAVCCILMAPSILLIQKLVK MPQCICHNI
8361	22262	A	8422	1	228	RHEVFIRLNHKKCN TVRGVFLBEPVP EIKVEVSHKYKTPMAHRCYSVLCLEPSY VAAVHSEEDLRTPPRVSS
8362	22263	A	8423	3	182	SEDTGEEQVTAEF INRGEYEDLAGYR FQAKAKLYPVASLFTQKKRDKDMLSDL HGK
8363	22264	A	8424	1	70	VQVFVDVAVTDTVIRNNLRKGLFP
8364	22265	A	8425	2	151	ETVASSCTPASLESRRCCAFCRMPTGF FGSSPLWRPSSGSRSLKDGQQ
8365	22266	A	8426	1	187	EGRVGPGGERLVPVGVGAEAQQPAGEGV RAGPLQARPPAPVGVVQGRCCOAGAGAG PPRFDG
8366	22267	A	8427	520	423	GKYQLSQSFENFAFKAGCECWTERRSC GSHQ
8367	22268	A	8428	1	627	GTSGTRGVGTGYTFLYLETPKPSISS NIMPRAMEVTVLLTCDPETPTSYQWKK NQGLSMWTHFPQSGENRNLFLFSGVTKY TAGPYECEIRNSGSASRSDPVITANLLG PDLPRIPHSPYTNVRSQDNLLSCFANSN PPAQYSWTINGKFPQSGQNLFIPIITTK HSGLYVCSVRNSATGESSSTSLTKVSA STRIGLLPLINPT
8368	22269	A	8429	3	390	ILGCNITLRVEYSLWICVSVGSRKVIID LPLVIGSRSGLSRSTSSMASRTSSEWS VDLNIPTDTPAEPCCYMDVIPEDHRLSP TTPLLLDDMDGSDSPIFMVAPBFKFPMP PTYTEVDPCILNNVQ
8369	22270	A	8430	3	208	NGTHVILLCLTCTGTVNVNANDMIVAS NLGTGVNQTVPVSSGDLIRSNGLLIPG TCBITRLTYISE
8370	22271	A	8431	3	563	LPTSVDPRVRLDRMKKQBBREDDQGGP CBRLSRELPFVVPSPEDLQSLDRWYSTP FSYFELPDSQCFYSGCFSLBBERIVGFS LDVDEISKYQBBEDQKPPCRLAEVLM BAKEPRLVQLQSLDRCVSTSTYFOLHAS FQQRSAFYSFEEDQVSLADVDRFFPT LTVIRHIALPQMGVIFPH
8371	22272	A	8432	2	119	DGDNITLVTTFTYIKSVTSRAGSDITNAS WRCSERVAPSA
8372	22273	A	8433	192	1285	AGVLSIIEETDSGLQTKVVENQTYDNR LEINDSEVASIYTPTRHGLPRSAHL PNKAMADNSSDECEBNKKKKTSQLT PQRGFSNEDDDDDDDSSDTSDSDDD DESHGAPLEGAIDPADYEHLPVSARKE LFQVQNLRCVPTDVLHKLKPFIPDFIP AVGDIADFLKVPDPDKPNDLGLLVLDE DSTKQSDPTVLSLWLTENSQENITQHM

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						KVKGLEDAERNPKAIDTWIBSISBLHRS KPPATVHYTRPMPDIDTIMQBSPEFEE LLGKVSLLPTABIDCSLAHYIDMICAILD IPVYKSRITQSLHLFLSLYSBFGKNSQHPK ALAEKGKAPTTPSSNSTSQAGDMETLTPS
8373	22274	A	8434	3	251	TLQADHFNTRKISCGAAQTIDWARTGYLGS FVKTRELTDANGERHDALNVGALDSTL ELRGLRYHPIDETSVSRHRSIABW
8374	22275	A	8435	1	225	OTFNLEBSQIYEDSTVLQSVFKSARQKI AIEEESDESDNEBEDDDEYHEWKRYD RLGENMNCINCKNGGGYIV
8375	22276	A	8436	95	340	CGCGLAGLANSALFNQSLILVILLLLIC TCAYIRSLAPSLDRNKLTGLLGIPIWKA RIGERXS PYVAVCCIVMAFSILFIQ
8376	22277	A	8437	1	317	GPKPLVRITSEPKGKDVITSGYSVSITAC PTSSVDGGLGALPQPTSVLSLSDSHITQ PCHQARKSCLQWRPSPPESTVSSQQQV KRINLCIHSEEDDMNLGLVRL
8377	22278	A	8438	80	213	PHLSFNAGITTTIKVNRNANS LGGGPHC WTCDAARRRGTLLQSYLD
8378	22279	A	8439	3	767	IIBDNIRKLEKMEFTYLLINYIQDEINTIF NDYIPVYFKLLKENLCLNLHKFNEFIQN ELQEASQELQIHHQYIMALREYFDPDSI VGWTVKY YLEEKIVSLIKNLLVALKDF HSEYIVSASNFSTQLSSQVEQLFRNIQ EYLSLTDPPKKNBKLELSPATQELI KSQALATKKLI SDVHQQTRVYLQDFSDQ LSDYVEKFLAESKRLIDLSIQNYHTFLI YITELLKKLQSTTVNPNYKLLAPGELTI IL
8379	22280	A	8440	103	354	NGCECDFLFLFLFYFPETESRSRVQAGV QNHCLGSPQSPSPFRKRSCLSTLGGRG GWIMNGVQDQPGQHGSETPLMQAGLKT
8380	22281	A	8441	3	160	KLYPLKIVFGNGNRVWVGKTVQCTLL ANVLEACELMTLDCRILMFILAES
8381	22282	A	8442	459	3	CGGLHPVRASVLLCLPQWAMNKAFFP ANLPPCSLISDCCASNQDSVGVGSEPF GAGYNLLVRRFLSLSEKRSIRVRVTRFS RCHLSPLSLTRGNSLTPCTSRVRQCLA LLRLAHGALHPLSCAHCALPSEMTFVP QMNABITRL
8382	22283	A	8443	2	318	RQGNRTAALQATLLNPPINFTSQAVNDR AKGVILNVLFSFAMDIKRAVQSILDKNG VOLLNWNMYKGEPSPSNANMLLQWHE KALAEGVTSIVRVSTALIPA
8383	22284	A	8444	2	109	VTFPMSDLQSDCACNFPQAQHSRKD LRGYSHG
8384	22285	A	8445	1	69	LVLNSNPOVRRPMPKIVGLGV
8385	22286	A	8446	1	163	PSEKHNIWGVVQFSRCRLSPISLTRG NSLIPCASVRQCLTLRLVHGACTH
8386	22287	A	8447	1	147	QOAGLELLNSGDRPTSAQSAGTGVSH RARPSSIIFLILRGSVRKPF
8387	22288	A	8448	914	729	GLTMDTKDVPQPKQPMIYICGECHE NEIKSRDPIRCRCQGRIMYKRTKRLV VFDAR
8388	22289	A	8449	134	392	TCPPPPPEPSPSLTCAVLVQTRRRVGLG SLFRRACCVALLQLLLLLFLLLFLLLP IREEDRSCTLANNFARSTIMLRVNGPP

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8411	22312	A	8472	3	154	FLVDWGIHHVSOAGIKLLTSGDLPASASQSPITFFLFFFFFEKQLLAQAGS
8412	22313	A	8473	3	162	GLYHVGGAGLKPITSGDPLASASQSVRI TGVSHRTRPKIIPKLIPLFLVA
8413	22314	A	8474	266	107	LCLFLIIMRFPYVQAGVKLLSSHLPS SASQSDRI TGVSHCFWEPVFKRGIP
8414	22315	A	8475	361	169	KLPQFSNPFISASLAAITCARHHAQIL FVFLVWGLCQAGKHNFCKYSRVLYSP IYSPTHFI
8415	22316	A	8476	1	154	KKLIPTIMDHGAGFKS SVKEITTAIVEM AREVELEVEPEDGNELIQSRGKT
8416	22317	A	8477	3	193	SHYOSLISNNGHKCGRFQCPKPTKTY DLCSLDYOLTFPPLLTDPVKS PSVRNT QELSILP
8417	22318	A	8478	408	103	TGSRILTSSRVECSGVITATCNELIPGS SDPLASASQVAETTGWGHVWILFLIGIF LVKNASHYVAQDLDKLGSTDPVPSASQ SVGITGLSHAWATICYK
8418	22319	A	8479	59	166	NVNTGLGHHTHTHTHTHTHTANYFKE TPIHQYI
8419	22320	A	8480	394	253	FLLLLLSSGFCHVAQAGLKLSSCDLPA LASQSAIBSGVSHCAQPIA
8420	22321	A	8481	379	184	CFSLPKWDPRGVPISPGDFWNFITKLG VCPFOQAGFELLAPNDVAASGPQAGIS GINFWAWAL
8421	22322	A	8482	367	170	CSLSGLGGRSGRESERKKEREKERDRE KKKBSERKEREKEREVSSTYKDTNSMG SGPHVSYL
8422	22323	A	8483	324	136	QRESCLSLRSSMDYRMPHLANFCIFC RDGVLPCCPSWSQMTTSLFSLNFLICLV GILGSG
8423	22324	A	8484	1	57	GERRYGTCTYQGRLMAPCC
8424	22325	A	8485	35	339	GKLLRPFYWQWKNKNLNVSLIDGWSLY DTLGYNGILNCHMYLLTEGDSQKKKKKK KKKKKKKKKKIDPAGNSKIYNRKIPKT PRGFTKALGPLLLIFF
8425	22326	A	8486	330	66	RPGVSRNPWPLIFFLRRVFLCRPGWNA VVQSLITKISASQVQALFLGGGCSFPR SCHCTPAMATIAKLCFKKKNGKNPTDIM FSK
8426	22327	A	8487	3	209	CLSLLESNDQAQPPPHANFLMFNFCR VGVLLCCPGLASSDPPPLVVSQARITGM SECTWITFLSFK
8427	22328	A	8488	3	216	QQSITVSCATINS DVGSSNLVSYQSSN LVSWYQQHPGQAPKLIYEDNKLSSSEK KKKKKKKKKKKK
8428	22329	A	8489	326	62	PATYFSGSFFLFLFPFKTECLSVTRLEC SGALSAMCKRFPSSNSPASCQGRSE PKSHFTLANTTRAKLHLNKNKI KTVKE FLSS
8429	22330	A	8490	2	156	SSAGIGRTGCFIATRTGQQQKARGVD ILGIVCOLRLDRVVOGCGQQQR
8430	22331	A	8491	399	254	KNNKENKTNNKI TNKLTILKNISPLY FFFFFFFF
8431	22332	A	8492	2	130	FRRVQAGLELLTSGDLPASASQAGIT GVSHRAQPTFLKSC
8432	22333	A	8493	3	94	HLPAEFTPAVHASLDKFLASVSTVLTSK YR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
8433	22334	A	8494	327	70	KSGFSNVGQAGLKL/TSSDLPVSAQSQA GITGMSHCTWPLYPPGLGSRSPHSIEE HCWYQLAPFPSCRNPFTVVPFFVHRFYL TF
8434	22335	A	8495	97	219	PQTVAHACNPGVLGGQGNMTSGQEPQT SLASAAPKPRSTRP
8435	22336	A	8496	3	191	RTKGEITLVEIPTSNEELCRDPKRGY GVVPRFALLPLETEVYDDVDFCDPLENG PLPLGE
8436	22337	A	8497	144	304	SYFFYEETLESTVIKKNAIVSPTATNVEL EATILSELGTQKNTKYMPSLAVSGS
8437	22338	A	8498	2	90	LITILVLAAMKRVGFFKRNRPPEEDDEG E
8438	22339	A	8499	1	156	PSSQDYMIAPPHLANPKNFFVKMCLAN LPLRMNPNPQTILLSPPLKGLHV
8439	22340	A	8500	67	319	KLMSPGPTLLSARCVSSTQTCNNELNIN LDAMSVAATINNNKIMSFARIWMLKAIT LIIITLLEHKKTKYCMCLISGSLRMTQG
8440	22341	A	8501	3	299	ETGSHCVQDGGVQKHTSAHCSLDLIGSS DPPASASRVVGITSAHHPLLWSISSLPP LILLHPHNLIANLILLPLSLSTVNLHLTL PPLLPLRLCLSPC
8441	22342	A	8502	56	142	NNSAKKKKKKKKKKKKKKKKKKKKKKK AAF
8442	22343	A	8503	486	348	TGFHRVAQAGLELLSSGNPPALASQNGG ITGVSHHAQPAEYNFKK
8443	22344	A	8504	158	403	RIFPFFETVGFVAQDGVQGRGAILQPRLL FELKRPSCLSIPSSWYKRAQPNPNDFP KROMAFDPKTORISLGSKKKKHPIE
8444	22345	A	8505	3	78	DNHTAXVLLYGRPRVETVEESEQ
8445	22346	A	8506	164	291	TRFCCCHLEVVVFVCLVCVAVFPFMCII LPFIIVLFFETFFP
8446	22347	A	8507	372	69	CAPLEPLKFFFFFRGPTFRGGSSPIFFP PKKGVLKPNPKGFFPPPPFLKPAPOGA FNYPPPGKIFPSPRKGWAPGGFLKG APPEFFFTFFFTFLFF
8447	22348	A	8508	282	1	SFOHVAQAGLKLGLSRRDPTLAAQSAGI TGVSHHARFVLVFGSVLFSMEFLSTMSA VILPCICSFVCSLAVPSSCILQQFLPPT CTYIKTETCI
8448	22349	A	8509	400	45	TPDVSSLFFPLPKETIFFCCPPFRQSLFF PFFFFPPPLFFFTFFFTFFFTFFFTFFFT FFFTFFFTFFFTFFFTFFFTFFFTFFFT FFFTFFFTFFFTFFFTFFFTFFFTFFFT FFFTFFFTFFFTFFFTFFFTFFFTFFFT SKERNK
8449	22350	A	8510	241	419	TPLAGNKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK QNN
8450	22351	A	8511	317	28	QSLSPSPQTVYITLITLITVAFPTLITLIT LTPSPSPFMELKYLKCYFPADPYASLE FFFTFFFTFFFTFFFTFFFTFFFTFFFT FFFTFFFTFFFTFFFTFFFTFFFTFFFT FFFTFFFTFFFTFFFTFFFTFFFTFFFT
8451	22352	A	8512	124	292	MCCYIMSLRLVICTIKGFSTKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK KGGVPL
8452	22353	A	8513	1247	910	QAQLSDIGTSCYTCSMILCRNDYIRLF GNSGAAGACQGISPASELVIRAGQNVYH LKCITCSICRNRLVPGDRFHYINGSLFC

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
8453	22334	A	8514	99	262	EHDRPTALINGHINSIQSNPILPDQKVC MNRKFTLNKKKKKKKKKKKKKKKKKKGG PFKKNPQGAQIFPGGKKKIFFLKQGL
8454	22335	A	8515	85	2	GWGNAQWLTPTVPIVLSAAGGSRGQE
8455	22336	A	8516	244	423	VFAVFNFLGAVMDMLNLAVVITLQAC ISNHVHVHLVYIQLFANYTYSIKLGKKP SKSV
8456	22337	A	8517	3	114	KINGEDKQKILDKCNISINMLDKNQCV FFFFFPI
8457	22338	A	8518	413	91	QGVKKISFRGGGFLKKKKLKKKKK WQGPKEKKKKGGGFFFLNPPFNGV KKKKKKKKKKKKKKKKKKKKKKKKKK GRKEGREGRRKEGGGRQENMTA
8458	22339	A	8519	1	163	SRLPGRSRRRSRRRRRRRRRRRRRRR SRVLIFPNDONLDINIVYIEDVDA
8459	22360	A	8520	191	21	RPIITHVADAMTVIVFLYSVFLHVGQAC LELLPSDDLPAASASNAVTVGVSHRAWL
8460	22361	A	8521	2	144	AAATSGAAMCHPVPVPAWAEVGAISLKP GRIQLPLIMIALVHLVSL
8461	22362	A	8522	90	8	KPTPLPLTARTTALLPISPLILIL
8462	22363	A	8523	305	146	VFRHSOGIRGSVDVKITDGLVIRRIE NVPPGPNKNNKYALFQSSSIESQ
8463	22364	A	8524	176	2	LAMPFLFLCPKMDYRHEPLQASITFTV REWDKIGWANNITPVIPLWAEAEVGRSQ GQ
8464	22365	A	8525	2	200	CLIPSSNDYRHPMPRPAFCIFFFFLGD HVSQVLKLLTTSKIDPLAMTSQAGITGF SHHTKPGQFF
8465	22366	A	8526	2	217	SFSLFPFSFSLLLPPLSILLPPLPSF SLLPFSFSLSPFSFSLLLPFSFSLIL HPTFSGLVPSDFE
8466	22367	A	8527	2	186	IRGLEPLEKRRIRVGSRRFRRYHLSRLS FARKGNSPTPCASRVRCPSLLHGLHPL SDKPK
8467	22368	A	8528	3	153	CLGFLSGWDCRCIPCLANLKLPLVEMG SLFNQWILLPPNPLKVLGLQV
8468	22369	A	8529	2	388	RTAVHTFILLVLQVQCRHLSLALTPA HLVCSHRIISYLSIRGSMHRCMTTP GLVISIFFVEMKYAVAHGILLGSSY PASAYQSAEITGVSHAWPTDSIMQKPH MVICISCFNLVLGTM
8469	22370	A	8530	293	64	YRISIRKSNKPGWVSSFWIFFFVFVF SFFVFVFCFMMFLKQYLFKFINIIL TQLYICTTSKICYSFLYPR
8470	22371	A	8531	2	250	SLGLPSSWDYRGLPLCLANFCIPNRDG VSLCCQGSQTPGSGQIDEAVYSIYAY ITALLIVYVAQWVHLKHFCCILKYT
8471	22372	A	8532	2	201	PHHVGGTGLELSGGDLPASASQAGIT GVSHCTWPSLLYMMFNLSAVPIANVI EGNYTKRCI
8472	22373	A	8533	319	200	TTFTFLQKGLTMLPRIVSNSAQAICL LOPKVLELNA
8473	22374	A	8534	160	297	KTFTLVAHANCPSTLACIGRQVSSAH EFTKTLGMMTKPILYTKL
8474	22375	A	8535	333	228	PNRGHYIAIVKSHDFWLLPDDIDEVSS FLISYP
8475	22376	A	8536	3	325	PPSSILPCSNITLDCASNERDSVGVGPS



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8496	22397	A	8557	669	407	LVSSSSVVOAILPTVPHKVLRLQA AGVIGNRLSTLQPPRRFKRPSHLSPS SWDYRC/LPCPANYCIPLVKBRHVHG AGLELLTSGDPPAMVSLIAGITGVSHRA HPD
8497	22398	A	8558	195	352	LGLQAGTTASGYSTVILGGMKPKRSHW WPVVPATREAFVGSLEPGRSKLQ
8498	22399	A	8559	345	219	HLKRLNISLECPFPASASQAGITGMS HHGMLNPKS IHL
8499	22400	A	8560	137	2	VKYCLPTSLTKTVRPLSPSQATASPV CTYTPRMPEVTEESQKN
8500	22401	A	8561	324	193	RSSGNLPSAAQASRTVGVSHTRPKCI ISKKEYVAGNNHLKSTS
8501	22402	A	8562	326	121	HNTHHTHTKNGKHQCFQTHHTYHTQD IYVLQAASQKSLILISSLAIV
8502	22403	A	8563	3	85	HERHTHTHTHTHTHTHTHTHTLCAEM
8503	22404	A	8564	2	153	ARDRHIPPLTNFSVFWRDGGLAMLPRL VSKLWAGVAVHPPWLLKVLRLQA
8504	22405	A	8565	2	177	ARVGFHYVGGAGLGLTSGDPPASASQS AGITGMSHRARPMSLSLTLHLQDTWRAY AG
8505	22406	A	8566	353	212	AGFRHVGRAGLELVTDGPPRTASQSSG ITGMSHCAHPEKSTAPILF
8506	22407	A	8567	76	191	ELIFCRDGLTVFPKLSLNTWPIAVLPL WPPKVLGLQV
8507	22408	A	8568	1	142	GTRGFLHVGGAGLELTPSGDPPALASQG AQMTGVSHCASQKKEFLW
8508	22409	A	8569	250	95	SASRAFLPLFPFSLPLRLAGLSPLCPFR LVSSYPRVPLLPPLPVLGLQV
8509	22410	A	8570	3	226	HEHTHTHTHTHTHTHTHTHTHTHLV LVYSLCEHLMRTVLSRARVCCIVVVVF PEOGYADRRVADKMLKIH
8510	22411	A	8571	1	216	GTRGLGVGVSHVLSKNTHTHTHTHTHT THHTATASQLSVPKIWAQFRLCKGLT YISNSYCSKKFYLNH
8511	22412	A	8572	356	268	LIMLARLVNFRPQVLPQWPPKMLGLQ A
8512	22413	A	8573	12	175	RWGTHPVGQAGLELLITSDLPLTASQKA EITGMSHCARPSPFSPFLSFFFWKHL
8513	22414	A	8574	1	163	GTRTGPHHVGAQLELLTSGDPPVSASQ SVGITGVSHRAPVGLCIALLISNEY
8514	22415	A	8575	344	176	EPLVETGFRHIGQAGFHLTLGDQSTSA SQNTEITGVSHAPGLAIIFKSGNQAFP
8515	22416	A	8576	2	179	ARGILCHSGTFLKDSRPSMVAHTCNPST LGSQGORIAAGQEDITSLKVARPRLYG QIF
8516	22417	A	8577	1	100	GTRGFTMLPRVSSDSNAQVILLPWPPRV LRLQM
8517	22418	A	8578	3	114	HERHEILSYLTIYLSIYLSIYLSIYLI YLPITIRI
8518	22419	A	8579	1	264	GTRPCRIELHVVVSLAKAQETSGEEIS KFIPLMKNRNGFYHSRQCEISMGEAGL CMRYVFWNGKRIPGSPETIGDENCHIYF NVQN
8519	22420	A	8580	1	245	GTSGTSGILGFIYERDRLQLTRIDTIT LSHGYSYTSINRCDSRHMMNPMQMILYQ SPFLGYQLSHEVLARGLSIYNTYE

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8520	22421	A	8581	1531	1457	QARNETIARRLAWISCHLLGLPID
8521	22422	A	8582	191	2	TITTSYPTPTAPGSHYATPCPYKPDYSR YPIKVELWBAETGSRGQETETILANTV KPLRSRA
8522	22423	A	8584	2	212	ARAGIYPKRYKSPYYKDTCNRMFIAGLF TIPKTIWQSKCPSPWLDWIKKMYKQGPIL SPMLECSGEVSGFK
8523	22424	A	8585	2	192	ARGWSPASSSRVAGITGAHHHARLIFVF FLFVRFVFFSFLKTFKLVATISNFQPLFL FAPLHFK
8524	22425	A	8586	277	66	PLDPLRGLKRRLLPFPKKKKKSKFQVCV VCVVCVVCVCKRQCLVTLPRLVNSWAQA ILLSWDPKILALQV
8525	22426	A	8587	395	286	PHLGLTPKNDYRREPTCLAEVWLKKYVW VTYFSFR
8526	22427	A	8588	307	177	RYPSTINYSILNRDKINKELDRMYKAR PRVMCLPWPVKVLGL
8527	22428	A	8589	167	349	ENLRELGEFFFFFNFVFVVGKFS VFLLVGNLFLFFGGIFGLSRVMCFKFF RCFS
8528	22429	A	8590	375	240	LLSRPSWFCFVFRQGLTMLPRVLNCA RGILLPWSPKVLGLQA
8529	22430	A	8591	347	215	ETGPFHVGGAGLLALSSDPPASASQSA QITGMSRRAPQSAKRF
8530	22431	A	8592	340	114	HRTAHCSLYLSSGSSDPATSSSQVITG KQHTWLLPKFYFCRARVSKINKYKSLNK FYFLNTQTITPSEYGRASQ
8531	22432	A	8593	86	253	LRLCCGLSCSTAKKKKKKKKKKKKK KKKLLMPKRGQFELFPFPFGGKRLP
8532	22433	A	8594	3	135	GFCHVGVGLLELLTSGDFPALASQAEY TGVSHRAWDPVLPFF
8533	22434	A	8595	2	274	PRVRTISLLGLIVRSHLISLLCLEGT ILSLFIATLITLINTSHLANIVPIALL VFAACRAAVGLALLVNSINTYGLDYVHN LNLQCC
8534	22435	A	8596	3	316	SIPYSWGEREGIPCMAPFOTGTSLRND FTALSILNLTHTHTHTHTHTHTHTHTHT QGITALILNLLRHYCPCLAFPSLSPKQ NLTVRHCILSRDTWLATASK
8535	22436	A	8597	385	291	KAPPLPFFFFFFFVFVFVFVFVFVFVF KKILGV
8536	22437	A	8598	275	369	GVQVLKILITSGDLPALASQAEYTGVS HRR
8537	22438	A	8599	98	344	VHYEFMVCVVCVVCVVCVVCVPRVRGVD MNPVKHPFGGTHQHGKPCITLRNNSA GRKVLMAALWTVRIGTKITVTLRKT
8538	22439	A	8600	328	195	THVPPLAKFVFLVKGSLHIGAGLDDL STSGDPPALASGVFR
8539	22440	A	8601	2	214	HVDVVGTFALISLELHMLHVDPENLR ILDVNLCKLANHGTDTFPVQAAYK VVADVANALAHNYH
8540	22441	A	8602	89	181	GLRHNRLNSGGGCGSEPKLCHCTPANA TE
8541	22442	A	8603	340	57	KGGHQEMQARXGGHGRKAPGUSPWTIG ELPKSARGHTGLFVSYRGCRTOFRKKV LPGGDRNGIAMLPRVNSWQRIILP QPSKVQGLQK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
8542	22443	A	8604	330	132	TGFLHVGQSGKRLKLTSGDLPTSAFQNGAG ITGSGHCTRPFSLFHSYLVLFYGCSSSQ VSLSLIARM
8543	22444	A	8605	546	279	RPGPTVSPRLLECICMIMAHCSLDFFGSG VSPPTASRVARITSTHHAWLIFYSVVE TGRHVAQAGLELLGSSNPPPTASQSGAG ITAL
8544	22445	A	8606	3	249	NRPNLGGGCSSEPSHACTPSWATEQET CITLYLEYCFPPVSHNTNVPKPLAVTIR SDYCIILHASSITGSSDSLITDCHD
8545	22446	A	8607	159	324	VIQYRTLTIAHLHCENLVNFWLYFYFLK KTYTGIGQMRWLTVPVIPALWEAAQSGS
8546	22447	A	8608	334	179	TGFPHVQSGSKLKLITSGDLPTSGSQSAG ITGVSCHTLELVYFYFNLSITYPS
8547	22448	A	8609	278	202	QQPSTLRQDPPPAKRRLISESTIGH
8548	22449	A	8610	236	66	AASTFFLQKTRHLLSGTVAHACNPTSL GGRGIRISRGREFKLTSGNVRPRVYKK
8549	22450	A	8611	29	177	GKQVWALHCFYFFHFFFRKSLAVLRLV SNSHWQETLPPWFLKVLQLQA
8550	22451	A	8612	1	215	HTSRITLVHLRLKNNKYLITKQGLSKLP RLVLNSWAQAVLPPWPSKVLGITGMSHC TWLYLHLSTDLLKLC
8551	22452	A	8613	3	91	LRHGNCLDPGEGKCSREPSCHCTPAWVT E
8552	22453	A	8614	2	167	FTISLGLVDRSLTRHINNIKPSFTRE NTLMFTHLSPILSTRKQALQHLKRLK
8553	22454	A	8615	2	281	FCILVETGPHCVAAHAGLQLLSSGNPPAS ASQSVGITGMSHCTSPNLSLLTQSKSPC LLIQHNPYAFINSQLTSLTLLFSLSYFI FYDSLFLFV
8554	22455	A	8616	282	182	GCAWHLTPVIPALWEAEVGLLEPRSSR PAWST
8555	22456	A	8617	379	207	SNQTTKRYINFFFYEMRSHYVQAGLKF LGSSNPPPTASQASITGISHYVMPISP S
8556	22457	A	8618	705	483	DKSFALVARAGVQWHLGSLQLPLPPGPK QFSYLSLSPSNWDYRHAAPRPAHFILSR DGVSPCWPGRSTPDLR
8557	22458	A	8619	359	220	RQSLTMLPRLVNSWQAILEPNLRLLL GLQALAPIPGKSYNEKTP
8558	22459	A	8620	3	186	HEVSWVKRKQDOWTEPDDDTVTSIVAPED ILRLSAGGDCHIAIVLLYGPRRVQILEE ESEQ
8559	22460	A	8621	1	116	GTSFCRDQGLTVLQGLQSSFWFQILPFP WPPKVVELQA
8560	22461	A	8622	369	188	NYSLEMGFTGNHAGLELLASGDLSALA SESAGITCMISLRYRTRFSFKRATCGDL SLQS
8561	22462	A	8623	202	22	YTLGFFYMPVICYQERKKDKNNNEVTTI NSFYVICMBLGAIIISKLMQEQKTKYHI FSQV
8562	22463	A	8624	387	315	SNLGGGCSSELRLLCHCTPAWATE
8563	22464	A	8625	2	135	TRDLCSLVYLLTFPPLSHDPAKSPSVR NTQELSIKKKKGRPP
8564	22465	A	8626	3	232	HASAFEEPPVYIKSRKKRKNENPPKIVSS QPHGLKKKKKKKKKKKKGRGLKKKKK KINKKKKKKKYKYNFRGGAF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8565	22466	A	8627	97	373	QHGLPKKKKKKKKKKKGGPLLKKPLIG GPNFTGDKKKFFPKKGGLIKCPGPEFLK KNLFLGGKKGKGNPKKLNPLGEKKNFK GKKGKNPP
8566	22467	A	8628	2	188	RYGCPPPYHTFEFPVYIKSRKKRKNWNP PKLVSSQPHGLNDHFKKKKKKGAAVLCD PSGSPS
8567	22468	A	8629	287	68	GEEGRRTGKERNGGGGSEERKKGEHEAR RTGRGGGGGKAGKPPRSARRGRGRSG SKSCTPSRHLPAHIITN
8568	22469	A	8630	364	136	VSLLLGLLEYSGTTTAYSLNLLPLTIVET GSHVVAQTGLKLLGSGNPPSTDSTQTFEI TGVSHGAQPKVQVQFSKGLDT
8569	22470	A	8631	355	70	LFPDKRFFPPFSLPLKFFFSFKGFNFF REFFPIFSPPKKRLVSKNSPGGFYKPPPL RGKIFTFPPPVKFGPPRGLFKGPPPPFF FFLFFFFFLVI
8570	22471	A	8632	2	266	AFTISLGLGLVRSRLYSSLLCLSEYLL SLVITATVITLNTSHLLANIVPIALLVF AACTAAVGLALLGISINTYGLDYGHNNIN LLQC
8571	22472	A	8633	1	186	LTHHNINIKPSFTRENTLMFIHLSPLL LKKKKKKKKKKKKKKKKKKKGGALKKK PGGGQN
8572	22473	A	8634	2	80	VLETAVALIQAYVFTLLVSLYLDRNT
8573	22474	A	8635	713	333	EGPPPPRSKKKGTGGGGKDPSPPEPKT PGNQGRKTKPPPPORPVTGPPPPGSGP TRGGGRSSSSNTNAPKEKLTFSKNPR KTFPPRAILLVTFSPFLKNTFFSLRLLI FLGQCAFFPPDPK
8574	22475	A	8636	389	1	FTFSFLGLTITFFFLNINFFPYFSSLSF FFFLNFMLLKHTPPIILFFFLSLPIFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF LLRARGCKQYKQKLIWYLT
8575	22476	A	8637	2	192	VRTGLRDTATPQRLYQTTFPTATRGVY YQGNRYICGANSFMPIVLELALATIFE IGPEFTL
8576	22477	A	8638	1	87	PIRPLETAVALIQAYVFTLLVSVYLHDN T
8577	22478	A	8639	2	132	INLASTLIIFTLITLLTLTAVALTQA YGVTLVLSLYHDNT
8578	22479	A	8640	2	113	LFFIABYTNIIINTLTITPGLTGYDA LSPELTTY
8579	22480	A	8641	375	22	FTFSFLAYLFTLDPFFFPPLCLCFFFF TFLFSLFSLFSLIFFLSLLLFLPPG LEFFFPDPFFFTFFFTFFFTFFFTFF FFFTFFFTFFFTFFFTFFFTFFFTFF FFFCWLPHRMVIAKVGISVSKKI
8580	22481	A	8642	180	34	WFISDSINLGMVAHNTNPSLTVGQGW TCGRSRSPVPKRTPSQTCAPA
8581	22482	A	8643	338	133	NIPGLFYSIQKKKKKPLRPQTGLGAPK GNPQGAPLFGKKAFFFTFFFTFFFTFF FFFTFFFTFFLEK
8582	22483	A	8644	156	287	LTYPFKPPLLCGQKKKKKKKKKKKKKK KKKKKGAFKKNPWGAQI
8583	22484	A	8645	1	325	LRHCHTNPVTKVVCFTKKKKKKKKKK



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
						KKKKKKKKKKKKKKGGGPLEKPPGGPK PSGGKKKLPQGGGUYKKPPGGFLGKTL FLOGKNCBNPKKIKIPGSKKIF
8584	22485	A	8646	370	3	PURASRLICLPRQANAMMGAAPPASLDP CSLISDCASNQRDSVAGSPSEPGAGYN LVMHCLPSPSEKHSIIVGVTRPSRCPS PLSLTRKGNSLTPCASQVRQCLALLRLV QGAGTHRTRG
8585	22486	A	8647	341	88	KKKKIPSPDIKRGPPSVYFICDPPPPPP FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF PIWHKLCGDL
8586	22487	A	8648	1	108	PTRPTRGVASVLYFTTILILIPITSLI ENKILKWA
8587	22488	A	8649	3	96	ETCGANHSFMPDIVLELIPKIPETGPVF TL
8588	22489	A	8650	457	297	SPSFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FYILIKDNMFPQC
8589	22490	A	8651	84	352	YKTDVKIISILFNTIDMLEYNVLHLTG QLMLLIKKKKKKKKKKKKKKKINK FWGCLITLTLGIVLSPLEALKISPSF GFLEK
8590	22491	A	8652	2	111	NNIKPSFTRENTLMPHLSPIILLSLNP DIITGFS
8591	22492	A	8653	1	305	EQQQQQQLRNEDFLVYNRMTELCFQ RCVPSLHRLADAESEACLSGAKLIH SNHRLMAAYVQLMPALVQRRIADYEAS AVPGVAAGPGVSPSGS
8592	22493	A	8654	129	268	LSEVLYLFPKKKRLITLCLEFRNPGSS NLQKITKEPIIDYFDVQD
8593	22494	A	8655	281	117	CITITLSFINTLQAVIINLVFSEVCLYV LSIYLSIYLSIYVFEYRIKISPHL
8594	22495	A	8656	3	177	DLHAHRLGVDPGNLNLGHCLETLAGH LPGEFTPAGHAFCLKDFVSTVLTYYK R
8595	22496	A	8657	3	270	RRRGRMHCSDLLGSRNPPASASRVAVT TOTRHLANLIVVGFLFVLRDVLVRPH ATDKIPKIQGFTKERGLMDLQFMVAGK ASQS
8596	22497	A	8658	107	11	QREHKPTPPLPTLIALTLLQLISPFIL LILL
8597	22498	A	8659	21	136	VPIKHVDPVENSRAELKMGDIRDAIA QAVKGLITKA
8598	22499	A	8660	1	395	LYTALYSLYITTTQWGLTHISNLEK KKKGKGGKKKGGALPGIPGGSIFPGV WELLFFLEKGGIKTILGFLGKTLFFGG GLGAPLPKIKGLREKKNFGEGLGVKN RVFFFQNFSSGLVYLKY
8599	22500	A	8661	1	255	ETRGTRGRTGRGLTRGKKKKKKMKKKK KKKKKKKKGGAPLNRDWGGPIFWGLPKF YFLPNKGSFFNLIGDPLKRPFFWGGAYF G
8600	22501	A	8662	136	358	PHIVEGVSILKPKCVLLKKKKKKKKKK KKKKKKKKGGKKLKKGGKKKKGGKK NKLFWVGFFYKRVWGYF
8601	22502	A	8663	198	368	LNLVQVTCILGTLGILFYLFLRRAL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, - =possible nucleotide deletion, + =possible nucleotide insertion)
8643	22544	A	8705	429	319	PGATIAHRSTNLPGSSDPPISASQVAGN TOVSYCARP
8644	22545	A	8706	426	245	RAATPSPIKLTKKKKKKKKKKKKKKKKKK KKKKKKKKKKRGAPLKKTLGGPQINRGK KKIFFFF
8645	22546	A	8707	1	108	KHPRGGSFGYCFALANVAPFLLALVSGLI YIELRKRRE
8646	22547	A	8708	3	146	QIEBHTLSALGUGAAMPVQGLIRHFRPE LEBRMORFAQCHQARQAS
8647	22548	A	8709	2	83	LVLLEIAVALIQAYVFLLVSLVLYHDNT
8648	22549	A	8710	1	81	EPLSKTVRFNVLKVTQKQKTKQKQKQK
8649	22550	A	8711	156	4	EPLSFHPSGKKRLFLKKKKKKKLCVAHA CNPSTLGGGRGIRMSGDNDHNG
8650	22551	A	8712	440	233	TPSYFVLIVVERGFSMLERLSTVLTSGDPP ASAPRSAGITGMSHHAQPRTRGRSKAYLP FLIEPDLKIIFFP
8651	22552	A	8713	92	302	AMHPTMGPDQDGHGTGOLYAHITPLHPHSH THANTLILSHIYAHMSHTIPATCPKQK TQPYLCLLSPHIEL
8652	22553	A	8714	2	166	KKINSFFSQGLTOAKVHGGRPSLQGPOT PVLKSSCLSPSSWDYRHEPLYPAN
8653	22554	A	8715	1	129	GFRHVGQADLELLTSDDLPAASQIVRI TGVSPCAQHFFKSN
8654	22555	A	8716	381	105	RRSLIHSVLNQAQGVQRDLGSTQPPF PSSLPMWPKVPRLQPLQGRHPVWEVRV SARPPVINDVRSPSAHLPSLESEERLCL AAIPSGK
8655	22556	A	8717	385	125	FFFFLPPAPLLSGXMFYYYYIFSTFFF FFFFLGSPPPLFFFFFLLANKIFFFFF FFFFFNMLFFFFFFFFFFFFFFFFFFFFF FFF
8656	22557	A	8718	409	264	KTDQRWSTSSSKIMSQSQVSKGVDFES SEDDDDPPMNPSSLRNER
8657	22558	A	8719	3	269	KHIVKRVLSHLKASCEELHLHFSWQOL LEQLQMGSGSHTHMDQRTTHMHPHYT HARTHTVIAKLNELPNVBNLLSLGNFQ QRLP
8658	22559	A	8720	430	141	LFFFLSFPEFGVLICHPGWSVVASQLT ATSTSKKKKKKATPPGIPKFLIGKSGK PPRVLLIGHNAPFKFFFNPLIAFF
8659	22560	A	8721	386	290	RWELTMLPRVLNLYWQATLLWPPRV SGLQA
8660	22561	A	8722	3	137	HEVFLVETVFLVIAVGQGLELPTSGDLPT SALNRAEMGGLLEDRSSQPMET
8661	22562	A	8723	493	186	PSQGGGKRAILGLRLNCLPGVKDPSAR PPKEVGNBGRVPKTLFVFLKKKGFP LIGGGFKSRPWSPRPFPQKVGVRQINP PPGFFFFDLIWPNRGS
8662	22563	A	8724	3	186	GGGTPPPGPGVWKGNGGTPPAKTLPPF PSPLRFFSPSPSGEGSREPLLSPLA CICI
8663	22564	A	8725	370	67	FADPPNIFYKADPIFFIIFLFFILFIYFI FFFFIIFKFLVFLFETGPHIVSQEDLDL VHLQPPPKVQVLQWATTGQFPVFLI ETGLHPVNDXGRHLLTL
8664	22565	A	8726	966	652	LGSLEKPPPTQFKRFSCLSPSSWNYNHA PPCPANFVPLEETGFHVQVSLLELTS GDPPITASQAGITGMSRDMGQHLIV

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
8665	22566	A	8727	85	425	NHCTLFYQGGHKTTRSLDPPPP HMHSAFHEHATFLHTHTNSHTNSQNSP TYSKSHTHSYMKFTDSDHSQMQQTHRH SLLEMTQGLYTCCTHTHTTRTVPLDHLHS VKGWLNKVALGGRTSHGRSHLAGRLLA
8666	22567	A	8728	393	124	LQSGEPOLFQSPFGSGGPPGPKSHANSNG NANPPVPPYIIESAPPPPHFPFGQAQSKY SGGQAARLCPCPPFFLKKKKKKAGSOT GTFSFQ
8667	22568	A	8729	25	217	AVQPIRVQWRRLQSKFQBIILAPSLAK VDMENLTQLTQENADFATDRYHSSLVN REQIMPHY
8668	22569	A	8730	1	611	PGIPYSATLSDTSLNQLCFIMHRYRK NLTAACKNELVQKTKSEFNFSKTYQBF NHLYLTMVGCWNTSKPKFGKIYIDPEIL EKTGVAEYKNSLNVVHHDSFLSYAVSFL LQTSSTSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSPSEERTVNVSSIRGKKWSNYLD YLFSGQLQGLKLFIRSSVHSSIPRAEG IYCNQNY
8669	22570	A	8731	120	378	VVEKTLASLQCKSTPRALGFPRERTLP LRRCPCQSPPEAQMLERKRALSSQAQML MPVFPALMEAVGSSLEARSFETSLONI A
8670	22571	A	8732	2	68	VYVCVCVCVCVCVCVCRAKVM
8671	22572	A	8733	382	258	NYHSSLHLETPGLKQSSCLSLPKSWOYR HSPCPALIFNSL
8672	22573	A	8734	479	326	PPLYGFFFFFWMGGGFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFQITF
8673	22574	A	8735	422	2	GRRPGLYFFFFPGKKNFGGGLFF FPKGFFFFFFPFGFFPSSELGKDMP PKKKVFSQRFPPFFPPDLEFLFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFNKQVIERLRCARHCFRPAS
8674	22575	A	8736	7	75	IAVALIQAYVFTLLVSLVLDNT
8675	22576	A	8737	2	176	NFGLLAETGFLVGHGHLVRSBGDLPA SASQRAITGVSTAPGFNRYFYKQTIYK YG
8676	22577	A	8738	408	111	GSSPTPRAGGDNFLKNAQGNFPGGGG GGCPYFLYPKKFFPSKGFIPWGGGGGK WPKKGGGSKGPKQVFFTPPKKKKFF WFGSGWGPKNW
8677	22578	A	8739	5	249	YKGLKLLNQASPPQKGGPVNHHKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK BGALGGKFLAQTSFKGKQKVFYKY
8678	22579	A	8740	1	226	FFLRQSLSVTQGVQNCGLSSLLQLLAFQ GSSNSPTSAQVAQITGVHHHQLLIFIS LVETGFHIVAQAGLEINLO
8679	22580	A	8741	4	96	DGLINLERLYSSNWPQGLPPNPSKGLG LQV
8680	22581	A	8742	19	112	FORILLVREKKKKKKKKKKKKKKKKKK GGGL
8681	22582	A	8743	362	234	KMDQKCLSEVLQRNFPCCCCCCCCCC CCFSLPFIPEPSRS
8682	22583	A	8744	3	419	LTLRRFQLNLTLATFKKKKKKKKKKKKK KKKKKKKKKKKKGGPLFKNSLGGPIPG GKKIFFFFGGGFLKPPGDLKTKTFFLG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: of USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
						GEIRGPPPPKRLTPLGKKKIFKGVGGKN PPLFLRRKKFFSGGFFKILFSPGLGF
8683	22584	A	8745	444	1	KKPSKBI LYPENSRRFSPISPLKFFFS KGNFWGGGGLCPPIKCNFFSNGP FFSPPLKIKIFPPPPVNLGPPDRDLFG APPFFFFFFFFFFLMMFYWLSLSSGSQR LPQGVPTVPSLGGMGAYFVSIRSTYL QSGMRPR
8684	22585	A	8746	104	222	NKTECLIKKKKKKKKKKKKKKKKKKK KKKKKNWOGAL
8685	22586	A	8747	403	201	NBKYHVQPHSGTILSHEKQALPPIA KMRQPCSLSIDEMRNIMSSLTVEYTT AMKRNKQLYSQ
8686	22587	A	8748	1	90	RTKGAVYAAERNGLDGCVEDLSRLQR GP
8687	22588	A	8749	444	85	SPPPPPGLFFFFFFPKKITSPPPTKGGF SPPPPPQKFFFLKPPFFLGLGPNFPPP KKNFFSKNPPRFFFPFPPKKKNTFFPPP FFFAAPKPPFFLTPPPLEFFFFFFFFFF FFFFFFFFFF
8688	22589	A	8750	2	309	EFFPPYVBSFLKINACMPSPEIKKKKKK KKKKKKKKKRGPPKAKTGGPQIPRGKK KKI PPLKGGQKKPRGRGLEKNPLFGGGP FGPPPPPKINPPKKKGNP
8689	22590	A	8751	3	76	TASVSRGGGLQGITMKDSDEERE G
8690	22591	A	8752	433	145	SFFFFFFFSSFFFPKSSSFTPL
8691	22592	A	8753	2	124	GHLDMHLIGSATLALSTINLPSTLIPT ILI KKKKKRPP
8692	22593	A	8754	80	201	FINANSKKKKKKKKKKKKKKKKKKKK KKKGGGLLKKTPQGAQF
8693	22594	A	8755	415	1	IYPTTPEKFGPKETLKGAPFFFPFKQ KDPFFPGGGQKGGGQSLTLPKGGKKI SRPNPPRKRGKDAAPPKGVFLKKGK VFPGGGGFKTPTPRDLAPPAPLPGAL FFFLRQSLSLSLRLCSGTLAHAS
8694	22595	A	8756	3	136	FTATREGVYVGQSEICAHNSFNPVLV ELIPLKI FEIGPVFTL
8695	22596	A	8757	80	326	KKFSLGSGGGRAGVPRPPLGRLOTAL NSGAKOTPPFLFPEPRKGGPPPAAGWE GLCPHFPPMGKGGGLMHTGEGPH
8696	22597	A	8758	1	164	SLISSTGGRQCRRPQPLPRKTRDPCS HVILLTPPPLLSDYDPAKPSLRNTRQ
8697	22598	A	8759	431	79	FFFFFFIPLKIVSTQSPFQVFFFFFKT FFLQPLKKGSGWGRGDKPPPLAPFK KMGVFFFFFFFCCFVFFFLPLFFFFFF FFFFFFFVFVFVFVFVFVFVFVFVFVF FFFFFFFPRCVLTRL
8698	22599	A	8760	60	194	ARPCFATAVTQKKKKKKKKKKKKKKK KKKKGGGLKKGQGGK
8699	22600	A	8761	383	38	CASMTFKKKKKKKKKKKKKKKKKKK KKKK
8700	22601	A	8762	399	164	HTVKSILAVPMDDPFKKKKKKKKKKKK KKKKGGFKKGLWGGKLTGEKKILPFF LKGKKKKPLGIF
8701	22602	A	8763	353	48	NFFFKVFFFLKDFSHKGAPEKKGGPPKK TPPRKKFFFLKIKPLFFIAFFFFMSLFG FELISLSEFFFFFFFFFFFVFVFVF FPIVFITLMMFKLYLH

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in US 59/015,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
8725	22626	A	8787	336	10	WLTRSSSTSWVHALLPOPPE
8726	22627	A	8788	1	147	CLSLPSSMDRRRLPPHPASFCIS
8727	22628	A	8789	3	130	IFVYLLTGPHYVQAGLELLTSGDSPAS ASQSAGITGVNHHALPEIHVF
8728	22629	A	8790	206	3	DLEEGITFLNGRLSDGSRRTGQLKLDH SSEFSKTRELVPVF
8729	22630	A	8791	124	390	VPPSGPIKKGDKCKNLVLIPLIKNVNPK KLKRGVSPLALPFFFFFVFLLETGFH VGAGLELLTS
8730	22631	A	8793	2	301	RAGAQNLMPPPSGVKAIFFPNFPKKM GNGTPPPAPLIFGGLKKGVS PCGPGGS EPAPCGPSPLAPPKGGNGRDLPLPP DKFLN
8731	22632	A	8794	1	285	HEERERERERERERERERERERERER ERERERDALFAFFPPPGARPPPIERGV FVGAGSVREIYPTLSIFFPSPPAHRGRE LRSRCVSHSLHLSRA
8732	22633	A	8795	1	321	ARGERERERERERERERERERERER RERERERERERERERERERERERER PLFFLGRGGLAFAHAISSPPFIAGAPPYI YIFHNGARPERYLCAQRETRPAL
8733	22634	A	8796	2	140	ARERERERERERERERERERERER RERERERERERERERERERERERER ERERERERERERESLPPDAGCAKAGWG E
8734	22635	A	8797	2	223	SAREERERERERERERERERERER RNLSSGGGVPPPLQANRHSGGPARGT LHHIKKGTSLTDVGLAQ
8735	22636	A	8798	1	176	ARGERERERERERERERERERER LOGGRGTQFAIERGVICQGRYTTGRV RN
8736	22637	A	8799	335	27	PPTKFFFFFLVEMGFCCIAQGLLELS SSSLPASAYQSAKIIGVSHAMSVF
8737	22638	A	8800	342	191	STSLSLPFCMDYREPPCANLSYFFPD PFSKCNPLRYWGLGLQHRNPG
8738	22639	A	8801	104	332	AVPLMVKICPLMKRVRFNFKSKLELP CDPAISLLSMYPMKMSLQQRDVCTPRL STGPLTLAGMWNPKRSMD
8739	22640	A	8802	563	258	FFLNLETRSWYVACARVCMLEFGTVIVH YSLDLLASSHPPIASGVAGITDACAQ LTLPLFKLGLGLGGGVGYPSYFGLG FHNDCSRVRVLCMWSYQ
8740	22641	A	8803	2	199	ARGLVRRFLSPSKRSIRVGVTFRSC RPSPLSLTRKNSLTPCASQVRQCLALL RLAUGACTH
8741	22642	A	8804	266	108	KLVSCKVALPPPSFSSSCSHIGCAPFP FPFIYCKFPQASQALLPEQAVEP
8742	22643	A	8805	1	140	KVWFKKFTYGCSEGCANHSFMPPI VLELLHLKIFEGIVPTL
8743	22644	A	8806	2	90	SSAAABENDEKSEAEKTEDDMFGLF D
8744	22645	A	8807	229	34	KKKIFFFFGFWPDKRFFFAVPPFFP FFFFFFFFFFFLLDLITLILISYTK LISIRAAPI
8745	22646	A	8808	43	173	NADSGHAWLTPGMALMAREAGGSQDQ



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SEQ ID NO. of nucleotide sequence	SEQ ID NO. of peptide sequence	Method	SEQ ID NO. in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
8746	22647	A	8809	259	134	EIETILACAGKPRLY IYIMIFKNNKPPNRDRGLPMHLRLVNLMAQ VILLSWPPKVLGL
8747	22648	A	8810	391	193	VLEPKIPGQIFPPPCRFKGRPRFRPKPKPP PKRKISFSNPPKINPPQGYFKRGPPRL FYFFFFVVL
8748	22649	A	8811	304	3	TTPPINIFFCFLFFIFIFLWYFIFIFIF FFFFFFFFFFF QCFLHQQKRWVHTHTQSSHLQLGGS NPQGGQSPGWVLC
8749	22650	A	8812	395	268	FIVETGFPHHGGAGLILPASSDLPALTS QSAGITGVSHHGS
8750	22651	A	8813	782	1174	LSRLFYFCVFLCYNHTQLDYPFRLVLC LFVLRQGLTSLSSRLCSGMIAACCSLN PGSDTSPTSASRVVTRTGVRHTQLIFV CFVEMNFHYVACGLEPLGSSSPDALSS QGAGITDVSHHTPLELCP
8751	22652	A	8814	95	236	ATNPOLSNITFLSNKDKGLNLPSSLVK SWARVILLPWPVKVLGLQT
8752	22653	A	8815	381	58	SCILFPFVWGARGGGPPRAGGSGNPPGP GLTPFPKKPKINYNARGGGFIPPPREG WAGGFPLPRGRVPLAPGSGNNLEGLPL SPDGQKKTTPSKKKKKKKRKR
8753	22654	A	8817	441	158	FFFFLRTDGLTMLPLRLVSNWPGAILL PQPPIMLGL
8754	22655	A	8818	415	342	RLVLDSWAQETILLPWPVKVLGLQV
8755	22656	A	8819	400	171	NFFPPGVKFLGGGGQFPFPQKRGFFQ KPGGFFKPPPKKKKFPFPFPKIGPPQ GLFKIADPFFFFFFF
8756	22657	A	8820	2	268	INITLAPTISLGLLVRSGLVSSLLCL BGIILSLPIATLITNTLSLANTVPI AILVFAACEKKKKGAVLKD PWGQQLSR VLAR
8757	22658	A	8821	2	258	LCLPNQAWAGSGPPASLLPCLSLSDC CASNQDRSVGVPSEGVGYSINVRFL SPSEKRSIRVGVTFRSSWVRVLTVIPA T
8758	22659	A	8822	250	456	GGGDKPGLTETFPFGLKFFFLNLSGW ELGPLAPPPFKCFKGRGFFFLPRFVF VANLLLTCCKKRD
8759	22660	A	8823	492	376	QENCLNPGKRICSELRSCLCTAFAPATER ACLKKQKNTQ
8760	22661	A	8824	1	116	LTPLPSPAPPSVDDNKTPPEWVCSLPF HPQRMILSRN
8761	22662	A	8825	2	191	FIVETGFPHHGRAGLIKLNSSGALTSF QKAGITGVTGVSHCFEVRNVRVTGTQYF LCYLLKS
8762	22663	A	8826	393	75	PPFPFPDPKIFFPFPFPFPFLGGFPPI PPFPFPFPKPPPPFPFPFLKKKIFP PPFPFPFPNFPFPFPFPFPFPFPFP FPFPFPFPFPFPFPFPFPFPFPFPFP
8763	22664	A	8827	81	380	KIITKHNIATINPTTCINMNYLKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK NPGGGGNPPGGKNNFPFPFGGKNNPPG FPKKKPPFGGKFGAPPPPN
8764	22665	A	8828	354	13	TKPKTPPLTKGPRRGFLAPRVPGGGPI TPPPQNFLOGKGTLLARKKVFPPGRPAK RPPKKKNQFMRPLKNGGPGWKLGF



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US95/09515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						YRPLCLPNQTTNSAMAGAPPLASLPFCS LISDCCASNKRDSMGVGPSETGTGYNLL VCHPLSPLEKCSLRVGVTFRSRLSP SLTKKGNLSLTPCTSRVRCIALRL
8850	22751	A	8914	258	9	GATPCTHCETNPSTSTQSTQTPEPOL POVPLELPPPOS CPKCRKSGHWAKECPQ PGIPPKPCPI CAGPHWKLDCPTSPRL
8851	22752	A	8915	326	42	EKIHKKTCYSPFVFLVENGFTFYVQAS LKLASSDLPASFGSARVKAMSHCVRP VLVLPKRLQNTENSTKIVTYPPTNPG ILTFCHWCPK
8852	22753	A	8917	3	106	GLELPTSGDLPASASQAGITGISHAR PIMTYS
8853	22754	A	8918	320	171	ASTTTDGYKCLCLPGVPSDKPNYCTP LNTALNLEKCPGLPHLGS
8854	22755	A	8919	1	201	VKPSDRVHLMPIPTAYPHQNTSTYNVVP STRMVAEERFKQGRKLSLCSDLRYKDLR TIVDPVVS CAT
8855	22756	A	8920	3	182	LLRPLEKRGIRVGVSRSRYHLRLPFA RKGNSTPCASRVRCPSLLHGLHPLSD KPO
8856	22757	A	8921	142	1	SCHFGNSAVVRPOLLRLRYINCLSLGG SGCS ELGSCHCTPAWTTG
8857	22758	A	8922	1	117	LFPNYAWNGSTTTLGRLSINSNVVILT PWPPKELGLQA
8858	22759	A	8923	357	121	LGAFSGLAHLNDLKGTFATLSLHCDK LRVDLENFRLGLHVLVCVLAHFGKEFT FPVQAAIYQKVVGAVNALAKYH
8859	22760	A	8924	343	133	LFPNPLLETRLEWLIFFVSVEYTFPI LRAGLQASDPPARSGSQASISGMH YANPCSNRAFKCS
8860	22761	A	8925	321	44	PDSGGSFASASQAGITGACHDANLPI FNMDININIPSAERDKLSMDKNEIIF SLLINRLSSPQIMYPLCSSRIESRKRNL KQTRKKE
8861	22762	A	8926	335	106	HPVFLIETGPHRVGHAGLELLTSTDPPA LAYKSSGI TGVYSRFTKLHLCAVCCLC IYTYLGLNLSTTPGSWEKKT
8862	22763	A	8927	2	160	LSRVPPRSANLSISVFAEKRCFTMLFR PISNSWAQGI LLSQAPKVLGLQA
8863	22764	A	8928	3	140	RVITEERNPKAFSLRLQANARLPFI RAKRAKENABQVEKKK
8864	22765	A	8929	126	59	NSGGGGCNELRSCHCTPAWATE
8865	22766	A	8930	3	104	KNMACYCRIPACTAGRRYTOTCIYQGL WAPCC
8866	22767	A	8931	311	112	MENLYSKMQQELEKNITRELKAAAELE SGS IASPLGSTDESNINQDLVWKASREY VQVLKKNYMI
8867	22768	A	8932	345	134	GGGSSPWFPPFWKPRRADSRLVGVLNPP GPGGGAPFPLKNPLLGWGGGARLWQILI LLRVLPENSDPCR
8868	22769	A	8933	262	39	RPRPRPHNPPFFPPNNGSHVAGGLEL LDSDPTLPQSAGTGTMSYQANPLDHI FENRDCVLLHCSSPVNNT
8869	22770	A	8934	84	22	TGANVMTLTPVPLAMEAKAG
8870	22771	A	8935	277	111	ERTINHAAGSHGVSGT FKKYDLSLMT VLEKHPMPWQFVRLGQIVGGIPSSG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
8871	22772	A	8936	2	106	DSATPRRLECLKEDVQRQEREKRLQHR YARPVF
8872	22773	A	8937	1	193	LMWDFSPSGLDGAFQRGYYWYNNKYNV KKGSI SGFTMVLGYNLFIYCLSYKELK HERLCKYH
8873	22774	A	8938	240	69	DGNGQLKGSFSGEARNLWTFPI PALWEAE VGRSLEVRNIIYILQNASNIGNHLLIK
8874	22775	A	8939	329	177	RWNLAHLPRFLVLSWQAICPSWPLKML GLEAEPCPARTNFKVISPRLA
8875	22776	A	8940	358	120	HUSNPFVFLVMSGFHNVQGLSELPFAR YVFTLAPRSGGTLGSHCAVPEWALPR KASPOLSGRRGSPHCATCSSKAW
8876	22777	A	8941	333	104	PHVYSNGHCTSLTLEDMSPALSVOQVC LSIISMLSSCKEKRRPPDNFSYVRTCNK NPKKTKMYGKGQEPVITF
8877	22778	A	8942	1	241	APLVAPTVQVNLDEKGLSKLVEATRINF NDRYDEICHEWGGNVLGPKSGVTRIAKLK KAKARELATNWKCTLLSFLYIKR
8878	22779	A	8943	1	240	APLVAPTVQVNLDEKGLSKLVEATRINY NDRYDEICHEWGGNVLGPKSVTRIAKLK KAKARELATNWKCTLLSFLYIKR
8879	22780	A	8944	306	150	AASLTCLPRLECSGALDARCSLNTLGSQD PPASASQVGGAGSLEPGRWRLQ
8880	22781	A	8945	284	2	GKSRSPDLCLCTSGPTGTHPTLLICWV PRYVATCPPIGLNFVPIKTMWSHYIVQA DLKLMVSNPPFVSASQSGNTGMSHRTW LNRLLUTYKK
8881	22782	A	8946	1	226	WSPALFAQAGLEPLTSGQPPASASLSAG ITOMSHRQAPVLSNLSYASTPCATSS YCAKMLKELKFWLVIDRA
8882	22783	A	8947	363	96	NTAFGYMPLLSIPFLVLSKAVFLPLGM FTAALLIAQRWQPKASDTDEWINKMW HMHTEHYSTCCGVHAANNISIQISEWN CWEW
8883	22784	A	8948	1	208	GRVQPGRLRLTSGDLPASASQAGVAG VSHRAQPTPALNCVLTCNVLQSYIKHSH GKRSRYFTIENDM
8884	22785	A	8949	69	298	SRGHQRVADAALLSPDVI CLGLMLWGS SSIVICILHRHKRRVQHIRTSVSPTS SP ESGATKILLQEERTSPRS
8885	22786	A	8951	2	201	LYDLIANRSISLPLPSLVCTHSHHTEHT YTHIHTARTYTHTHSHVLSLKKQKRV KHPRLSVWI
8886	22787	A	8952	1	285	GASPPASLPSPCLSDCCASNDQRDSGVG GPSRPGAGYNLVRRVLSPSKRSIRVG VTRFSRCRSPSLSTRKGNLSLTPCASRV RCLTLNLLVH
8887	22788	A	8953	341	256	LGLGGGCSRPWRHRTPAWVTERDFIS L
8888	22789	A	8954	227	43	TLFPTGKTHPTHTHTHTHTHTAKLEP PARFPTS PNSTNCTPTSPNANPGLV RAGLG
8889	22790	A	8955	310	79	RPRRFGLMRRVNFIFSTLRRSFYKIRI TNQAQCCMPVIVPTQTRAGRSLRKPXSL RLAWATQONSISKKNNNNFF
8890	22791	A	8956	374	198	FFFPLNRHGLANLPRNVLHWQAVLPO PPKVILOQ
8891	22792	A	8957	138	10	RPRRPRLOQAQWLMPTIPALWESVAGGL





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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, P=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
8915	22816	A	8981	335	221	FFFFLFLFCMTTSHCSVNVLGASDSPTS VSHIAGTIGT
8916	22817	A	8982	360	150	LSHMPLLPVSLYPDHRAPMQVIFPPFFPT ESPSVTRLBCSGAILAHCNVCLPGSSDS PASAS YAGYSFYL
8917	22818	A	8983	346	116	GQGRVETESCSVTQAGVQMCDHSHLSL LELLGSSDPSTASPVGTGTGHHYHTSS HFLSVSSSYFPTVCLAYR
8918	22819	A	8984	350	263	LHFLPRLVSNAPQALFLMPPKVLBSLQ A
8919	22820	A	8985	3	159	EEYNLLVCRLLSPLEKCSIGVAVTQFSL CHVSPLSLTRKCNLSPTCASVVR
8920	22821	A	8986	2	253	KHVGLKNDLSTCGTASVDYRLNKL TNISVTDSEKYPHMLSVKNCFTQGSVVR YMLPADEVHKLQLQDAARKEPLQCKQ
8921	22822	A	8987	2	115	QARIVGHLTHALKQCGYGLASTGNGGG ASAMLIQKL
	22823	A	8988	3	159	GFYHIGQAGLKLMSGDLPASASQAGI TGLSHCAQAGIFFFLPYDIFTVE
8923	22824	A	8989	1	123	SHYVAQAGPLGLSSNPASASRSGIT GVSHHAWPPSLFL
8924	22825	A	8990	462	303	LARTPSRPTRPPTRPPTRPPTSPTRPP FMLSVDCLLLY
8925	22826	A	8991	382	178	PPFFFFFPFFSPPFFFFFPQKQKGF PQKQFFFFFGKPKVGNFQKFLRAKGGK GEKPKQNKGVF
8926	22827	A	8992	532	432	RDAGLTMLPRLVSNRAQVLLLPGPVKV LTLQV
8927	22828	A	8993	418	172	KKKKKKKNIPLIFFNYFFFLIFFPIFF FFFFFPFFFFFPFFFFFPFFFFFP FFFFFPFGAMSLFRGGDSGEVKOTDSMS RQCQGF
8928	22829	A	8994	2	722	AVRLNYSYPPNLTATVFCQDGTASTTL RNGSALSVLBQQSLLHVCVDSNPPARL SWIWSGLTLPQSQSNLGLVLELPRVHVX DEGEFTCAQNPLQSGHISLSLSLQNEY TGKMRPISGVMLGAFGGAGATALVLSF CIIFVVVRSCKKSGARPAVGVDGTGMD ANAVRGSASQGLLESPPADDSPPHHAPP ALATPSPBEGETIYASLSFHKARPQYPQ EQEALGYEYSEINPK
8929	22830	A	8995	498	323	EPKARLNEGDIADVHTRKEEGNPRGTLQ RNAKTLGLLGS FVENI
8930	22831	A	8996	21	511	LITDGVEAYALNASGVVNIIVFDPKWA LFRSFVAKVEKCLDTRRGSNSELETAVKD LKRASVYKHYGDVAIVVYSGQTVENGV KNFLDPTNIVLGNVQAGRLRTYGCIQD ADAQREGINASAPYGVNVTQDPAREF TWIQAPILMLLNDDEFSVQLA
8931	22832	A	8997	178	306	GATHAINNPPFNVMGKCTLGPPNLMAL KQIPFSPVGEKTKR
8932	22833	A	8998	351	211	SIQSRLMQVPVPCYISGRHHYHSHHHH HHYSSYPLKYPOEYLRPL
8933	22834	A	8999	1	381	FRLPKFALMELCSIEISDQPLFPVPGF FPFGKASFGQGGRRGKFKLMEPLAK GVKGISCPKPHPCINPPKPKRGKSSP PEGPKTGAPGPAKKGLEPFLTKGKNWP GDKTKKAVFPKPF



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8953	22854	A	9019	3	209	GNLTLIQVQGRGA CPPLSPGCTNSARAEPVSVALPDALNNL RTHGSGDGPSSSDVWNRDPEDVYPQGIY VISAPSIYAREA
8954	22855	A	9020	504	20	NYAQMSYSTARASANESWAYPMGRKRFV ASRQASQMPFLCWLEEAIVRRVVTLP SKA RFSFQSARSAMGNCDMTGSGRMALDGLK EYQEAAMLLAEGLSTYEKECAKRGDDYQ ETFAQQRRTMRRAAGLKPANAAAF ESGLRQSTEEKSDSRPAAGS
8955	22856	A	9021	3	168	LPRLFAAARITHREERRERERRERERRER RERERERERRERERRERAPPPTLCET
8956	22857	A	9022	2	89	LCSLVYLLTPPPLLSCDPAKSPSARNTQ E
8957	22858	A	9023	508	371	FFCRDKVLA TLDPRLANAWPQVILPQP PKVLRLQPCITPLSKDL
8958	22859	A	9024	2	170	RTHSAGRPPQCNCCEKAPRHSSTLVHR RTHVGRETRINGSPLPSMSHPYCGPLAN
8959	22860	A	9025	3	185	PPAATPQGPSPINSPTPKKAKNRRTK KTKKKKKPPPSKKKGPQRTPKKTMGGPL KTTT
8960	22861	A	9026	104	319	LVFLSKYTPPLLVSLMTHGLSLLSFLPS LPSFLPSLLTYLLPSFLPSFLTSVDNPL PSLFFLVFKLSQFWT
8961	22862	A	9027	476	364	SLKRLTSGDLPASASQSAVITGVSHRAR PIIYFYVQ
8962	22863	A	9028	36	154	FLVQAGLKLTLTSGDLPASGQSARITA VSHRTWRTHF
8963	22864	A	9029	2043	1237	WLETHVAPALDERLACTQLQVPLDPSQ PYVVRCQCPYERQAQPPHCPAPEGEF GAPQALGDAPSTSVSLTAVQDYVCPLQ GSHALCTCCQPMEDRAERQDPRVAP QQCAVCLQPFCHLYWGCTRTGCYGLAP FCEINLGDKCLDGLVNNNSYESDILKNY LATRGLTWNNMLTESMALQRFVFLSD YRVTDGTVLCYCCGLSRELTLYQYRQN IPASELPVAVTSRDPDCYWGRCNCRTOVKA HHAMKFNNHCEQTRFEN
8964	22865	A	9030	15	389	TVDHVPCGPTSPGTVTQAGQWNLGP LQPRPLGLEGGSSCLSLCSWGRHAPPH LARGHFSSEVQLRSRLQGHAVFVKQRK GTPEDPQGLRTLSSCLHLVALALWF SLPFHGPRIHQ
8965	22866	A	9031	3	243	RHSIAFNRFSCLSLPSNWDCHPPSPCEA RHSITFVMEHHVQAGLELLTSGLPT LASQSGITVSIIHAWTCCCP
8966	22867	A	9032	1	245	PTFRPLAICTGMCNKHDTAVGLLRT THINIVSSYKPPPYGHDHWEYCADLP DPYSPTPQQAQARSPPPPYDGHARK
8967	22868	A	9033	46	124	QELMTHGAKSPDGRVHDAFLVTVT
8968	22869	A	9034	235	435	KKKKKKKKKKKKKKRRPFLLKGFPPK LKPGQGLFEAPFGGPPDPGFFAGGGA DPGPFKKKKK
8969	22870	A	9035	333	70	CPVYQPIILKDOVNLSSISPPSHLLKD LWKTLPISYITELIFVCVEMAPHHVAQ AGLELLGSSNPPTSTFQSAKITGISHA CLNT
8970	22871	A	9036	297	411	NKTMFAATNMOLEVTLISKLMBQKRTKY

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8971	22872	A	9037	461	167	CMSSLLSGS NKNYPLGGPPFGSPSPENLNGGFPLTP GGGGPINPNSPPPPPGGRPPFLKKKK KKKKEKETNTYILQDTCRCSAVLPMQ VKIVMICLIMHRLP
8972	22873	A	9038	466	292	NGCLLEPASNSLANIFIPCREBGLTML PRPQVILPPLPPKVLRLPLPPLSS
8973	22874	A	9039	34	124	GRNIRFSSLSLTPLAHKKTYCSHAAEH VK
8974	22875	A	9040	54	239	RERKRLRHWGLANLPLRVNSWQIALW PPKVLRIQACATTPGIRRMHGGQYSP GAGSV
8975	22876	A	9041	469	223	PNARVVCVVCVVCVVCVVCARASES QTCAAVPSLGPAGAGPALGCCAVCEDE VGSCPHARPLPRAAVKKAAGRGLCF
8976	22877	A	9042	491	380	SPGVVAHSYNPSTLDRQSHITRVRFPM TCLATEGAV
8977	22878	A	9043	144	360	IHSHWGYLWLVSLAARLAINPDCMYV YIFSCQCTDKLTEKFIEGTLANKEILRL IQEPQKVKREKMONA
8978	22879	A	9044	23	263	RWNSDGKGLRPAWATWPDVPSIKNTQN THITHTPHSPHTPHGQOPLSPPTFPW PVSSPSPTFPFSHTCLSPFGA
8979	22880	A	9045	461	287	PPSLANIYLYLYLIGRDGVSILFPLVLS NCAQAAILLWLPKVLGLQGFPPNLALK SL
8980	22881	A	9046	485	6	NNNSKAWRVVPLPATREAGAGESLES GRRLR
8981	22882	A	9047	475	307	LELDKGLTLPLRVNSWQIALLLPWL LKLGLQARATLHWACSCINSTQNLLO
8982	22883	A	9048	483	338	LRERERQERERERERERERERERER TTAFTQLLFQYVAIILLPCY
8983	22884	A	9049	680	303	NDLLFGSLYVQFAKSGTGRVTLPEPSE EQVVCLECFODLFGDENKNGFKMFDS NYHGQDLLFKDATVRAVPWGEKTYTRGW LGLDYVAALGEMSSQCSGAGRTGPPCR LPWCYSDDPTPEP
8984	22885	A	9050	26	165	AFGYHVRVQAGLELLTSGDFFASASQSA GITGVSHHARSQYFFVYV
8985	22886	A	9051	461	83	HKINLPSSKKKKKKKKKKKKKKKKKK K
8986	22887	A	9052	475	209	MAAPPKKKKKKKKKKKKKKKKKKKK
8987	22888	A	9053	531	404	SVTQAMQWQKINSLSGSLTLEFGQSLL SLPTINDYKHADLS
8988	22889	A	9054	66	416	KKTKNKIKMGGSPLFKISPPFLKRLS WKGAPKTPPLSMAPFFFGGKKNBPF KGGKIFFFFPKKTIKGPFQGEHTPPL GGGPQIFSLPPFGVQKNPPLIRGGL FFT
8989	22890	A	9055	1	104	LIVANGSLGVTHSQAVAILKHQRSTV TLTVLS
8990	22891	A	9056	3	106	LKRWGLAMLTGLVLSWQAQVILPWPP VLGLQV
8991	22892	A	9057	1	299	PTPRINILAPTISLGLVYRSILSGS LLLEGILLSLPIAIRYPDAPPLPL DEKKKKKKKKKKKKKKKKKKKKKK RKIKARRNTGGGL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
9007	22908	A	9074	437	79	NQREEEERKKRRRRRRRRRRKKKK KILRQKKKKRRKAGSREKKKILRHLPEK NKRSEKHVELINALSRIGQTRLI YQKMH FYTLAKNNWKILKIKYHLQALENKVPR HRWETA
9008	22909	A	9075	51	185	CRADFWFHEKTIUVLCISLVYLLTFPPL LSYDPAKSPSARNTQB
9009	22910	A	9076	452	310	QPSRCHLSLSLDRKQNSLPTCTSVRR CLALLRLTLGALHLLSDNPO
9010	22911	A	9077	438	326	LLHCWMDCKLVQPLMKSVRFLRDELE IPDFTLHF
9011	22912	A	9078	37	169	GTPGFRHAGQRRLQLLTGLDPTASHS AGITGTSURAKPPSTF
9012	22913	A	9079	1	408	RKRRLSKEETERNVQAEKYAEDEVR ERVSAKNALESYAFNMKSAVEDGLKXK ISEADKKKVLDCQCEVLSWLDANTLAEK DEFEHKKRKEBQVCNPTISGLYQAGGP GPGFGAOGHPKGGSGGPTTEVD
9013	22914	A	9080	31	168	VRRNPRLESGTITTTAYCSLELLGSSNDP ASASQVARTTGLQLLNLQ
9014	22915	A	9081	460	319	YFFVEMGSHYIADVLELLGSSNPASAA SQSAEPTDAHKPTDCRPLR
9015	22916	A	9082	465	326	PCVAFCTHTHTHTHTHTFFKCVGSHL HTNND
9016	22917	A	9083	33	269	PNSSRPISSVRGIHPPCLANFCPLMVPV EMGSHVYVLQGLIGSSDLSALAVQSGR VTOMSHCANPELIPLESNILL
9017	22918	A	9084	47	300	DLTSLFLCKQSSSLATNTQTPFRNTYF DLIKTLPLRFPICPIYFYFLPSYGG FSSFFFFFLKGSPLPRLNGAKTAVN
9018	22919	A	9085	437	220	NIAIKSLSLSLSLVCMCVCSACVC MCLSLSLFSSSSLSHSLFPSTPMNDIS HLPIILSTQENMLLLQ
9019	22920	A	9086	227	23	DCPRANILGLTPRLVSNWFOVILTWP PKGQSLCRQGGDRWTWHPWLLHPP PQARFPPTTHFH
9020	22921	A	9087	206	326	PHWQNPTFPVIALWEADGKSGQSEFE TSLANTVKKRLY
9021	22922	A	9088	364	123	SRVVLPLKAGDETSILPLASGGRCSL AMGSTPPIASIPTWPSVLCPCEIFPLL FLLYGDCNLGPTLIPDDLIMRSLP
9022	22923	A	9089	373	205	MPPRLANFCYFSRDWSPYWSGWQSTPC WDYRRPEFPFPPCVRTSYSVQYCACYAGL
9023	22924	A	9090	283	2	REFFSAAVVLAPKIFNKLFSPPFNRVRP EDWPIRGCGPNENPFPCCPPGVKKG PFFKKKKENFISQAQNLMPVIPAWE AKAGSLAP
9024	22925	A	9091	16	261	CPEDLIVGQNVVEDSDMGDPDRFPCW FACFYLLVYRRCCLANPRILYASNAQVI LLQPQPASLELQAATTHPALCLSF
9025	22926	A	9092	17	109	RQGLAMLPRLTNSWTOANLLPWPPKEL GL
9026	22927	A	9093	282	114	KKGKGAALVPIKTRGRKPPFFFLRQSLA MLLRVLVNSWAQAILLPPEVLGLQA
9027	22928	A	9094	205	337	NANLHGRMORITFCLPETWEASTGGSG QETETILANMVKPCLY
9028	22929	A	9095	62	287	BHSCAKLFCFAPESQSPYSACAGVOWHD HSLIQSQTPGLKQSSCLSPASAGFYKE

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						CPKYVLEKVFLLNVLAPFYLKYRNRNP GSVAHTCNPSLTGGKRGWITGAQEFETS LGNLARPSLIKRKKYKLF
9072	22973	A	9139	34	142	NCKRLNTHHTLTHSHTHMLTHSDTPTH THTTKYK
9073	22974	A	9140	146	2	PPPPFPEGVSLCPGWSAUAARFLTASS ASRVHAILPPQPPQQLPTRP
9074	22975	A	9141	3	102	PASASQSAGVTGMSHAQPIELPRCSS HRTT
9075	22976	A	9142	245	51	NREGHLLCCPRNSQTFGLKQSCGLPFC WRYRGGPHLAYTMSRKNTILIQMTFFY NNPCLLYS
9076	22977	A	9143	2	108	GAKCVSDRIKHAFLIKESQRIIVKVLQA AGSQKAK
9077	22978	A	9144	3	200	MGFLHVGQAGLKLPSTGDLPASASQAG ITGVSHRAMPVSGFFCSZAKKCFWBEQL INLDKNSQK
9078	22979	A	9145	405	227	WFFLLGFLLKGLKLPDPPFPAPRVYSDF FDPFFFLWPPPRILIFPPGKFFVVELAG PIW
9079	22980	A	9146	387	220	PLFPGVCGFFFFFFFFFFF FFFFFFFFFFFLOGCERNELIRKNNDN
9080	22981	A	9147	539	220	VINFKHLITRTVQLSFLFFERGSGCLPFR LECNMIMAHCSLNLGSSHPASASQV AGTTGAYQHTQLLPIFFAETGSCVYQA GLQLLGSSNPPWPPEVLGLQV
9081	22982	A	9148	3	141	GGGCGCEPRNSRYTWNATSAKLCLKKK KKRFLKSKCLTPLLKA
9082	22983	A	9149	413	240	FFRCRQDGLILKPOLISNTWSQVILPQ PPKVLGLQAYHADELPHLATWGVLYGLT V
9083	22984	A	9150	395	193	LLEFQCLNLITQPVSCHLIDIKLQMTL SEGYPFLNIQESPFPYRAPLDDPSVZHAR GEILPISLGP
9084	22985	A	9151	1	77	LVAATLVGGTGGGFKNIRRGSGGA
9085	22986	A	9152	365	181	IVDRDPDPCRDADAQRVFTLSARYPTIW VPPGDPAREFFFIQSAPVMLLAAPDELV SAQLA
9086	22987	A	9153	373	251	FKKIFFCRDRALNNSPRIVNSRQTAIL PPQPLKVLRLQA
9087	22988	A	9154	204	95	DYHNSQPGMVAHACNPSLTLRGRWRITR SGDRDHG
9088	22989	A	9155	44	280	AELFGTLMRRDGLSLGGGCKGPKSCHC NPAAWATEPDLCKRKKRSPYLLVVTPPD SSYSPPFFLLLPAPDNNDYFLS
9089	22990	A	9156	2	117	ERLRHENCLNLKRGCSGPGWCHCTBAN ETKQDSISKK
9090	22991	A	9157	3	207	HASAHASADANDYRVRVPCPANCILYV SHVGKAGLNLTLTSSDLPTSSASQAGITG VSHHARTPTV
9091	22992	A	9158	117	267	NRVLLCCPDNPOTPLKGCSSLISLSSWD YRHIDPRLAARSSVLAGGVYI
9092	22993	A	9159	415	167	LEFFPIKAKFFTSPLLEFFFPDPDX KKVFFFPFFFPFFFPFFFPFFFPFFFP FFFPFFFPFFFPFFFPFFFPFFFPFFFP FFFPFFFPFFFPFFFPFFFPFFFPFFFP
9093	22994	A	9160	217	41	SSQIHRDRNRMVRQGAHACNPSLTGCG KGEQITRAQEFKTSILANVVKPRLYKPC

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, /possible nucleotide insertion)
9094	22995	A	9161	341	164	LY FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFVCF VSVELKKQNYSFVDRIILRVBP
9095	22996	A	9162	190	402	ITGTGKHPKCYRNSYSVLFLSKKKKKKK KKKKKKGGGPKKKKNLARGGGEIIFFF WCPKKIFGGGGLKGG
9096	22997	A	9163	108	209	LSVKKCAKNPKGKVPAGIKETIRSHQ DSRDI
9097	22998	A	9164	2	145	KKCGRPKPOPLPRKTRDLCSLVLLYTF PPLSYDPAKSPSARNTQK
9098	22999	A	9165	170	402	TSRCHFPSSLTLYSVKTTTKAPKKSKK KKKKKKKKKKKKKKKKGGPPKKKNF LQGGGGEIFFFLGAPKKKRGK
9099	23000	A	9166	399	113	WRLRWEDCLSLGORGCEPSPCYCTPMW VTEQDQSGSYEGPGRPSSLSKARIPSA AERSMCQPCACVNCNLSVEHLSLYSLAQ QKALYKLINK
9100	23001	A	9167	3	138	SWITGVCHYAWLIYFAFLVETGPHRVQQA DLELVTSGDATTLRSH
9101	23002	A	9168	134	301	EKLITQSHSVTQAGVQRNLNVHSLRPFP FKRPSCLSLSSWDYRNLETVLQETHT
9102	23003	A	9169	201	1	GATILRFKTKIGNVFPKKKKKKKKRKK GKGWSGTESRWNLGSGGSSGLRRRLQA PAGQEFKEKLA
9103	23004	A	9170	2	191	FVPQPLPLGPKRPFSCSLSSGWDYRCTP PHLANFCGFFFLKFFFFFFKKKNFSPSR GRGGLI
9104	23005	A	9171	2	191	GGTESCFVAQAQVQGNLQSLQSPPTGF SETASQTVDPRKVDKPKLRITMFAELP KTIIVTDS
9105	23006	A	9172	3	143	SNFLYVQAGLELITSGDPPALASHSAG ITGVSHRRLQTGIFRAV
9106	23007	A	9173	361	174	VLGIILSSMSEITNFKLQDSGTVAHT YNPSTLGGQGRVIRAQEFSTSLGNTR PHLFKI
9107	23008	A	9174	493	351	LVETGFNHWQAGLELLTSSDPFASAQ SAGITGVSHLALVLIKRKSC
9108	23009	A	9175	1	115	PRKIWIYITMEYCAVKKKEMLSPTIYW MNLDFMLVR
9109	23010	A	9176	286	96	PLFFFRWGLATCLGNSVAIHRDRDHA LQSQTPGLKRSSCLSLSSWDYRRVPPC LANESHY
9110	23011	A	9177	399	237	RNTKWLFFLRSLTSLTGLECSGAI SAH CNLRLPSSSSDLANGIFKDLALLDM
9111	23012	A	9178	427	101	GRTGQGRGAPHTSHDGRPGRDAPRFPD VMAAGKRSSLPKMDGGRAETLLTFQTG QGRGAPHTEDGRPKGDAPHPPDGVVA GQRQSGHFRPRQAGRWEL
9112	23013	A	9179	193	41	IVFLFIYLFCEPVEYGPYVAGAGLKL VSSGLPAAQPHGVITCMSHHT
9113	23014	A	9180	292	119	KITIKIKQILNLSVTEGMLDTEICILP HPITATEYRFPKRAMOTFFPSGTKNSAMH I
9114	23015	A	9181	3	279	ALSPPYSSKCKLGSFNRELSSPSFGQG KSEIKVSAGPRPLRVQGDPSPLPASG GPRCSWACGQITAVSAGVTHSPPLHLH VCCVCL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
9115	23016	A	9182	402	238	OMQHHNLWPTQSLPPEVPTPLFCINLPNNWGYRWPPPPPTNFFFLKGVSLGRPGSV
9116	23017	A	9183	3	207	EPHHVGDGLLELLTSGDPPASASESAGTGVSHRAQQACRFLLHFFGTCTFLSQELS YLKLGRDTIIC
9117	23018	A	9184	3	106	YPHYVKSIVASTFTIISLFTPTTINCLDQ EVIISN
9118	23019	A	9185	110	248	GVLVGSPLRTRFRHSQLABGUBEIGVVTVMVGDGVLPVCVVLVDV
9119	23020	A	9186	925	1132	KCPASAAHPTSEIRISQGSQAQVVLVLPFLKMPQGVDPALWEARAGSGSQGFETSLANNAKPLV
9120	23021	A	9187	399	292	ASQVAGTFTGAHHARLIFPVFLVETGPHVYSQDENF
9121	23022	A	9188	7	82	PCDPFASVSQSAGTGVSHAWOTF
9122	23023	A	9189	1	117	LPISLPSFLPSFLPSLLPSFLPSFLPF FFPSSVTPYLK
9123	23024	A	9190	238	46	NKAFRIKAFVSPSNKRTSFSTFFNNHMKSHYVDQAGLELLSGNPSILASQNAKITGVSHHVRP
9124	23025	A	9191	2	282	LIFYPVDNNMLVRAGLELLSSDLPALAPKVLRFITGVSHHTRPELYQRLLAPATLLINSQAAGTNFPGLSRIKPTQSGHMLQEVWGTSGLR
9125	23026	A	9192	44	136	CLCVCVVCVVCVCSCKOTLMCCFLNFDV
9126	23027	A	9193	469	347	PCPANFVFLVETGFLVHGAGLKLISGLDLPNSDQKFVYN
9127	23028	A	9194	427	238	PPARPFAFFYIEFFVENVFYFGKAGLKLVLISGLCASASPGVITGVSHHAQPK
9128	23029	A	9195	34	178	SLMRYVEFERGRAEWLTPVLPALWEABAQSGRQGMPTLAWDPWG
9129	23030	A	9196	22	338	CSPIYSWNNSTKEERKEBKRRKKRERERKOKERERKERKEREGREKGRGRSGKKRKIONRKKVGLIGSPCIVFTWQAAYCBESGGVWPGGETHTQGLVO
9130	23031	A	9197	3	91	OGLSLGGGGCSFPGSCHCTPAWATERDSI
9131	23032	A	9198	1	203	RTGRNKSIDDTSNFDDFESDILQVPVNTTSPDYKSKDWFLNNTYKRFEGLTORGSIPTYMKAGKL
9132	23033	A	9199	2	144	PTRTMPCCCCCCCCCCCCRCLFMTGVLFTCCHNOFENISGCLPROI
9133	23034	A	9200	1	99	YAAKELVIDHYRPTIENBERERGLNWLVPRLSL
9134	23035	A	9201	3	149	LNAVORMEWQLKVEIDPAGHSLCVNSVPSFYVPMVDVNDVFLVLP
9135	23036	A	9202	284	21	KGPPPLFFFFFLRQGLVLMHRLYSQMTAHCNLELLVSSDPPTLSSQNAETTGVSHCAQPSALITSKPYIGFLHQIQKSLPVTFI
9136	23037	A	9203	1	77	LRLVLSNRQAILLWPPQVLGLQA
9137	23038	A	9204	529	340	GVLLWRQARAGELSLGGGCSLKVVRHCPTAAWTRATPSQKINKLIKSHAVRLTDDEIT
9138	23039	A	9205	413	241	HPPPPELKLFTCSLISRWCHRRAPCPYVFLAETGPIVQAGKHGTYYCCVSLP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSIN 09/515,1 26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
						T
9139	23040	A	9206	33	152	OLQGLSESWGMERCALPGYPVVTINLCRY RSWIEETMRDK
9140	23041	A	9207	70	402	HVDNEALGNDRPLVHIGICKLRASGTHE WVHTRTCAHTMMHTHTICTHCRSPRVV VINLGCTFELPGALKARAYPHNATKP MTSESVGIRPTRQVFKAPRAEQHCSTA
9141	23042	A	9208	46	262	GGIFPAAYRGGRSRLRDVLSRLAAGRR RRGTRRGGRAGGAGGGRVGSRRSPA NARTABOERAVRGKC
9142	23043	A	9209	15	206	FIEPLSERTNSAGAPPASLPPCSLISD CCASNRDSVGVGSPSEPQSDMQTSLNA KVPVSKD
9143	23044	A	9210	475	110	NLLAPHLVLSEKHSIRGVQAFSRCHL SQLPARKENSITPCASGVRRCLALRL NLGLGLHPLSTCHCTPGSEMNVLQLEM OKSPVFCVAIDGSCRLEFLFGHLPL
9144	23045	A	9211	420	132	PPPPNNYFGAGTFFPPPPFFFLRPPPPFF LPKKKKKIFPPRGPKKIFFLKAPPPGFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF LVRSHFILTIM
9145	23046	A	9212	353	87	FFFFKQXFFPPSLFFSSPPXXSRFPF* YLKYPLLPPSFLFFFTPPPPXFFFF FTFLPPPPPPPPPPPPPPPPPPPP FFFFD
9146	23047	A	9213	2	276	FIQLKRRRLCELYEYVLRHPYSYSHDLLP TNYHFFKHLNFIQRKFHMQDAESAF QSPAESQSMRFYATGINTLISPWQKCV CSVSYFD
9147	23048	A	9214	402	276	LSCSLPSSNDYRCPPPKGYFFFFFLF LVKTGPFHIAQAG
9148	23049	A	9215	386	37	GPKKRVCSPFFFTFFFTFFFTFFFRG FTFLQKKTKCNPNSSNKLTLGLQKKKE IQPALMKKNSIQS
9149	23050	A	9216	1	142	KDFRVQWYNBSSIQPPPGFKQSSRLS LPKYWDYRHEYLHCICLQAP
9150	23051	A	9217	402	181	FFFFRFFFFXFFXXKXFFFFXKXKX XXXXXXXXXXFFXFFFTFFFTFFFX FOQKLLFIFYVNIIVTF
9151	23052	A	9218	2	87	SGSLYFGLIYICNVCVCVCVCVCVCYPC
9152	23053	A	9219	420	271	YYCIFRETQPIHVGQAGLELLTSGEPPA SASQSAGITATAPSPFLTFLV
9153	23054	A	9220	139	413	SOYHSRTLQRRKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK IFRRGGGNNFFFLGPKNIGGGGLKKR GGGKKPPPPQIFFFVG
9154	23055	A	9221	134	236	LHRWGPAFLPRITINWQVILLPRPKK VLEQA
9155	23056	A	9222	364	280	STHSLPKYNDYRHEPPCLAKKDAQSFS
9156	23057	A	9223	1	147	TLLPMLSSGTINAHCSNLYASSSDPST SASQSRITSVSHCTOPPLF
9157	23058	A	9224	1	208	AGAPPPASLPSSLSLSDCASNRDSVG VQSPKQAGHLVVRLSQSKRSIRVG VTRSSLILLSIA
9158	23059	A	9225	1	145	FQHVQNGFKILTSGLLPASASQAGIT VSNVRPKTKQNYFTGNTRPM
9159	23060	A	9226	396	210	KQWDYRHEPPYPALNLFIEHSGYGA RAGLKLGLSSNPPISASQAGVPLSHH

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						AQPTP
9160	23061	A	9227	2	154	FHHFGQAGLELLTS SLDPTSAS QASBIT GMSHHTQPRMVFFSNPSSTAQC
9161	23062	A	9228	1	238	FFLLALGIFILHAIYLSIYLSIHPSSMH PSLSIYLSIYLSIYLSIYLSISLSLSLS IYLSIYLSIYLSIYLSIDPLSSAR
9162	23063	A	9229	3	65	RGDLITEPPLPKLLTKVGS
9163	23064	A	9230	25	188	YFTAMNQAMWYVP IVSATWEABAGGLL EPTSSRLRCVIAVPMSYCTSTWAVS
9164	23065	A	9231	44	232	YDLAFNNHVVVFLEFEFEPFSLSKVCEK GALSAHNNCLCDGARLHERRGKKTKK QKTLPS
9165	23066	A	9232	3	195	FPVGLGS PYVVQTGLELLCSGNPPASAS LNARI TGMSSHQVQNPTRLPS FYLGSS IY GSIHAMI
9166	23067	A	9233	380	244	SVPLAKRMFPHVQGASPELLFPVTHSSQ PPKAIGLQARATAPSLH
9167	23068	A	9234	11	101	LLLINTLMFIHLS PILLSLNFDITGTF EG
9168	23069	A	9235	411	226	FFFFFATNSGGGQTSFWGPRNNAAQVAGP LRNKIPTVGSPPKIFPSWETPVF
9169	23070	A	9236	404	262	QQLANLPRLVNSNWTQATLLPWPNQSA GGSGVSHHTQPIFISENIH
9170	23071	A	9237	369	152	HAFVVS IWESEFVNSNWTVTVMQHNL SIPLPDPHPTFRGGGLAMLPRLVSNMWP QAILPPQPPKVLGLQA
9171	23072	A	9238	389	190	RPKKKKKFFPPPPGGKGVFEGAPPPYFL NPIFFFFFFFFFFFLLIYTHNPLIL FLNCDKLYIT
9172	23073	A	9239	330	3	GRNEPPPPPTGAQNGYFGLSQNSPPEF KQFICLRPLPWLEYKSIPTCPNPSFY KNGIFPCWPGWPKPKKKKTSNWVWCA LAEGAGGLEPRMNRRLQSAKAPL
9173	23074	A	9240	122	248	KKKKRGGGLTPVTPPLWEARGGSGRQK IQITLAGGGKAPLY
9174	23075	A	9241	2	286	FFVQTEPHHVAQAALQVSSRDPTSSAS QSVSDITGVSHCAQPVIVSCDDQVTLVQR RQVITVTSLIAFCQVAYPKAKSQWPQSF FFSSPFLFSL
9175	23076	A	9242	2	95	HMKRCSSSLAIREMLIKTMRFFFFFLYI TCY
9176	23077	A	9243	377	293	PLSPRLVLSWAQVILLPLFPKVLGSQA
9177	23078	A	9244	422	147	KKGGTQGSFPRVFKGPRNFFFGPPKK KKNPPPPRGKIFFFLKGPSPFFFFFFFF YFFFFFFFFFFHXYFLGLDLLIYHLS EKNYSFF
9178	23079	A	9245	402	208	TIGRCHHTQNLKFFVEGSHSYVQAGL KILOSTHPSSAPQSGISGVNPAWTE IMPLYSTPI
9179	23080	A	9246	314	168	EPYHGHFDPHHYCYCRNGLIVLPLMVS NSWAQVILLFWPPKVKQLQV
9180	23081	A	9247	3	320	VVQKMLKSSCDOPASGLAVITGVN HHAEPFLIYEDVQSRVTLIRKWDN EQSNRTIFLKKDELTVNRSACKLYTMD INVNSGLWNYRFGMHQCRW
9181	23082	A	9248	22	303	KGSYFSFTYKAQFSCSLARLKCRGALS AHNLRLLDSSNSPASASRVARTDHTK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
9202	23103	A	9270	1	209	PRGVVFDVDMGHSAYQVSACAFNRGQLKV SIYFFSRRLLVVM IPNFCVFSVVVALAYGIYKQDLGLALERK PRNVVFDVDMGHSAYQVSACAFNRGQLKV SIYFFSRRLLVVM
9203	23104	A	9271	379	263	ESCSVGRLKCSGAVPAHNCNLCCLCPDSS GSPASSSRLLC
9204	23105	A	9272	312	3	FRREGLAALQPWWPNKYSSKKKKKKERE RKERKKERKKERKKEDGATADGTSEAE VIRVHPYVPVGGVPLSEGDWNTEDMRAGR RPHAGESQTVMLPQAOE
9205	23106	A	9273	405	246	FTKKRKYLHAPLPHFPFFFTIPNPNFFFF FFFFFNNFFFFFKTKKCEFLYPSY
9206	23107	A	9274	2	227	LVEITGFRHIAQAQGLQLSSSYPPTSASQ SVGITGVSHQPGPSHFIFERKSLGLKTL LCVKVGVRACFALFQGS
9207	23108	A	9275	70	304	NLFLEASTYPSSEHLYLHPTPIVTVRKR LDAMAHACNPGTLGDGGW/LARTPDLKC SAYRGLSKCWDYRHEPPRPVLV
9208		A	9276	2	260	TVFYHVGQAELLELTSGGPPALASASAG ITGVSHHAQPFLLTLVLSLFCNQS FHI SPYRFSTQLNHFNTVLYPLVINISEI FF
9209	23110	A	9277	406	330	PRVLNSWTQTILLPWPVKVLGDV
9210	23111	A	9278	2	160	ELLTSSDPFASASQSARITGMSHITRLK YIVYVSRKSKNIPLKHIGIQSPF
9211	23112	A	9279	1	91	GLTVFPRLVNNSAQMILPFPNPKMLGL QV
9212	23113	A	9280	3	107	LAETGFIHVGKLELLNKVHPHPNAPR VLGLQA
9213	23114	A	9281	336	234	AHYKLLKLIKLPQQAQWUTPVITLMEA EAGRS
9214	23115	A	9282	3	241	DRFPCMDADAQRGINASARYPQNNVT TGDPAREFMTIHATPMLLADDPDLISV QLAQSPWFGALASLGRSPCKRN
9215	23116	A	9283	404	277	IFFVETRSHHIAQAQLELLGSSDPFPYFF QVFTMSLSQALF
9216	23117	A	9284	399	231	HYVAQASLKLLYSQDPPASAFQSAETAG VSHCTWPTGSINKIQNNHRSISM
9217	23118	A	9286	394	231	AFVFFFFFGERGPHHARTVLKLDSSN PPAVVSQASGITDVSHDFLSLYRIY
9218	23119	A	9287	420	311	LNFCRDGLAMLPRVLNSAQAQVLSQP PKVMGLHA
9219	23120	A	9288	398	173	LLSFFLLFFVFFFLFLFLFFVFFVFF LMFKALLFSCHYFPAMVTFKFLSLISGV VRTSGYIMLFSYLLCLKM
9220	23121	A	9289	270	23	TPEQCRGILKFTYISLLIVRDGVLCCS GWPVVAIHKCDHSTLHQIPSLKQASCL SLSSWEYRYAPLHASANFLKVTUV
9221	23122	A	9290	273	46	HLINMPLFTIWTTERLGFYLICFVPLV ENGVFTTOAGLKLLTSDDPPAYASQSA ELIGTSHCTRPICVWVNI
9222	23123	A	9291	424	230	CLPFTTSLSLSLSLSTHTHTHTHTHT TIYMNK
9223	23124	A	9292	2	146	NLFIVETRSHHVARASFPLLSSNPPTS ASQSSRIIGASHRTWPVVF
9224	23125	A	9293	393	202	GRRRKKRRERERKKERKKERKKER





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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
9247	23148	A	9316	3	235	TMVNVAGGFIIRTTLDNSTVQYACLLH HLTKAKASTVRDIDPQNDLTPLRIRSKK HEIMVAPDKKEYLLILVQNPCPE
9248	23149	A	9317	253	71	LEFFFLFFVDTKPHILAQDGFQQLSSSN SPTASQSGGITGRSHQWPPYVHLLTLQ KLAV
9249	23150	A	9318	425	95	CLLFCKPKKKKKKKKKKKKKKKKKKKK KKKGKPKKKKKKQ
9250	23151	A	9319	25	214	VRIDRPFECMDADQREGINSSARYPK NNVTTGDPAECOMIHSAPMLLLADPDE FVSVQLA
9251	23152	A	9320	50	231	GHRPEFGDRDADAQREGIASARYPNWV TTGDPARECTRIQSAPIMLLADPDEFVS VQLA
9252	23153	A	9321	401	226	QNLFINNLIHGCSELLIGPSNPPIASR LAATTGTRHHAQPSKFRNLKGLCAKRA RT
9253	23154	A	9322	410	159	LGSLQLFPFGSKFRSLSPSSWDYRGC SESLRLRHCTPAWVTQDSVPPKKKQIQ RPFPSYGESLGVLRLHLCPSKPSRPF
9254	23155	A	9323	310	25	KWGLFFPSPPKKRGFFQVFPVCPVPV FFPPFFKGTGPDIFLGLPKKKIIFPPPG GKKFFPKRGPPPPPPPPPPPPPPPPPP PSEVSCVCLCK
9255	23156	A	9324	406	289	PSFVHGAGLKLITSGNPSASASQASR ITSISQTRPH
9256	23157	A	9325	1	116	LHSVLLFFVFVCCVCCVCCVCCVCKK YVAGGAPGR
9257	23158	A	9326	2	158	FIFLFTVGLTGLVLANSLDLVLHDTY YVVAHFHVLSIGAVFALIGGPIH
9258	23159	A	9327	3	107	RGCSEPRLEHCTPAWVTGDCVSKKKKK VPEAWG
9259	23160	A	9328	257	2	GFFSNISASVILPPIISRKNLFPFPRVY FGPPKPTFKGPPPPPPPPFLSPLECSG VIMACSLITLPGSSDLPLSASCVMATVS I
9260	23161	A	9329	66	384	GNLCQNMKSMANDNFVREADNGQIGRES LEQCPNTGMLKKKKKKKKKKKKKKKKK KRGGPFLLKISWGGPILQGRGKIFPPFFG GGILTPRGVFWKSPFFWGGKKK
9261	23162	A	9330	1	98	TIIGQVASVLYFTTILILIPTISLISNKI LKWA
9262	23163	A	9331	33	412	NGFVVMARITLHTHTQLCQVQLHLSVPR PSLPLLCWNPVSLVIEHSQPASEKKKK KKKKKKKKKKKKKKRGVFKKKPGAP FOCGENLFFFFFGSLKTRGVFGKNT FWGGEKRPDPDY
9263	23164	A	9332	401	311	PTRVLDLLVDDSVKESLIGYGPTEDSKE FS
9264	23165	A	9333	5730	452	TRSAFRAASNLDEDPREVSVCLSATPFT LSLQKPRILLFSPSVVLGVPLSVGVQL QDVPRGVVKGVSFLRNDSPNNVPCSPK VDFTLSSERDFALLSLQVPLKDAKSCGL HQLLKGPEVQLVAHSFWLKSLSRNTNI QGILNLFSSRRGHILFLQTDQPIYNPGR VRVRFVFDLQKMRPSTDTITVMVENSIG LRVKKVYMPSSIFQDDFVI PDISEPG TWKISARFSDGLSNSSTQFEVKKTVLP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in US 95/15,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion
9265	23166	A	9334	46	324	<p>NFEVKITPGKPYILTVPGHLEDQMIDTQ ARYIYGKPVQGVAVVRPGLLSDGKRTF FRGLSQTKLVNQSHIISLKAEPDQAL EKINMGIITDLQGLRLVVAALIEYPGGE MEAEILTSWYFVSSPFLDLSKTKRHVL DGAFFLLQALVREMSGSPASGIPVKVSA TVSSPSGVPEVQDIQNTDGGQVSIPI IIPQTTISELQSVSAGSPHAPLARIITVA APPSGGPGFLSIERPDSRPPRVGDTLNL NLRAVSGATTSHIYVIMLSRGQIVFVN REPKRLTISVSVPVDHHLADSPFYFAFY YHGDHPVANSRLVDVQAGACEGKLELSV DGAQYRNGESVKLHLETTSLALVALGA LDTAIAAGSGSKHKPNNNGKVFPAVNSY DLGCGPGGDSALQVQAGLAFSDGDQ WTLRKRLLSCPKEKTRKKNVNFQKAI NEKLQYASPTAKRCQDGVITRLPNRS CBQRAARVQQLDREPFPLSCQFASLSR KKSRLDKQAGLQALILQEEDLIDEDD IPVRSFFPERNLNRVETVDRPQLTLNL PDSLTWELHGLSLSKTKGLCVATPVQI RVFRELHLLRLPMSVRECELELRLVL YNYLDKNTLVSVNVSPIVBLCLAGGGL AQQLVPAGSARPVAPSIVPTAAVNSL KUVARGSPFFVGDAVSVKVLIKEKGA HREELVYRIANPLDHRGRKLTIPGNSDPN MIPDGFNSVVRVTASDEPLDTLQSEGL SPGGVASLRLPRGCGEQMTIYLAPTIA ASRYLKTQEWSTLPPETKDHAVDLQK GYMRIQQFRKADGSYAAWLSRDSSTWLT AFVLKVLISLAGEQVGGSPKLGQTSNNL LSQQQADGSPQDPCPVLDRSMQGLVGN DETVALTAPVTIALHHGLAVPQDEGAEP LKQVREASISKANSFLGEKASAGILLGAH AAATAYALTLTKAPVDLLGVARNLMA HMQSTGDNLHWGSIYSSQSAVSPTAP RNPSPMPQAPALMTETATALLLELH BQAPMAQAAAMLTRQSGFQGGFRSTQ DTVIALDALSAYLIASHTEERGLAVTL SSTGRNFKSHALQNNRQIRGLEELQ FSLGSKINVKVGGNSKGTLLKVLRTYNVL DMKNTTQDQLIEVTVKGHVEYTMKANE DYEDYEYDELPAKDDPDAPLQPVTPQLQ FRGRNRRRRREAPKVVEQBSRVHYTVC IWRNGKVLGSGMALADVTLISGPHALRA DLEKLTSLSDRVVSHFETGPHVLLYFD SVPTSRCECVGFRAVQEVVQVLQPSAT LYDYNNPERRCSVPYGAAPSRLRLATLC SAEVQCAEGKCPQRRLALERGLQDEGG YRMKFACYTPRVEYGFQVKVLRDSRAA PKL*ETKLTQVLIHFTKVKRAANQMNF LVASCRRLRLPGEKELINMGLDGATY DLBSHPVLLDSSWLEHPSLELCRST RQRACAGQINDELQEVGTGCGQV</p> <p>SKYLPVVITFQHEIHWGNTIQTISDNLV ICCPNSAVTQSRLLAASSTWAGAMSSS SCLGLSSSCYKHTPPCLANFAVETK LYTMIPLGIS</p>

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
9266	23167	A	9335	338	178	EVD IAVSHRRKQAPNCLLKKCKPHNNCL NLEGGGSSSELKLCYCIPAWATDQSL
9267	23168	A	9336	396	254	KLSTDCYTSKELINRHPTWEKIPANYAP NKGPTSTIHSSCLMPFYLF
9268	23169	A	9337	454	359	SSWDYRHAPPCFANPVFLVETIFIQGEI GLL
9269	23170	A	9338	540	328	LKKRGAPRROVLFPFTRKKKFFSYKKK TKERVSPFLFVAPGCIQSGKKKKPPTKKK KKKKKKKKKKKKK
9270	23171	A	9339	21	209	ASEFFDEKLYTKANQNTTRQWNRTETS EITPDIIYIGIQLVSNWPQVILLPWPVK VLGLQA
9271	23172	A	9340	345	2	KIFFFLIYILFFPFFPFFPFFPFFPFFPFF FFFPFLNRMFLMENPIKGRGHVKGPLG QARDHDSGRNRWRBQCRASQLPGVRR SILQVQAGGPVHIRISGLQDARQGRVGA
9272	23173	A	9341	15	252	LERVIRQSAALTDSEFNILLILFLIYLF FETGSPCVSQAGLKLGRDPFVSASQS ARIIGVSHRAQPALTDFFPSISF
9273	23174	A	9342	484	276	RHAPPCQANFFVQTRCHVAQSGIKLIR SRYLFASAFQSVRITCMSHCARPLYFLM FKRLQYLKSPTKS
9274	23175	A	9343	464	326	LIVETGPHHVQAGPELLAPCDPPAPASQ SAETTGMSHRARPANFV
9275	23176	A	9344	486	280	SFSHSHSCSLPSSWDYRCTSSHLANFPF KRWGFTLLPRLILNSWPQVILLPQSHRH EPLCLETILKIANV
9276	23177	A	9345	276	179	DRDFTMLRDLVLNSPKTILLPLPPLKIL RLQS
9277	23178	A	9346	45	143	RWNRSQENCLNLOGGDCSEPSLCHCPPA WATE
9278	23179	A	9347	229	73	PPPHMIFFFFFFFLFFPFFPFFPFFPFFP FFFFFFFFSRLQSVYCSSVLNKNVD
9279	23180	A	9348	391	139	IPSLKRSSSHSLAKCNDYRHKPPQVTFP SFLANRYIATKFFFLSTPLAANSKYWYLV FLLSPSSKYLYTPISFLFLTHNVSSSIF
9280	23181	A	9349	53	191	IYVTVIYSEVSHAYNSSTLGGQGRIT GAQEFKTSLVNIAKPLLY
9281	23182	A	9350	373	235	EGEELLEPGVQGCSESLWCHCTPANGTE QDHCVSYNNSNTHNNNVY
9282	23183	A	9351	476	82	YLATLYLPTLYSLIYLPYLYLPIYLYL GSHYLAQGLKFLGWVGINGSCL
9283	23184	A	9352	286	142	ELQPMRPGWRHSQTSWGLSLLPRLIS NSWAQVILLTWPPKVLGIQA
9284	23185	A	9353	3	102	FFETESHVARLEYSGAISAHCTPVKIL YLYT
9285	23186	A	9354	3	270	TAGAPPRPANFCIFSRDGVSPCWGMSR TFGIRCDPPASASQLGRIRHENCINIG GEGCTGAILAHCTSTLRAQAILQPPSC PAPQ
9286	23187	A	9355	1	112	GGGSAHCNCLPGSSNSPASTSQVAGIK GVSHRAPN
9287	23188	A	9356	1	63	VALIQAYVFLLVSLVLDNIP
9288	23189	A	9357	244	140	QRRHTHTSHYTYHTHTHINRKIPILT ILKCLIA
9289	23190	A	9358	464	181	LGAGGHTGILFSLGASWLGVAQMLAP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						APTSTTSLPTSTTSTTITSTTSAPIS SNLHKKKKKKKKQKKKKRNDTRQD TITKIHGGGSL
9307	23208	A	9376	69	160	ETHHTHTHTHSHTHTHSILPERFFCVIN SL
9308	23209	A	9377	336	199	EGITASARYSKNWVTGDDPAREFPWIOS APIMLLADPDEFVSVOLA
9309	23210	A	9378	321	128	EPGFPMWASLAPITSSILQVIRLGLPKCN DHRREPHPATHSLYSGPSVQNGEREK INPIIKMG
9310	23211	A	9379	440	286	SSDPSASASKSAGPTGMSHETQLTSSYS EGGCLSYLVFLVLV
9311	23212	A	9380	392	154	KGSSPLSPPIISLAGGKPPPRKFFPINFF FFFNDRVSPCLPRIVSNWQAILPPQ PHKALGLQAYATTASFIFLIVTV
9312	23213	A	9381	403	178	GRRHETCRDAHALEGTIFSAPYKSNWE TIGDGAREWIMNSAPMLMLADPDRFVS VOLA
9313	23214	A	9382	303	206	DPVSTKICSLQPPFPFKRFSCLSLPSS WDHR
9314	23215	A	9383	215	116	SNNFVCCCCCCCCCLRWSTLSPRLH SCGTW
9315	23216	A	9384	2	285	ARHLIAQLSGGATLAISTIDLPLSTLIIF TLLLTLELVAVALQADITLLGSLY LGDNTYKKKRGAAFEETKTSAGMQSK NFFLGLIAWR
9316	23217	A	9385	12	123	GVENFLPLTLHTQTAHRTHTHTHTHI HSDPMFY
9317	23218	A	9386	3	230	KCWGYRCEFLRLAPLCRFFTPPGISLTS GEALLSNASALAEVRGQCLCPPTPLPT LIALTLTLLPISPFILIL
9318	23219	A	9387	590	396	ARVQWPDFLGSLOPPPPGKFRFSCLSLAN SWDYKCAPPCCRADFCIFSRDGLVCSWPG WSQTPYLE
9319	23220	A	9388	224	79	GLGPVGHACPTLWEGEAGSGRQSTIAL PANTVKPRFLKRKKKGKGG
9320	23221	A	9389	249	72	LVYLIVKKLLFPVHIRTFNKIDHMGH KTCNLKQMTRELQSVFSDYNRIKLAS NH
9321	23222	A	9390	400	254	LRQPGSTNSPVASASRVAGITGTHHTQI IFVFLVEHVVLACNPSYSGG
9322	23223	A	9391	3	64	PPQKSDPPYKLVFVHDSIL
9323	23224	A	9392	266	106	LDANFLPVLSTGSPHYATVGLLELLASD LPTLASQRAIGVNNLQNFVQWPF
9324	23225	A	9393	430	348	PKQKQPPKQKSPVNNLQNFVQWPF
9325	23226	A	9394	481	311	LALSBRKRTIRVGVTRSCQPSLISLTG KNSLTPGVQSQKHSPPMFLAYSVCIH
9326	23227	A	9395	3	136	VFPRLVLSNAGVLLCMFPKVLISLQAC TTRPSHPLPLMSKYY
9327	23228	A	9396	143	347	NFVFLVETREHVQAGQLTLLTSSDDPAS QSAGITVRPPEILTLKRTHFPSSGILGTE GMVIMAYLLKV
9328	23229	A	9397	2	231	LELLTSSDLPASASQAGITRGSHHARP SFTFRCVIHLLENFMRGARERLHFYCR WVIRRLTTFGRGYSPASD
9329	23230	A	9398	383	200	QHLYNRLSLAQWMPVPVATQRAEAGG LLEPRSSSLQCAMMLPVSISICTLAWATH

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
9330	23231	A	9399	3	416	REPHL GFLHWGQAGLKLSTSGDLPTSASQSGAI IGVSHRAGCLKSIYLTFFPIRKKFFVQMSI CDPKVELEGKLGFLSVPLSQSLILHIVN NFFPFLSTGSPFGWRAMEKFGLLIAPLA SGVKGLPLPLPRENLGWRSPILPA 9331 23232 A 9400 400 151 FGYQVFFPLPPFLKPGKGLFFTPGLKRN PPFFPGLKIFSPKRAPPTFFPRKGLI MLLRLVNSNWAQVILPPPPPEVLGLQA 9332 23233 A 9401 324 154 FFFFFKKKKKLLFFPPPPFFFLPYIPFF FFFXFXFXFFPPPPPPPPPPPPPPPPPP F 9333 23234 A 9402 413 312 PKLVNSNLQALLPFPFKVLGLQARAT ITQPK 9334 23235 A 9403 363 3 FKKKHPCLOGAGVVFVFFYDPPPKKIF YFPKKIYPLSPASSFFFFFLKPPFFIF PPPPPPPPFLNRWFLMNFYKGRGVH KGLGQARDHIDISGRWRWRQCRASOL PGVRPRV 9335 23236 A 9404 401 82 SELTHDPINFTGGYIYKKNKNSVCPDI CTPMFTIALFSIAKINQPKLSKRITTI FMFIVTYSQLFCINYPILPYPFFPALP SSINHYHTLLYENILLDSTYE 9336 23237 A 9405 382 219 WARMHGLVPTSPGGAGSLRPGKRRV QLTQLSPFLSSLGKGVPLPKCKGN 9337 23238 A 9406 3 195 YLYSIVETGPHVQAGLELLISREPSA LASEASITGMSHSIQPKSAFYIQTIPET FWQPAFK 9338 23239 A 9407 371 1 FRRLTGNRLNGNGGCEPRILCHCIPA WETRAKLGKKEERKREKGTQYNNMY RMYLEINLTCEPASPCKMTQRLVLS NPSPTGTFQICKQFKFCCPALRVSIY LIMGVFEYCS 9339 23240 A 9408 326 229 RQGLTMLPRIVNSNWAQVILPFWPFRVL GLQA 9340 23241 A 9409 81 231 LESASFPDGRVARTCNPNILRGCAQMA WAQKFTSLGNMAKPCLYKIK 9341 23242 A 9410 367 256 HFGWENWLVSVPTLREAKVGRSLEPRS LRLAWDTWG 9342 23243 A 9411 2 192 VPLVEMGLHWQAGLELPSIGDPPASQ SAGITGVSHHAQALTFLINIPINSHPPK ACCSKQL 9343 23244 A 9412 3 83 KNCINLGGGCGSELRLCHCTLTWATE 9344 23245 A 9413 371 301 EDHPRHVLRLGRYIVRLVVRMH 9345 23246 A 9414 486 337 AGLELGGSSNLPAITSHIASITGMCHHT WLAVYFVCAFWGLDLDCLAF 9346 23247 A 9415 378 254 TVAKSIDLSSDPLTSASRVAQPTGM CHRWLVVFFVC 9347 23248 A 9416 160 309 VVRYSNPFLLPLFLYKSNPFIYVCC YCCCCCWRQSLTLPPLKRGV 9348 23249 A 9417 162 339 RPSSCFRFLGDSVPEKALPMKARPEKSR RSQVSNLMPVIPTPEAKVGRYQARSLI PA 9349 23250 A 9418 1 147 GGGCGCEPRSCHTPAMATRVKGLPKK KKKINFLVPPPIPLKSKTGV 9350 23251 A 9419 283 126 KMYKGAQWLIPITPAFWBAKERGLLE VRSIRPAMATEQDSTATNKNRNF







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9395	23296	A	9464	104	336	NHVSQCBEIPLFDEYVIFSRVAVSMFVW DABLGSDIYLDGKLKNSFLLSPLGFFFF FLFGKKVFFFSQNGGLRPGQ
9396	23297	A	9465	410	0	LNLAGGGCSEPRCLCTPANATE
9397	23298	A	9466	254	61	KKKKDAPFTIPLYPSSQNLPAFTQMDPD TNISQQLTWTVLQGFRRSPPTFLDKPF KQTSINFA
9398	23299	A	9467	403	255	PAPQLGGPMMPMMPAPSSNMMPMGCAP AMRLPIGGDIINLCVPTQLSP
9399	23300	A	9468	1	1428	PAKFDLALGATKAVGLASTFEMHTVAF RDLFPRMVSSTCYRAETVQSPRGLY RVHHPTKVMPGVGTGPLEQSSQLLEEF LSLQWEILTELGLHFRVLEMPQTEGLPL AYRKFDLEAMMPGRGRFGEVTSASNCTD PQSRRLHIMFQTEAGELQFARTVNATAC AVPRLLIALLESNQKDGSLVNPALQS YLGTDRIITAPTHVPLQYIGNPQRKPGI PGCPAGPRVGYKALQWPAPRIASPVRP PCRPEGQPLSCCCGCSGWRGLRLAE VVTEVLTVGQVORGFTALLHKELOSTE PHGCASTEBKILLDFFKQBAQRSS QEVDRDEEEVAEERTHSEVQQAIRMQ GHRQLHQEEDDEEEKERKGRPMETFD LHQHLENGELQKRVASKASDKETAQF QAEKGVVVLQDRLSLMQAERGGERR FDLPIHHHHHQPEARTQEKASERE
9400	23301	A	9469	265	170	GTESHSVTQAGGQNLNLSLQLPLPGPK QFS
9401	23302	A	9470	289	110	ROLELASPLSFFPSPLSFFPSFLESFL PSFLSFLSFLISFPLPSFSPISFSLSL FFE
9402	23303	A	9471	67	210	TVTIGQALTEAYNFTSLGRGGQITRQ DFETTLVPGDLNFSRVLASS
9403	23304	A	9472	2	186	TSLNROAKNKVEKTDKYTEVLKTHGILL VCTQKSCSFLKNNKAMGLQANAPARK VEIRC
9404	23305	A	9473	417	265	FLSSFLFFPPPPPPPPPPPPPPPPPTV
9405	23306	A	9474	430	120	ASQKKKKKKKKKKKKKKKKKKKKGGAL
9406	23307	A	9475	1	150	PTREVVQAGFVLSSGNNPPLVYSQCFRI TGVSHRAPHLLNLRAPNLPVL
9407	23308	A	9476	404	109	PPPLFFNFGPPFLVEAKLHIVQAGLKL PTTSDQPDASQAGPTGVS TRAQPTLI TLV
9408	23309	A	9477	391	235	PPFFFFCRDRGLTMLRLISNSNAQVIL LPWSPFMGLQARATVSGLNKRYL
9409	23310	A	9478	438	277	KRAPFFFFCRDRGLTMLRLISNSNAQV ILLPWSFPMGLQARATVSGLNKRYL
9410	23311	A	9479	399	279	PPPEVKNPFPKKNGAFKKKNISPPPG RKXVFFGDP
9411	23312	A	9480	247	26	LKAGDSRTVLGKRVHSGPFSLLFTFQ VSCRDSGLTVLRLVLSRPOAILLPQL PKLLDHRCKPPHIANHG
9412	23313	A	9481	2	176	HAPHPANFLFFPEEKESCYVTQVSTIKLL DSSNPALTSQSAGITGNGQHGPMNCL SG
9413	23314	A	9482	2	178	HAPHPANFLFFPEEKESCYVTQVSTIKLL DSSNPALTSQSAGITGNSHGPMNCL SG

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9414	23315	A	9483	2	151	GRVGGGPELALVLLDQEPVGTSDHRDA TQIGFQPLMSDLGSGTGSTEGA
9415	23316	A	9484	420	325	FFVFTLETGPHHVSDGLDLVTCPPRPP NTFV
9416	23317	A	9485	400	104	LPFFLPLPPPPPPPPPPPPPPPPPPPP PGLNFTLLKLKFNPPPPPPPPPPPPPP
9417	23318	A	9486	117	280	SSTNQANNCPFFFKRGLAILPRGALNP WAKGILLPWPFGKLGKRGGAIGPQQK
9418	23319	A	9487	76	353	VLAWTLFCLTYLDDLPLLPFNKRAIR KKKKKKKKKKRGNGKKKKKKTPWQEK AGLFLGDTLYSRGAVLNKSGGETPHET PSGGIMPR
9419	23320	A	9488	3	122	HASERIVPLHCKSDLGQVLLAGTASLQ DPSFFQKSPPP
9420	23321	A	9489	1	155	PTRPVTCGAMLAHCNLCMGSSSLAS ASQVAGTACTSTPDPFFPPPSL
9421	23322	A	9490	3	212	BTGPHHVGLSGPKLLTSGDLPTSASQA GITGMCHCVMPQFAYFCLLLVYLDLKF TIIMLVCLLFYD
9422	23323	A	9491	2	163	ETLFRHVQGVSEPLTSGDLFASASQA GITGVAMPSPWIKFFLAFYSCINC
9423	23324	A	9492	474	296	SQAGTADCLLPLPFGSCFFPTPCRAAL VPLPSFSPSARIMPQSLHQLLPLPGTCS SCT
9424	23325	A	9493	7	151	LCAVEFVYMPKPAHEBARAFSRGPVRY APWTASSSEGRDDMGQFRA
9425	23326	A	9494	52	363	TTAFSLSVFLFTFTGELFVYVWVGTLE TSFISFFLFFPFSFLEKDFSPSAGRFPW NFGLIQPLASGVGGLSRPNPFSRWELRA LPFPFGGLGFPPFWKKGGPG
9426	23327	A	9495	383	118	WKPFPWFGQVGTPTPCPGQETPLMK KKKRGKGGLPQPPSPGGQGETPLTP APKQGEIYPPPPPPPGGKKKSLQKKK KRIR
9427	23328	A	9496	554	419	FFPETKPCVSQGVLMRDFGSLQPPPS QVORDSPCQASQVAND
9428	23329	A	9497	428	281	GSYVQLTFKPYFSIYIVTHLRLVLYTH IYVVYHICIKYKGYITGSVLA
9429	23330	A	9498	144	16	KVKKKVSQCGIVAHNCNPSITLQGRGR IANGQEFETLSLQKN
9430	23331	A	9499	2	155	NTALIGSSDPPVSAFVSGIRGVHHHAQ LIFPPFPKRAWFNPPGGRKGBE
9431	23332	A	9500	2	184	FTYGRDSLTMPLRLVINSWFOAILPFRP PKVLGRCBEPHPLASLIFYRDLFTIG LRSV
9432	23333	A	9501	465	153	PHKVFLNRGPFETPQGEISRGEWKIRPP PDRERSRPFHRRGGPGSPPLRQGPFPV FSPWPPWCPPPKKGARPPQKGFYFPPPP FPNPPPPPPPCFLFFFEIV
9433	23334	A	9502	429	11	CRTLAGADKVCVCVCVCVCVKAPFPI SYSCHLVPSDLLELLGVQFKCWVHGLSF LTCFPPSPWPKGQKQPCSWGLGCLL FACKLAGARLTQTLGIPASGPTWATPL GSCASVLRLLPGGSEKUTDLKVSVLG
9434	23335	A	9503	436	202	LPQGYIFQEGEVKTEKPSLLRENNFSS NTFPPKKNNGGKPHIPPPPPPLKKGKGV FTIPKFPADPRPKKKFPKKKKK
9435	23336	A	9504	3	112	SPDLSSSDPPALASQSGITGVSHSHG

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						QRVYICNM
9436	23337	A	9305	426	208	VGHNLVVRPLSPSPSEKRSIQGVTRSSR CRISPISLITRKGNSITPFASRVQCLIL LRLARAPTDLRPLSGTP
9437	23338	A	9506	441	189	CPANFFVFLRENGFHVQAGLLTSSDF PASASQSAGITGLSHCARPTVGSVDVLSL PSGQQTALTGPFMLGSTTVHSNAATA
9438	23339	A	9507	117	278	NKALLCHFGWNHLKAVNRLGMEHTCN PTTLGGQGOEPFENLGNIGRPHLYK
9439	23340	A	9508	3	126	FFVWHPFHCVGKGLRLITSSGLFVLAS QCAGITGVSEKI
9440	23341	A	9509	421	134	FIVERESHHAQASLELSSSDSPSTAS QCAGITGMSHCARPCYTSFFLHRHNM ATPTKLEPTLASASQVWVCLYFLLPST SKGBIPTQLV
9441	23342	A	9510	2	200	POPTTFVPSPLPSTPEPPAFYPRLPFST PASRLLPQPPAFYPSACHLLPQPTTFYP LSGNARLHL
9442	23343	A	9511	414	204	ERDRKFERKYEGRKERERRERKREGRYK KKERRKEGRKEGRKEASKGQRVVVIMVD T
9443	23344	A	9512	1	211	FHRVHGAGLGLLTSGDLPASASQASARIT GMSHARHRRHGFDNLSCALAPSTPLW RRHRRRGHPTVPEK
9444	23345	A	9513	390	265	VPLVEMGFHVQAGLELLTSGDLFPLE SQSAGITGVSQQFS
9445	23346	A	9514	438	180	IGFRHVHGAGLDFLPLQDLPLSLASQAR ITGVSRKAMPAMAFVNCGAGGSVAMKT TRGHSCHHIGIGGFPAISLLQVLSAGS L
9446	23347	A	9515	126	11	RHLDFPLSLGLAMLSRLVNSWQVIFQA WPPKALRFQV
9447	23348	A	9516	2	249	FLHVQAGFVPLPSTDFRPHHTPQSSGI TGVSHRTRPLRCYFLRLANIPLYVYAY ILFIHSVISGVYGGCTAHYCHPREKV
9448	23349	A	9517	403	37	PEGALVPQKIKKKKKKKKKKKKKKKKK NIKI
9449	23350	A	9518	406	140	PHYNHTFVYNGVRLLEDLQWCLBLTVD REPLASNDFLVGVRLGVGTGRIPSPLIT CLKASCLFYSYHSRPTQSSSVMTVVF FPFS
9450	23351	A	9519	3	75	GIEWNVGVNRVNRPPRQDIT
9451	23352	A	9520	183	6	LTLHLITSLALIGINVAITLQKNSGSE RECLRLVNLVNSWQVQILLWPPKVLGS QV
9452	23353	A	9521	89	339	LQCLQKSGKLEPGMTYTLIDADVNGN ITSVQFIWKHLLFEDSQNKLGAEVMVIT SGKYGYKSTFCSQDIMGPHLLQMLKPC
9453	23354	A	9522	3	329	PSLMFPWLKISFPGRPRGRQTYRYQT LRKKELFNYPNTRKRMENVFHALGLTE ROKIWFQNRMRKKKKEVDNLBEAQN EBKVREKQIEKKKKKEKKEDND
9454	23355	A	9523	1	156	AKTSFNVNVEIFPAIAKKLPKIEPQNPQA NSARGQVDLTETPTQPTNQCCSN
9455	23356	A	9524	1	272	AKNSFALLGLLYRSHLYSSLLCLQRT IISLVIAATLITANTSHLLANGPLIALL VFAACEAAVGLALVSIINTYGLDYVHN LNLQCC

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9456	23357	A	9525	1	62	GNDANVCINDMPKLAHNG
9457	23358	A	9526	1	111	GDITHNNNRQRGRDICYTLRQTRQNTKQRIDEPEAL
9458	23359	A	9527	427	340	IPIGNIMSCDSHSHHLEVMQAQNAAPHD
9459	23360	A	9528	439	27	PRRTDKNLTVMENIQDGHQVSLLSGBLTVQDRASIIQRFDGKKEVLIPTNVCARGIDVKQVTIVVTFDLFVQGEEDPYETIYLRIGRTORFOKKGLAFNNIEVCELPSPKIQALFDGRNKKLANRVCIOQAMED
9460	23361	A	9529	1	236	REVLITTNVCKRGIDVQVTFVFNEDLPVQGEEDPYETIYLSIGRTGRFGKKGLAFNNIEVDELPSLMKIQHFRXS
9461	23362	A	9530	437	240	QQVSSARPEPEAGEVSPFVGVGWNNSWAFKYGPNPKQSGPEPKKQTVSFLLRKEASOPRO
9462	23363	A	9531	413	260	LPDQVVKVASPSGLRSTSTRYGDEPERLKLLESILRQQAKRGASLSVRIENV
9463	23364	A	9532	431	260	ASSGQMFVSVQQAAPVWRDLPPFGTSLRGGQIYDNLSPRPPOGIVAPPGGRGNINLIG
9464	23365	A	9533	2	134	IHGVCVHMCVCAQCVVACVCVGGYDGRIFLALSGSTVSPMWNIM
9465	23366	A	9534	419	53	LLLLTNGDRQTREREIACACQSYFDAVVVGQRREKPAFSPFYCCNLLGVQPGDCVMVGDITLTDIQGLNAGLKATVINENGIIVPLKSSPVPHYMSSVLELPAQLLSIDCKVRMT
9466	23367	A	9535	439	109	NCIVTIDSTPVRQVVEKVALPQKKYGAKVTPREHEILYGNRSGIKQCKYDERKKNAKISSLEVERQQQKVLACIASRPGCCAPADAYVIEGKLEFSLRKKIKRKK
9467	23368	A	9536	1	185	NTTSSHHPTPCILVLYSCTSTWTHLTHTHTHTHVVRVFSYIPSQDVKEGCIPAPSVFSW
9468	23369	A	9537	168	280	NPNIRLITSCCCCCCCCWSSPYNVNRLRLTGFTFP
9469	23370	A	9538	142	324	KIVKMGFPFHAGQAGLELLTSGDTPOSTSAGATIGVSHRSRARSIFLYPYLPSVYLPHRRV
9470	23371	A	9539	3	139	YIGGNGQAWALMPGKPRNDYLSPGVQDOPGQHSPTSLQKGFEN
9471	23372	A	9540	383	318	MTQNNIQSYPIGDEESES
9472	23373	A	9541	372	207	YGLNNCRQCFRQYADIGFKVGVCRRTPCCLGREGCGGYFPRERQTRDSSLW
9473	23374	A	9542	2	360	ARGDDHRSRDRGDVLEQTERLQEKVRSASHSEKQNLFLVIFQVIMILTEHLVRCETDGTSLVTPWYKNCIERLQOIFLQHHQIIQDTHVTLENLLPTAELDPHILAVPOQFCLA
9474	23375	A	9543	379	75	THLQGFAMSHGSAQVKGKGVADALTNAVAVDDMPNTLSALSDHAKLGRVDPVNFKLISHCLVTLAAHLPAEFTPAVHASLDEFLASVSTVLTSKYK
9475	23376	A	9544	380	36	RDLNVRMKSMPATGFCPTALMGMPNSIFDGRVAKLPFTPLSYIQGLSHRNLLGDDTDCSFIFLYILCIMSIRONIQKILGLAPSRATKQAGGFLGPPPPSGKFS

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9476	23377	A	9543	304	92	SKSRVINNTLRSTRKDTMITLNTHTSLIA NIVFLAIIVFTACRAAAGLALLVSI YGLDYVHNINLLQC
9477	23378	A	9546	394	108	KEIDPSLVQVTDADDAGNYSQMYQTKSP FWASRPSDQLKILVTVPGTSSNYSIG NFVRLGLAAVIVVIMGAFVBAWYSRNV SPGESEAFKPE
9478	23379	A	9547	1	335	GNVAVGLNLHRINFPDKYHFGYFEDGMKH YHLHRNQSPFCFTVNLDKLRLFSBQTRL NAAKHTGTAPIIDARSVYKVLGKRGK LEKQPIVVKAKFFGLLFCFRIWILID
9479	23380	A	9548	326	188	NELKWTIVAKSNPSILGGLSGRIAGAQ KEFTSLGNIITPCLYPKK
9480	23381	A	9549	381	152	VTLLISLILLQVVIQVGLVWVARLNNE VRKQRLNQLNNAATILVFTTVINVPFI TAFGAHKTGFLAARASRNL
9481	23382	A	9550	170	65	IHRSEINKKKFHLKGGINLNGRDYIFSK AIGDAEW
9482	23383	A	9551	544	361	RRLAQENRLNFBGGGCSKFRSCCTPAW ATBQDSSSKKKERNLKGNTVKSVPPLP LTSHA
9483	23384	A	9552	369	181	GVLGATSGDMQIHTFGSMIGSITGMVS ELGYKFLTVSTADVMQITLNLHLFSSHS HQKKKSY
9484	23385	A	9553	1	516	SLVHVVEPGQALARRLKFPFQVRFLYTG RQRPBEEAAEPQABFVSTPELAAQSDFI VVA CSLT PATEGLCNKDFQOMKETAVF INISRGDVVNQDDLYQALASGKIAAAGL DVTSPEPLPTNHPLLLTKKCVILPHIGS ATHRTNTMSLLAANNLLAGLRGSPMPS ELKL
9485	23386	A	9554	386	56	LFACVLRMQFASDGDGIGGVFLKTKH GBQQSARENTFVLPSQRVNAHVPEDGS LTCLQAGVYVLRFDNTYSRMIAKLSYT VEVLLDPKASRETLQSLKMRPSPPTQ
9486	23387	A	9555	375	150	IUVGKTSFHVSIPLSLFFGGLVLYDLLQ HILKQSKPRILPSFFPHGNSIHTQPEV ILHQTHEEGTGRGFSFLA
9487	23388	A	9556	3	354	CLPTQASAMVDTPPPALLFPCLSLISDCC ASNEQGSVVGIGSPBGAGYNFLVCRLLR PLRKHSIRVGVQTFSRCLSPPSLIRTKG NSLTPCTSRVRCLALLQLTSLKLPHP VPSV
9488	23389	A	9557	463	40	PIKVRDPRPVKPPKQKRSIKEMPTTC DRFNGVSPYMSKRILTYNQINDVIKEINK AVISKYKILBQPKSMNSVTRNLYHRFI DBTKDTKGRYFIVEADIKETTLKADK KEHVLNLIRHCRRLSESVRGGLTRVI T
9489	23390	A	9558	338	104	NFKKKKKRRTKKKSLTRERKGRGANKKT FRGPKKKTGSGNSRSPGKOHGAKKEG ERRRPPKKKKKKLLARYDFTCL
9490	23391	A	9559	1	152	NTCVVCVYTGFCVAVQVAHRLSSSLNP SSASQAGITGISHAWPGGFF
9491	23392	A	9560	517	238	SGPGESVPHPSAVRTPAKKPGGQCLL QSAFPLWCSSERTTWAERKLNTEYFGV SGRFLGRSSRGGRGGRGNGTPRRNPT SLRAGTGV

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9492	23393	A	9561	709	280	NTS FALTAPCGRRPGRIEPMQCARVPAP SSACPAWQLPSLCRLSTVPAHPSPAAH QPCELSQHHRGGLLEPALPGTRQLCSKRT WHRCVRFLEPGAQAGELGFAACATGRLEP VSHSTDMQAPGLTSLHCEPHSTARGGT ATH
9493	23394	A	9562	3	130	YRGFCHVQAGLELLTSGDRITSASQSA EITGVSHRAQFQMS
9494	23395	A	9563	409	160	NFGVKRSFCLSLSSSSGGYMSNPCLLAY KKKRRFLKDGGLTMLFRLASNSCAQGF SHGLGQSWYKHREVLTAQFLPFL
9495	23396	A	9564	1	241	GICLGSHSGGAGGTSSCLSPYSNTLHQ NLLSTTKPPFPVPSVTGNGLEPMDSGVT SGLGKMLFLYYYYLLLSQNTPOS
9496	23397	A	9565	2	215	THMNGMNGMNGMNGMNGSCVRAVTPGT SSPHSTTCGHAVCVVCVVCVYTCARHVL ALFGVEKNMYFLWKA
9497	23398	A	9566	244	117	DHQLNNSVTFISFSPVTKARNRKKGL NPDSSMETSDFDF
9498	23399	A	9567	414	77	FGG/FFGTLVFPFWLFPVRVFPFFPAFL GELSPFFPFWKGLAPPLNFPFSPGQR GFPSPGGKGRFLPRPAGFPGFVAKPPF RPPGFSSTSDCGGLPFFFFF FKKKV
9499	23400	A	9568	418	198	FPVSLTEVI VSKSHKELVFWNMPGLE HPEGDNNYMEFLEVLTEALERVLVVRGG GSEVITITSYPTLNAGA
9500	23401	A	9569	549	415	ROENRLNPGGRGUSEPRSCCCLAAWATE GDCLKKNINKPSETEK
9501	23402	A	9570	546	1	KLECRGATTACHSCLNPGPGDPPTSATO AAGTTGTC
9502	23403	A	9571	415	215	SRLRKITYIYNYCVCVYVYICVYICV VCVYICVYICVYICVYICVYICVYIY MHEPTFFPSI
9503	23404	A	9572	374	138	LAASAALQELFKRISQFTFMFRKAPL HMYTGGMDMEFAEASNNMGL/SEYQ QYQDATASEGEFEAEAEVA
9504	23405	A	9573	370	233	GSPFVRSVHSGVSLGTQVDEGVRSGS KRMVAPPGGRYNTLS
9505	23406	A	9574	3	399	YSSPGFIALALRDFCAHKKPSNNSTSP AQGHPARAQOQPOOQPPSHLGSIDLRF HVAHTRGALHGAPAPAGPAPGGSGGV AASMCAPRPRAGGTGLSVLTASHPAS AGCAHRDAYVCAPGRAVF
9506	23407	A	9575	314	48	SILPHSDPERCFSTQPERGTHTTAAPLD REARAHNNITVLA TELDSSAQASRVQA IQTLDENAPOLARFYDTFVCDAAAPG QVSN
9507	23408	A	9576	505	264	IFVVEHEFHHTGQAGRLTLTSGDMPASA SQSAGVTMSHCTRPDTFFNF KCLPGAV VTFLLCOMQVGRDELSDMWAHS
9508	23409	A	9577	508	314	FAHWKGLSNFSSYLKADFTIEQ/LSL WQVPDGFIFINERFKSTTVVLNNAE FVCKYKLL
9509	23410	A	9578	512	1	EMREAFSPGRLPRGAALPLRGPAITLVP NMPTPGKCMVLSVSAAGEKPYKSCVSE SAFNKDKLKRMLIHIEPFFKYPPEST FTGCSKRFNRPDKLKHLTSHSGMKLHK CALCSKSPRRALASHQRAHGYLRFR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						CAGCARGFSRHYRLKHRCRLGPKQDKD PV
9510	23411	A	9579	3	487	WDLIYVGRKRMQVEHPEKAVPRVRLNVE ADYSYWTFLAYVISLQGARKLLAASPLSK MLPVDEFLPVMFDKHPVSEYKAHFSLRN LHAFSVBEPLLYPHTHTYDGGYVSDTET SYVMHNEHVCITDRKRSQWRFRQALS REAKNSDVLQSLCSAARDEL
9511	23412	A	9580	1	840	SKYLYDEGEEREVEFNEGWAAGVAVPT LNALERSGPLSAMDHILYTDPREIFEVLS WLESCVAGQGRMRGWYTYTDLCLVLEQ PTWQALGSLCQRLLVLSCLLAVATVS VALAVASVAVIHQSLGLSCTPTPGPPDL GLTNRCLLSPCIPSPQCLPSLANVSSC LEGSMGLRSLGWSLLASITPPPLPPDP PAPPTLLHCHLCOQLQDSPTCHACLH PNRTPTALSSPWHYITGLAPNPNWSPV PLSLPQPOQCSLSVMEIARLKSFPVPG
9512	23413	A	9581	2	158	THAGFISVSVDLNTITYCNVCVCVCVCV AHMCACISEHITHAPRLPEVFTYP
9513	23414	A	9582	3	144	YTAGVISVSVDLNTITYCNVCVCVCVCV AHMSACFSEHITHAPMLP
9514	23415	A	9583	503	3	GKCYCISAVWGSLSAPGSGSLVCLGSG FVCLAVRGSPVCCGRKCLSAVRGS VSGVCLSAVQSGVSVCLSAVRGSLVCLL SGAVCLSPCLLSGAVCHLCRAPTPCLSR SLAHRRCSSVNVCMITQLSVSYFPCWGN WRHRRNIHLGKCRILRLMAYTQGGP
9515	23416	A	9584	2	1358	AGLDSLHRFQVKIEKEKQVVRASQALQ LQRRTKVMACISPSAGYSSSTNVLIVG AETLRQBGFSDRIVLCTLDRLHSYDRPK LKSLDTQPBQLALRPKEFFRAYGLEVL TEAQVVTVVVRTKVVFKDGFKLEYSKL LLA PGSSPTLSCSGKEVENVFTIRTP E DANRVVRLARGRNVVVVGAGFLGMEVAA YLTEKAHSVSVVELEETPFRRFLGERVG RALMHMFENNRFVYMQTEVSELRGQEG KLKEVVLKSSKVVADVCVVGIGAVPAT PLRQSGIGLDSRGFIPNKHMQNVPVGFPAAGAVTFLAWRNRKNTPEWQA HAQGRVAQNLMAQRARMSVTPYLHWAM FGKSLRYAGYGBGPDVLIQSDLEELKF VAPYTKGDEVIAVASNDPISVKVAEV LASGRAIKERREVELFVLHSKTDGMSNLT GKGS
9516	23417	A	9585	360	239	QCRKGLGKLVSPFGGLIWSLIDVLLTGV GYGVPHGSSV
9517	23418	A	9586	160	1156	MPRLTFAPKGWPHPTSLHPGQVTDQTT NWLFQELPTPSNSMPGLSTPTASQEG AGVPVDPQPTTRQIRLSSPERQLSSL NLTDPDMEPPPKPPRSCSALARHLES SPVWGVLVQSPQALVMEKEKES*FS SEEEEDVPLDSVBEALQ*FAK*SGTM NNYPTWRRTLRLRAKEEEMRFCIAQTI ORLINEIEAALKELEAGVLELALRRQ SSPGQCKLWVGGLLQVVKKNSLVAE EAKLMTVQRLMLEKQWLLDRLAGYM NREENLKTADROQLEDQVRLKLVLDVYQ

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
						RDALIRFQERRRSLALSTGAQG
9518	23419	A	9587	419	130	RRDPHLPRIMGRTRLNKRNABETRNAQL PLTDKGRMARHVLDSNGSESVTKQVIL LRTLRRLRSLEYLPLRCQVLITGLAAISL LYMLTHYLLPYA
9519	23420	A	9588	2	399	FSCEFNVEANQCEPLVSPSYPDLVINVG EVTLGSENRKIKLQKIQRDQEKERVRAA CALLNSGGVIRMAKVEHPVEMGLDLE QSLRELQSSDLQNFETHQGRCPYIF VKSWSGPPPEDSVKPRH
9520	23421	A	9589	19	205	LYCLVERHDLCSLQRLSPKPRQFSCNLN LSSWDYRHMPPRPTIKLSSYSSIKLIYY LFMLVL
9521	23422	A	9590	500	407	KLITNEVRSVKRSQQLPPSPNCKSKLGN TNI
9522	23423	A	9591	727	236	RRSRGLGKREALALCPGDGSHLLCRITD SSFSFMAFFFTFMAQLVISIIQAVGIPG WFGCGMIATISFFGTNIGSAYVMKILPTV NFTVMGVFSFIALSMVHEKPYRSGSGSFS KAQREMTTGAWKNPHVQQAQNAAMGAA QGAMNQPQTOYSATPNYTSNEM
9523	23424	A	9592	381	278	HPSVYKVASGLKESLISLGLLNCRHKCW GEKLLR
9524	23425	A	9593	412	156	SQRCLASLGCKEHLNAYALITCDNGFSA LLGPPPLPGWIDIAQKYDPSFYICGLILY MTGILFLLIQPCIRIIRQSRKKYMDGAH V
9525	23426	A	9594	263	50	KHAAPPASISLSYLLHQGQKRCPPFAP CRDCOLLEGSPAMLPVCFAKILLVLEQV CLLCALLIPPSGSR I
9526	23427	A	9595	432	309	GTFSERGGPFLEPRSTQTVTDPOQEMDK CTTDEQPKDYT
9527	23428	A	9596	457	29	TLLPGWITTAQASEGRTGASLPSLPLPL YLPNWRCSPSGALHTPAACPTQGRSSSA LLPSLPQAPPGFCGMTGLRPLPSPSVGC CSAPSPOLLCTQLFPAPESSEGGCES RCVANVKYTRDLGDFLEKCTNGEASALE YP
9528	23429	A	9597	864	407	PSRRLSPTGRTTHGSSAACAIPPPFLER RSRTSRPPWGPSPHASARTQRACTTWS RSWACSCSWITSRSPWMTTKTCMIPST IPTTPRTALMRGLSLMKDAMILLTRLKIA PSSPTSMPPFTTCTACSTYMTCCGPAR WASTPMRSTT
9529	23430	A	9598	421	145	LQYHNGDANSLIVABQYVSAPSKLAKD PNTILLSPNPGDVTSWVQMGVIGALT KAPVCTGPDLSLSSGSRVQGTASDLSLE ELDRVXMS
9530	23431	A	9599	1013	604	FGRPTRPDYCLLAREMKQVKNVKTFR EELYNIRKAFPEVRQELASNNKKKMRQA LOAHNAKSELYLNRRMKVQDYERQNLNR QRINDCEYNNIKIKLEQDVQVLEQQLQ QRKAIYQLNQEKLYNLGAEER
9531	23432	A	9600	409	191	HHVGQGLMELTSSDLSLASQAGITG VSHCARTVIGLSTVFFSSHRGFASVTRP PSNENFPDRPISLAHP
9532	23433	A	9601	367	1	PPRYSLPGLGGVRGGVPGGPGLAPFPFK GXPPFFFFKNPNLPRPGGGAYSPFFGGV



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US9515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						GRGISFNIQGGQGSPPQKKPPGPPRRKTK GFFSKKKKKKSTKLEPVTSHTTCWFLPE AIDLELDPLV
9533	25434	A	9602	1722	394	GRNGSWNDNTVIDTSPLKRDPIQDTCRRY MEDLKIKLCFYRELNSKTLKPVHTS PHG VGHIDYVQLAFKVPGPKPPIPVPEQKDED PDFSTVKCPNPREGGSVLELSRLAEKE NARVVLTADPDADRLLAAELQENGCMKV FTGNEALALPQWMMFCKKNSRNADV KNVYMLATTVSSKLLALKEGFHFE TLPQWNTGSHITDLNKGKVLFAFEE SIGFLCOTSVLDKDVSAVVVAEMASY LETMNTLKKQLVKVYKGVHISKTSY FLCYEPTTIKSIKFERLNKFDSPKBYPKF CGTFAILAVRDVTGTGYSQPNKGSVLP VSKNSQMITFTTFQNGCVATLRESGTPEK IKYYAEMCASPDQSDTALLEEKLKLED ALIRNFIQPSKNGTSGRSCIGVPPNTV MTLOGAGNRRATRNCHTLEPCG
9534	23435	A	9603	14	356	DFVERTQYTHTTQTHHTSHAVRLSPRP VQSRPRASQTGPTTRTKPALGPAHPSPRG APCPDDPGSLRMLGYGSRASHNSRRGRW GHGRCKDQRAMOPHSHWEEAALPPGALS SP
9535	23436	A	9604	477	264	LVSTGTFVCGQALRLLLTSGDPPPTSASQ SAGITGVSHRTWAALSTFTVLGNVHLP LEVFIHDKLKLSPH
9536	23437	A	9605	1	378	EGINFSDNLRCTVAVQKPPFNIRSAEL QERMAVLDQTLPRAPQAPDQKALVENL CMKAVNQSIGRAIRHQKDFASIVLLDQR YARPPVLAKLPAMIRARVEVKATGPAI AAVQKFHREKSASS
9537	23438	A	9606	417	254	MVSLTGELCPVAMRVAEGHNKLNVAE RVTVPNRFIRGALLEQAGQDIONKLE
9538	23439	A	9607	404	272	PFKFLLESFIRVVDNWSLGLMYDLT GAVGAQLKACIIGLC
9539	25440	A	9608	409	205	HMGSLGSDGIDGLFKNLSNNTSISGNSP PGTPRDDGRLGNGFLHSFQNDNYSPPSL PCSWSLFYSLPF
9540	23441	A	9609	449	263	VWICPDPPASASQAGITGLSHHLPKC WDYRLSPPRPAHCFYFTMRNRNLLS LVKYSR
9541	23442	A	9610	366	75	TPGLKRSSCLSLMSRWGYRIKKRTIIR SVRAIKSQDGRVDWYFGLGLFTSEN LNVHVLCHKKTHKLTCDSSSIYYPT ELKKGQPVKKNQ
9542	23443	A	9611	1	801	PGYCGSWFTCGALRQSGORDLSRQAR NGNSALRAHVKTAKGTQVPLQKRGTE FPADLQKLTNSLRITIDLSNNKIESLPP LIGKPTLLESLSNNNKIIVLPDRICNL KKLETSLNNHRLRELPSGTQGLSALKT LSLGNLGLALPPQLCSRLHLDVMDLSK NQIRSIPDSVGLQLVIELNLNQNIQSI SVKISCCPRLKILRLBENCLESLMLPQS ILSDSQICLAVEGNLFRIKKLRELEGY DKYMERFTATKKFA
9543	23444	A	9612	179	329	KGAFCCPPFGRGGPPPLWPPPPSYK IFGLKTPKSGALSPPPPPPGNT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
9544	23445	A	9613	410	298	PRPTFFPSCLSLRSSNDYRCPPPRPNPL SLSSVLHGT
9545	23446	A	9614	1	130	NPQSHCVAAQAGLQLSSGNFSAASQSA RITGVSHCAWPNNTTI
9546	23447	A	9615	1	146	NTWRLHMVPRLVSNFWRAGILLSMPPKI LGLQKRATTMPGPETVYTSIN
9547	23448	A	9616	552	26	RLSIRNLTHAFFAEDTGRVETAEEDD CSNSSLAIRLWVEDPKLKKGRKDNBAI EFSFMLETDTPEEVAYEMVKSGFMHESD CKVAKSIRDRVTPIKKTRKKPAGCLK ERRDSQCSKMGNVFPQPNATLPLAPAQ QTGACCEATVQGHVRQGLQREBPQHIC SSVTGDI
9548	23449	A	9617	420	48	FSQILRASVTEFDSPPMDISEAKDPIR HLLEDPQKRFTCCQALRHNIWTDGTA DRDILGSVSEQIRKINFARTHWKRAFNA TSLRLHRIKLGQIPBEGGASEQGMARISH SGLRAGQPPKW
9549	23450	A	9618	190	285	RQGLTMLPWLVSNSPQVLLPWLPLVL GLQV
9550	23451	A	9619	392	308	SPIKPKIPLSAPRKINISVYRLKFRFG
9551	23452	A	9620	166	23	FCNPFPSSLPSSLPSPFLPCPLPTFP LPCFLPPLPPLSPFLMTLTF
9552	23453	A	9621	49	374	DREGIRIMAAALFVPTGLGTHGPSG AAGIVETTA*YLGSKILLTCSINDSATQ VTGHRNLKGRVVLKEDS\LGKRPERNV GHPHPNGDKSSFVFPSPSCPRLTF
9553	23454	A	9622	85	472	SHVFPPLRLTLTLHSKAVPETRPNHTY INNNDKIKKDELKKSLIATPSQFQHN DILVRLNMMQAPVIFKEVSSATNSL RSMQGFPEYDKPMRIQYATYSYIIAEN KGTFLSC/DRELIK*TPQ
9554	23455	A	9623	170	2	IFFFFCFERGSQCSVA*AGVORRSYSL* S*TPQ\SSNTAGATSVAAGTGL\HSHAE
9555	23456	A	9624	2	469	RLCSDEGLQSLGSGSAATAGKLARA PADPGKAGVPGVAAPGAPAAVPAKIP EVLEDPSSRRRYVRGRFLGKGGFAKFE ILDADTKKEFPAGKIVPKSILLKPYHR*X MPMEIFIHRSILGHQHV\*PHGYF*EHDF MSBELEL\CRPSFLF
9556	23457	A	9625	661	1393	ASPPFSQTPPAFGCSAEVGSVA\GLCL QERRLDVVAQGSIFIPSYLDHPQPSKA EQDASIPPTHEALLQTLSPPPPPTRP VSPQKAKEAPNTQAQIPISDDEAS/RWG RNPG*CS*SGSPHQWPLHLP*GRL*A* PSPCCPG*VG/PVHSQAHRRPITTSIS QKSWKFWKPTVTPRETSQGWAMPRSM PSSASISLSPTRSSQGRQTLGCGVN HVVHTQERATCGDVRANIESPR
9557	23458	A	9626	1	286	PTWAKLIALTLGMEALFNHQAQST RLKALREVQPA*LPNCNLAVGS*TTGSD F\KILPNGLTIFISSGLEPNPH*RLDP\N SPGKMLIMLINE
9558	23459	A	9627	173	491	EGPLPLESSSNWQADLDKKSRELLNKT VYLL*LNIGLPYNVHPILGINPREHT C\HQMCTRIFIATLFTKAKA*K*PRCP *AREW\IK*/IWNHIIIEY
9559	23460	A	9628	351	1	VLDATQSRGSSREAGSYLLSRSP/CS

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						EGGRCGCWANNLTWSSVASGHGAWVR ELTS*AWPEGPAGQREGRPPTPCPT CAHGPPAQ*PRGKAATPG/CLGLQWPD *SAFNP
9560	23461	A	9629	599	11	KMR**H*AKSQIRNAIFPTIAHK/RDL KSLKIQLTKEAKDIYNENYKIPL/NEIR DVTNKNINIF\CS*IGLYSTYKYKCIC LVNIYL
9561	23462	A	9630	226	1	KCDLADYSTFFFFFFFFFFFEIGSYFVA QYV*WNIYSN/DASAFQVAGTGTGVCH HAQLINL\FVYVGHSTQAQ
9562	23463	A	9631	241	1	VSGCLPGR/RPPQ*QSPPPSTPOTSD HCTPCR/PAIR*SP**LPCLDLPAS GPPSTSGNSTGTWQPT*PKLNSSSS
9563	23464	A	9632	201	1027	MTLPAPGQGGQSSQCLMRPFL/PLPG PDSEEPGSGAAG/PQSSL*SPDLPPAAP PKP*TSS*EMNTVGSTQBGSLAQRTTQ HCPVPPST/RVDILGTCLQFPFALCLTS APVLWRMPSPQSSREIP*RLAFL/SLR TPIPAHSAQPSHQKEP/PSPR*DHGD* PPP*PPKTHQTLAQAPRSGGGLARPT LPYPPSPLEVTPIRCRVH*GHLRRPRG PPPSARRPTMDWRVGLPWIEDLE/VLCR GPANLLARTSAPFSSLP\THACTGKKT TF
9564	23465	A	9633	103	379	YKCTILVLKCTIFFFFFLKPCILSPRL EARGILLGH*NLCLT\SQLRLLRKSP LTLEGGVCSDPSPHCSFANPTKGNFFS KGKKKILD
9565	23466	A	9634	155	405	VPAFESVNTNISVSFFFFFTEKGFVQ ARMQGLDIGNQPPCPKLSFA*ASQVM GTTGPRH/HC*ALIFLVKGFPHVAKTN F
9566	23467	A	9635	4	423	GAMRGDRCEGRGRFGSRGGPRGRFPF VPHIPLDFYLCMAFPRVKAPDETSPS EALLNRNQDLDPNSGQASILSLVTMT YEIDNLTVAPGTLDLVLEERQGGGYIK GTMTT*RH/SVADLTVILQILITNESVA S
9567	23468	A	9637	2	492	GSRATGFGLAHELREHLIKTWLASTVR* DLA*LMNWSG\SHKDLAGKYRPILEKAI QLSGSEQLQAFKAFESMVNENIVSLIS RQMIDTPTCTILNLPSPSTVKEIYHFLE KIQPIVISSEQVSLIRGFASITHEKEE DEWBAQVLVQIPL*TGQRYNVQYKLE TYLKIARLVLEDDPVAV
9568	23469	A	9638	1	417	VQQLGLVWGSPPRRQLKVPVITCPKSV LLITYTFIWTIGVILLADGTVKGVSLN YFSLKKDKATIVPFI\LAQSAITIFG ILLCIFSV*HYVP*LLLVTFLL*LLVFL NKNWISPHFILLTFNYLFLDIIIDNS
9569	23470	A	9639	125	451	IYRKPLKIRRVGGLHLAKTFFFFFLKQI WGNARGLMPC*HFGRLKKGDCLTIGID /SRG/RYDHDPALQPRQSKTILSLKINK IGWACWLMGPIPAWEG*AGRSFGAGI
9570	23471	A	9640	670	927	GHVLLPRAGCAQPGQPARAFAPVQR LPGGQVQPSGPGGRAGQGLRG*AGG NPGTGF/GGPHASALLPSPAPGSLLES



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						TFSPKSTTSGPPQVEDSSS*PPTSPFP P\PPSLSSLPPLSSAPPF/VVHSVSP TISAPLYP*YNS*PHFP\PFPPKVKQL ARPSPKTARPPWTIRRI
9584	23485	A	9655	1	394	SLRYCFVLEVI\CFYL/L/PIMYSIS*G I*LMNPTILCIQV*LIQPPFVVVKS FYNFIRIPFLLFLYLCLLVF*LIFFDL SYF/WCLRLIIFNLFY*LELLYSICLW WVLLLSKLF*F*FCGRFALIQ
9585	23486	A	9656	122	371	SPYLLLQCGVSLVWLLVSESINSFL FPTSHSCVQCGVQCGRGLS*TPC /SQS*VAGITTCMCHAS*LEKFFVEMG
9586	23487	A	9657	425	3	KTSMNSTIVPHISTPTLVNGLVFLER YRIAS*IKIHQPSICCLQTHPTHKDS KLVKVGWE*IFHANGVGVALLISDK/ TDFKATTVK/RDKEGHYIIKGLVQEN TVNLCA\PNTEGALKFKIK\QLLELLR NANT
9587	23488	A	9658	179	373	VESWLLWQSQSFLVFLRLTD*MKLTH/ YMKGNLLESKSTLSVNLQKHPHNTQ N/V/AQNIWVSWNS
9588	23489	A	9659	103	373	LKHVIRLCIQSEKRLHYLFNDQWGRFY TWDDLYECISSKPTTHFFSFL/FFS* SQGLALSPLRDCSDAI\HCHLEFLGSS HAPTSAS
9589	23490	A	9660	216	424	TDINVTTKIKPLDENIGITLYDLGLGS GFLDWT*TAQVANEKIG*WDFIRNLK TCIGHYEVKKTNP
9590	23491	A	9661	276	2	PRIGKLPNHLIEPLIKEMLLNLAMRPH LSPVMAI/IKIKSNRCW*GCREGI/ IYHYWECKLVQPL/WSSKLE/FIR*LP IDLFSVPAIPLL
9591	23492	A	9662	239	356	ICITERKK/WSGTVAHTCNPSLGGQGG IA*VQEFQPGQQ
9592	23493	A	9663	1	340	RHEIMTHAFAGMKRVPTISILLFLFNLA YSRGVISRDAHRSEDARPIKDLV*ETFK ALVMIAFAQLHQRPFDHVLNNE\VT EFAKTCVARESAENCDSLHTLFQDX* CTV
9593	23494	A	9664	759	1039	KRIPFGRPRVRDLRSCVRDQPLHDET PS\LKIQKLAGQGGICL*SQLRLRL*E NHLNPGSRGCSRPSRCHCTPAWATE* DSISKKNTKIS
9594	23495	A	9665	1	355	ITDLYSMFHFG*VDLATITSLWGKNBQ KGR*TLERLLDVYPWTHRFDSFNLIT SASALMGNPVKAHKKVLTSLGDALMH LDD/LKGTFAQLSELCDLTHVDPENFH ENPCDGS
9595	23496	A	9666	364	3	APNIPPSVTRIPALLAFKSSQCLCSGFL PLATEPVGLLLSMSFQAPCF\TWVYEA WLTGTSWPPDFLLSLCT/HINTNAVIF RKYRPRVGVAVAHICNPSTLGG*GWIYA AQEFETSLGN
9596	23497	A	9667	1	357	PISNAMRHLGQEETATITSLWGKVNVED AG*ETLGRLLVIYPWTHRLFDSFNLSS ASAIMCNP*V\KAHVKKALTSGLDAIKH LDDLKGTFAQLIELHCDKLFVDPENFKL LGNVLAT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9612	23513	A	9683	1900	1988	NLVFEEFHHFFSLFTFPPSLCHIF/CSRD RVSPY*FGWSESDIL/RVLP/CLDLPKC WDYRRSPCPASSRFLMFLFY*NTTLW Q*KTIPLLF*SGDC/S*FF*YNFLAHTS STMVNSGISRNSRPVFKLADKAPSHSPL SILAPGVEFF/NLGSILQPKLKLK*ASH LMCLSSWDNRHAPCPDNFFFNIL*RWG FPLLSRMVLNS*/PLCSLSTASQSSG/ ITVSHCKQGLV
9613	23514	A	9684	69	358	LLIVVFVFHTQKPRFVRLSLQSLQON LLPERKWTBQKTCVSSNTERCHKEQV ITSHWLMVAHSCNPSTLGGGGWIT*G QVFT/SLANTVKP
9614	23515	A	9685	66	344	YGERLLLTOKERNVYVLETF*APGKDSVN IDEMT/TR/DLEYIY/N/TDKAVTGFERT DENFKSSIRGQSL*YSII/CAKGSQKQK QLSLVVPYFKKLQ
9615	23516	A	9686	269	1	PKIQNGHCKTLFENPQSQDTRIFPLFTS GSSPQPHKLSFCFSAGPTLFSKTQLKIH L\WQGTVPFAYNPSTLGSRRGRIT*QGE FKTIQ
9616	23517	A	9687	229	361	DRYYSKSHFKPGAEAHAC*LVLSFFWC YRAIMINK*HLYIRKL/VYQVIRH*KYR D/I*THVTLTTTL*DRYYSKSHFKPGAE AHACNPSSLGG*GG*II*GQEFKSLAN KA
9617	23518	A	9688	318	46	KLYALNDMANNTCKEYDNLQYYRYKLY KRLIQHD*VEFIPSEH/NWNT*/RKSII NVIIHYIHSLEWEEKNYMIISLDVADVSDK IKLITFLIF
9618	23519	A	9689	168	3	GNSNTMIFFTLLYLFLFYFF/LFPIFDH KSHSVARLCSGVILAHNV*LPGSSNS P
9619	23520	A	9690	192	3	NHRKASLSNPQAGCMQPRNALHEAQITF VNFLKTLNAG/VFAHAYNPNTLRGRGR IT*QGEFK
9620	23521	A	9691	388	1	CRSAGVCRSTPDVPCIMITSSGCRTE IVACSFLNKLHSGAPARCQPELSCHRC R*TL*GVQSQGGTVGRDPLKEAVCP AELENGARSTALFRASQDSSLKLKLR POLPLFLGALSQTEGI
9621	23522	A	9692	226	3	WFLPQVKLADMTFRLYFPNLPPFFFF* DRV/CTVAQAGVQWRDLSSLLSLGSS SSPTSASRLTGTILLQHAE
9622	23523	A	9693	305	1	NIAITTVN*FGLIRHLVTRAANSNGEVD IV/SIKDPLIALNTYVIMFHDSHKGK RGTVK
9623	23524	A	9694	320	1	PRDPPASASQASATITISGHPMFWLLY IENPKSSKNPLGLINKYSKVAGYKINT OKSAAL*TNMYLQNP*MRITPTPTIAT KKKYLETYLIMEVKDLYTENYKM
9624	23525	A	9695	263	1	VRILLFSESTALSPEKCSGVISAHTCL CLPGSRGALSILSRVDY/Y*VFLVKAGF RHV/QOAGLEFLSSGDPVPSLPDFNDY RCKPR
9625	23526	A	9696	262	359	IRKIKHINSGVVAHTCNSTLQGR*TRA HEGSLYCLRVGKIVSNKVGTR*FFRTQ K*V/HLEFS*VHHLNHS*SRFST*IRK

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						THKIWSGVVAHTCN PSTLGGRVGM IT*G Q
9626	23527	A	9697	166	473	TQDTSQPWKN IWSFSGLKVFENVDIRK LYLELDNRHRSWMTDILLFFYF*DGSP VT*RLSCNGAILAHCNLHLPGSSNSPAS AS*VAEVOGVTLEPRRLRLQ
9627	23528	A	9698	456	59	LPLWKLHLRGGAGYVRCRLA*LLGASQ LGYSQVRDPLEEAVCPFSDCLKLHAGRT TLFKAVERYGRHLCLQKFLLPVRLCPAPT GOVFTVRQASHSCDGLLIV*VSERH*L PKXQQFWELVYKFPVRLKSL
9628	23529	A	9699	4	375	VFCSSVTIVSELAFLWHLKQALLLVYRN ASDFCMSSSLYPETSLTKVTGQAL/H*N G*LT*EQYVNTDQKAVI/CQQSTGSS GOSSQAREIKGPGAVAHTCNPSTLGGRG RWIT*GOEFETSLA
9629	23530	A	9700	239	361	RNDTFFFETESNSVA*RLQC*GVTLAH *NLCLPGSSNSPA
9630	23531	A	9701	169	1	IFPYKALFFETESHVSAYAGVQ*SNLGS LQLPSS/GSSDSPISASQEAQTTDAHH
9631	23532	A	9702	37	348	HAQFVDSILPYTKTEHFFVKEDINIAN KHVKRCSATLWTKRIPQGS/TLKWLKX* PPC*QGNRGRTGSPIC/CWNECKIVQLN KIV*PPFKKLSIYL/PY/DPPILLLGI
9632	23533	A	9703	16	339	ARLNTPAAAKC*SERKS/RN/SILTNH KLQMIKLIBEGMLKAVNGQKRLRLYQ/T SQFANAKDEILLMDIISATPATV*MG*Q NSLIADLEKVRV*LDQ/TSENHHLSH
9633	23534	A	9704	276	2	GLSKRSLSKPPFP*DFPLYLGGSPFC KVKRNS/RPRTTKSLPDDPPLFFFF EKVSQAISAHCKLHLPO*CHISPASASRV AGTGTRH
9634	23535	A	9705	352	2	CNSRSPFQDMMCFERNAVS PRVECS/ GVI*TAHCNINLNDSDVDPTSTS*VAGTT GHTP*HYNLIIII I*VAGIFLFLFFLFS FPGRDGVSPCCPSWSQTSEFRQSA CSL PKCNDY
9635	23536	A	9706	6	351	IWNSRPRRPLGQGGRIQDWPKLHGKTR SL/LKKLQKLARRGRASLWSQVLKRLRL TWVDCLSLG*GCSQP*SH/IHCS PAW
9636	23537	A	9707	76	359	CPLFVCLDFVIFLAYFCN*YLFPLLSH TFFFLKKGILFAPGVNLRDQNKPYFTL FDVFFNIYC*IFPIF/CLVLFFPIFF FFYCFVMRFVL
9637	23538	A	9708	342	3	GRLLIMDEQSKWFL*TPGNGNATNVD LTTEDLRYISIVVDKAAAGFERIGSN*N STLELXTVN/SVPHAS*IFCKRLQSVWQ TSLLPLTRN*LP*SPHPLVSAMLIQGS STLK
9638	23539	A	9709	211	350	RQDIALPLRL*SGTITTH/CDPQLSGS SEPPTSASLIVAGTIGACHYV
9639	23540	A	9710	253	3	VKCFSRHEMLIRRSALGGKKHLEKGLLI MSPVVVVYSQSEH/NLCHYAY*SHIKX VWLGTVADVYNPSTLGGQGGRT*GOEF E
9640	23541	A	9711	80	324	LITLTASMCSNERKSHTSLTSNQKLEW SKPTEEGMLAKATS*KLGLPHQT/SQVL KTKKKFLERTKSTTPINAPLMRK*NSL



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9641	23542	A	9712	246	3	QLAKHGLFFLPFFFMGSH*LRLECS\LT ALLSKTSAHCNINLPGP\SDPPTASQV AGTTGACLLAQLIFKNFVVETGSHYVA
9642	23543	A	9713	2	359	AAASTTKEQDNLKPYFFLYFFETRESHP VTQVGVOMCNLCSLOPPPP\GPSDSPAW VTEQDSVSKB*KRKKLILKINVYLQVTTIH P*HSPQHIVRVLSVLN*LNKINRRVTX SSSKEKOR
9643	23544	A	9714	278	33	KLPGELANHRKFPQTRCGLFFFLFTYP* DGA/YMALSLELCSGTTHAGSLDLIGSS HPP\ASLAA\GVVVTGSPSC
9644	23545	A	9715	166	402	RLSLKKNNHTSRKNNHVPVNSGVWKAEB R*SLVPSRLRI\HCTPAMA
9645	23546	A	9716	168	1	VDCTIMRRSIAKSPRCKRGTISARCKL RLSG\SOHSPASAS*EAGVTGQGHDP
9646	23547	A	9717	1	553	TSIRLFFLLTITFFFSRANRLNPKTYCN GVRAGRGQGGWGTGRHENTMTWGPQL LLSWGRGMKRGDQGWGGRGEGDTCI PPPPGTSRPPWTPRSPPWPLRLHLSASG PPGSSSCSP*LFPLTDSQVGRCSGPDN PPYHLMKVOPLPALLPLKPHRFPISLG Q\PDPPSSPPSP
9647	23548	A	9718	13	364	PPNR*RNPLTELINSLIYLPTPS\GIS A*NFSGILGACLI\QITIGLFLAMHYS PIRIQIAFSSIAHITRDVNYG*ITRYLH ANGASIFFICLFLHIGRGLYSGFLYSQ T*MTGILLLAT
9648	23549	A	9719	82	351	GEALEPELQWPLSH/HARTLLAPLPT PFUCTKVTIVGCAW/HOAL*SOHPEPP RRDVYLHLSRNGQNPIS\TKNTRI\SWH WRVPVIPA
9649	23550	A	9720	179	365	FSLPLASLKAQITDSKPPFSNTLNT*K YEVINFFLYI\IKLHPNLTSLCFYCHS VCTILL
9650	23551	A	9721	2	320	PIPPGNESSPPTACEDMCAANKH\IRRY STSLAIRET\QL/KTTIREPYAPITWAT TETSANTTCWREYGESGSYCWVGCKTLR PLCKTVNQFLKPSM*LAYDEPALTIF
9651	23552	A	9722	1	344	PLPTQNNPQGSFLHYFVLLPAVSLWS SFFFFWQKILLPRLRG/NGQNSG*W KFLPLPGPSLSPSPQTSNGYGPQQA ATFWKFKIKTGFHGVTRGLNFLTSGSA PLGS
9652	23553	A	9723	156	3	VTRAYFILFYFETESHV*WHDLSLKS PPPG\SSNSPAGASQVAGTIGALH
9653	23554	A	9724	76	337	YLSYLSYLTATVSTIYLTPTHESTSI YVSSYLSINHLPLYNSHLSSTHSSYI YLSTISILSINLLSTLSYLSYLSYLSI YDSSIHLSINHSLYLYT*YLSYLSYLSI YLATVYSI\TYLSI\HLS\SHYHLPIL SIIYLCITIFLPTV/LSTHSSYLSYLSI LSINY/HTSYLSYLVFVY/HLYYHPT
9654	23555	A	9725	249	436	ELAG*IQDHP/GOHHTLTLQOIKNLAR RGRHL*SELFRIRQEDHITPGVRCSE L*SHHSTP
9655	23556	A	9726	177	3	HLN**FSLNLPFETSPSVT\ROTISAH RNRLPGSSSDPTASRVAGT\TOT
9656	23557	A	9727	272	233	RKNQRIYQIARGLNEMARISPLRSMYI

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						LAVSGLNPFLLKRCRLASWTEKKK\DP11 CCL/QKTHFTG/KDIYRLKIKGWKKI PH ANG SQ*Q
9657	23558	A	9728	368	380	RKGQRISRTATKRI NKMARISPIITSTIT LAVSGLNPFLLKRYRRAEWTEKKK\DP11 CCL/QKTHFTG/KDIYRLKIKGWKKI PH TNG SQ*RR
9658	23559	A	9729	294	2	KGNLSFKKKKKNLKNFKVTPQNFGLADQK TQKPTLKVSGMQKKPKFK*NLKGRFL KLFKKKKLNFGRSRYFKKKK\ANLID GTLVBQJNKKKRNQ
9659	23560	A	9730	7	284	SQGLRLRRRNYL*PETESHVSARIVGVQ WRNLSLQSPPPG\SSNSPASASQVPPV T
9660	23561	A	9731	1	322	RLSKKKKKRKKKGNQPGQGHGKTLFLPK TPKI*KIKKIYTP/RGTHLNSQLRLN RKENHJNSGGKGNDFKLGHCI PAQMTK TPFKKKGAKQNGKLLQLTYGK
9661	23562	A	9732	168	2	GFYKSLSLCLSVHICFADFFFFFEMVSR SVA*AGVQWHDLSMRPPPPG\SGDCFA
9662	23563	A	9733	43	317	LKLQPRDTHCITLWSTSPFTYFFPETES CSVAQA*MQWHDLSLQPPSPG\SGDSP ASASCTGMHRRHTLWKCINSEFDPDML GLGLNSHI
9663	23564	A	9734	8	296	NVVSACSLNGLVKRLSCITLNLQIL*MI TLITTERFLKAEGRQKGLLHQTA/QVVN /AKSIFLNEVSSATPVYBGII RKLNSLI ADBKACVWIEDQT
9664	23565	A	9735	3	300	TRPSNVAALSKCSRRRT/R/TCLITAN OKLEWI KLSKEGILKAEGRQKGLLHQ T A/QVVN/AKEKFLKEVRSATPVYBGII R KNSLIANNEKA*VWIEDQ
9665	23566	A	9736	352	1	PFYFLINPFTFFKGPPLIHFFLESFLEN FPGQAPFKLQNFAPFLSLLNGP FLEN PFYFKFPINC/KFLGNTFYCYPLGFF* RSPPPPPPPPPETESRPVA\RLCSGALS AHCKLG
9666	23567	A	9737	130	3	KIFFPPPPPPFLRQSLVAQAQVQMC/N* LGSLPFPFAGLKRPLV
9667	23568	A	9738	167	3	YSRSVPFFPETESCVTQV*EQWRNTG SRRPQPP\GSSNYCASACRVARFTGLV
9668	23569	A	9739	140	419	INVKYLRRHFFKGNISQRIKRLKATREI QIS\*TDNNKQ*GOGSVQYFTHCCMCE MVHSLWKIVW*LLTGL/HIELSDDPAIL LGGIPPEKMT
9669	23570	A	9740	93	371	KLCNGYYQESKREPTERN*IFANHKTG CLSKTYKELQLANFNS/NPTQKWARDLD ISPTQWQFANQVVKRCSTSLVI RMQI YTKSILDIH
9670	23571	A	9741	1	288	GTRDHLRSGVRDQ\POGHSTSLLLKIQ N*CGHGGCSLSSQ\LTWRLRQVNCLS
9671	23572	A	9742	296	563	FIKHLNSYMLGQNIARISYICKLPPT EK*IQAGYGGTCL*SQLRRLRHNCN LGGGGCSSEPKI\HCCTPAAWATDGSVSK KKSRR
9672	23573	A	9743	32	400	DALVPHWSSYSFICLDLNLVGIYLFSDR VSLLVPRLECSDAIMAHSLDLPRLR*S SHLSLPRNMLMVLVETGFCFHA*DGR

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						KLGGSSNPPLA/FLKC/WRNMRKSQL* PLLLGLLSADHSD
9673	23574	A	9744	60	356	HSEVDSITITPILQGRKQISEVRPQRMCE REGGLFISSETLLFLCPAPSCS/HPI/TPA Q*SYF*KNVSWLGAVDGTCNPSTLQGRG GWI\RGQEIKTILANMV
9674	23575	A	9745	2	446	PMVNVIVKRCASLVIRAEQIKTIMRSH CTPNS*M*KIDNTKSW/*GCGATGTPIH C/WMKYKVVQPLWKKKQQLAKHIIHLPY DPINLLGLGIS*EK*NHLG/YKTYVVRIF IAAF
9675	23576	A	9746	257	1	VNLRLSPFSPFLPILFBSSQGLVCCFL MVF*RDGVSLPIPAQVQLMDRSS*P/P SPGSSSPASAS*VAGTGMHLHAEPYAS C
9676	23577	A	9747	148	3	IKLCEQPHK*THVLNKH/L/WPMQVAH AYNPSTLGGRGWIT*GQEFDS
9677	23578	A	9748	769	1	YPQLFRTAKKKKSNVPIKSTNVSQYGH *ENKKHVLNKHGATLQ/BGKGNFGDTPK VTLDKDIKAVAKTRQERLPQELKLFPLL EAKILKQYNHPSNVKISGVHTQRRPIYV IKELVPGGDFLSPQRKQNELK\VKPSSL DADSGWCISKKCIHRDIAVRNCL/VGE NNVLKISDFGMSRQEDGGVYSSSLLDKI PIKWTAPALNRYGRHSSEARSFGILL WETFGGL/VCP*PGMTNQQPQSQVERRY WMSVWQC
9678	23579	A	9749	607	986	SFSSSSSEPTISYGCGLDLPNRDPVPI HPAFLNPLFLALGNFPLSPSPSPLEIYF LPDPDPDP*HSPD/PPDPLTSLFVFL PPDPGVSPSPNTSPHLPVVRPPSPSP TSTHLSPPPPSPH
9679	23580	A	9750	313	339	AR*GLSCSG*S*TPGFVQSSCLNLPKW DYRC/RATVPSLCFV
9680	23581	A	9751	213	453	NLAVNVDEINLFFFLFLIVTASLKPCS /HLVGR*FIQSCHYSLFFIFDTSRSV T/RAEMSATVLAHYNLCPLGSPDSSA
9681	23582	A	9752	368	3	PLSSPRLPFLPFLDPSYFLPISSTSTFL SPPCYFLCVFLISWGFSLVSDQGSLL SS*SAFLGLPKCWYRL*PPHPAWRELS FFFS/SFFYL*GSLSPSLSCSGMTIGH CSLDILVSSARA
9682	23583	A	9753	2	335	ARAGFSGGDWNGMQSTASGLSLFHCPI S*GELPILYILLKCYITL*IN*LMFGS PFPRDLQHFLLP/TSIWGKRPQTVAAH YNPNTLGRGKWTQQGSEFTLANNVK
9683	23584	A	9754	467	120	SQLEFAPRQTHLKSQV*DDQVQHEST PSPLKIQKLGRGW/CAPIGPRLGRP R*ENGINSGGRCVCSRPSRHCPTAWVRE RDCLKNQNKTKSGVLFBPHQCFLISNT SRNLL
9684	23585	A	9755	137	368	DGVTLWTRPITYGGLSINFGSVIIVLP* VKAYGMMVLISLGDALQPLADPECS*G QLRELRCMDLHVDPEDFRLGK
9685	23586	A	9756	172	267	SKSGNKPNHYHLNNGSVWVCIRTV*QLL KRLTTELPGPAVPLGVYAREMKAVH MKTYSLQKMC*IFIAALFGIVKKNK*A K*LSPDWSIK/M/WCIRTVEYITLRS

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9686	23587	A	9757	56	318	QPMGVSFFPPFFCFIDETICSVSQAGVQ WHNQSWLTA\ P*SDPPASVAS*VASTIG MCHHDQLIFFFFKQALCPRGWSNAQSQ TCHSS
9687	23588	A	9758	179	1	KDTRVSRGNTQDTLKPPPPGSSSDSPT SAS*VARIIGVHNTWLI\PCILVEMRFH FRA
9688	23589	A	9759	219	208	NFCNPMPLQYKILFWVRVSLSPRLC SGTIITTCSL/RTPLK\SS*LSLGVG CSKL
9689	23590	A	9760	133	371	AMAYQLYRNTTLGSLGSLLEBLQ\LR NRVNFRLSLTYFCONVGVPLNDEVF REVTELT*VDKVKIVSL\DGKQTGF
9690	23591	A	9761	813	3	CGEGNAAGQDQSGRSGSCILPVRARQL GSLFPAFQVYCCSCQTRSSQSGWHTK RSLPGNNPAPQDS/ASAPKYQTGPGVLG VQSPPLNQCSCHTALSPEASSAFHTTTP ATLLHQARTLSLTQSRPTTVPVLLKMP A*RPRESRH\GR*ERTKGSQARSQEA.DN ARPRKALGLSDPAPSLHPSGLSDPKFS LGAPKAPPLPASSPTAQBTQSHSQQP TATGFLGARLCPSPQHICQRRGFGVTP LLLIGENGVGSHSPFVULV
9691	23592	A	9762	96	377	RYHTNAAQYIPESDQIKQTGPHHVQAG LELLTS\FKEPLGTZKNLTET*FLDCAK DPTTRKRSBETTLSEHCLPKYSTMT\H RTSLT\FTDNI
9692	23593	A	9763	164	399	TDELLLEDEQ/RKWFLEKSTGTGADAV NIVEMTIGLE*CNLVNDKVAERLETE TNFE/RCS*TVRQ/MLSKSLACCTE
9693	23594	A	9764	225	25	KCKITWST*LE\TVFKDYVYHLVYCKL KNLEKTDKVLTHNFRLLNQ*EPEVLTR AKMYKIYNDIE
9694	23595	A	9765	128	218	FFKDLDCFPKMSHCFILLAVVGGPTF ST*LVIREMQIKTP\I*YHFSNRMVIM KKSININKWQGRGESKALHC*ECKTV *PLWKTVMQILKLLIG
9695	23596	A	9766	194	551	KNFFLEMEF/SVLLPLECNGVISAHR RLRLPLSSYSPASSQVAGDYRACTTTA G*ILYF*RGQPHVWGQGLELPTSGDP PASASQSAGITGVSHCPQLKKSILHETP KGLTGVTS
9696	23597	A	9767	238	3	SFLKKLCPRGAPACRLCLSA/LLGVS* SGYMGVRDPLERAVCPFSELEHHAERT ALFRAPVPGCLSLQKLSAFCSC
9697	23598	A	9768	343	1	RGASHSRGDCVRFGFCAPIPVLNHPKP LFFFF*KEPIERSLLGPPLEKSNRP PFL/VPRFFKNIPFETFKLPLPFPF FFFEHSHSLA\RLSHGAILAHCNLSL PGSC
9698	23599	A	9769	191	2	FRINH*TSH/LRGQKKKKCNKATGRK QITKIRA*LNETOPPESIQRINET*SF SGIKILI
9699	23600	A	9770	165	2	GKPPNCFYILNPKKKGQDVFNRI/KLG VVAHACNASTLGSQGRIT*AOBCKTS
9700	23601	A	9771	97	912	VILSTGCSGSPFLPGWSVLEHSLTRCPF SFFLSSPTPME/FSILLTLRECNIGIS AHCNLLLGSNSPASASGVAGNTGI/C

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GLHAC*AS*FLYPHVSVEGTGFHIVGSGSLG LEL LTSDD\RPASASQAGITGVTPRV* PLNFSRHRGLSCFF\KTRVLSCCPSWT* TPGLK*SSCLNS*E/C*GYRHTPAHPAQ DMVFIFITY/CPFFVFWLL/VYIPRELE LRWSPFLIVQAGVQWRNGLSLQPPPG\H KQSETFQOI*INKY*LLN*LTTEFSIK
9701	23602	A	9772	3	363	HELRSANDEVPASZIGCFILSLFENLL IILVPLILTRTSYILSN\RLAVTTQQ* LILKLSKLMITTHNSIGRS*SLTLGSLI IILATNLLGLLPLFSPTPTQLSINLAM AIPL*AGAV
9702	23603	A	9773	38	385	YLIILDSPEKRLCGCCNCHSSLLDH NLNT*SS*MCLYANIHIYVALSCIYFI* F*SI/YIFII*YFHSIAYIVIV/IYIY MYTHAHIMCI
9703	23604	A	9774	13	1350	DRVSLLLRLRLCNGSISAHNRNLGLGSS DYPASASOVAGTIGVHHHTRPTFALFLV ETGFHHVQAGLELPTSGDPPPL\ASOS AGITGVSHCTWPHLSTTGKILSSGTICP GINGQRWAFLL\SLFWL*LWHPCLSS IMCLSLFFFLCQ/RCKPLISD
9704	23605	A	9775	376	1	KFFELMYIPVLAICLNFSEVFLNK*QFF NLTSQSGIQNLRLILSNEVESILKSLP TVKNLQPGDIAATF\TYKCOLTLILKL QKHEEARILSNLTSETST*LLRKQQPK KVPNEHIVKILV
9705	23606	A	9776	192	2	NVYQFPFVFLVPPGVAGV*PF*SPDPV RVK/LGF*GSLFFFFFETKRSVTRL ECSGVILA
9706	23607	A	9777	77	350	WLEKFGSRNSCKLTLVLYVYLTSTFFF FFFKIGV*LSPTLECRGPINVN*NLCPF G*RDFFPILTS*VL\GPRVILEFGFLEKT GFSHVPQL
9707	23608	A	9778	133	325	FRWVRFPFLGDCTPRVSEMLGLQGVVPS SSPFFVCFET*SCSVAQAGVQ/WCDLG SLQPLPLG
9708	23609	A	9779	145	362	RLAFGSCSTCFPLT*TVIYYLI*FNIFP VFEMESLSVS\RLCSCGAISAHNCLTP AMTTERVDAAANSRMN
9709	23610	A	9780	260	1	QKQKQEKRRKIFIPNIRKIQRDYNEQ*YG /NKLDPEDMKP*ETRYT*/ENLHQEE IGMLAPVVTNKVL*LVIKIPLTKRSPEP DGFV
9710	23611	A	9781	230	1	SSDSKIGSSVVLVACRFFFLGTGSSGV TQAEVQMHDSLQPPPPPPK*/PGTT GA*STLAS*NARTIGVSHIAR
9711	23612	A	9782	20	322	SOHFGNPKGNPKIPRNLINFPRLNAD HMIISTDAQKVDKIQHLEII*TS*QT* TERIFLNLIKAS*KKPTANIILNG*RLN I\FPKTGETHIC
9712	23613	A	9783	158	379	LVKIIICNSFQYISFFFFFPLETKCFEFP QVEVQGNFG*LNLPPLGLNHFS\ASAS REPIPIGPHHPG*ILVF
9713	23614	A	9785	54	312	KVDKSTKIGRNGSRMAKSNQNQASSPP KDHNSSPARKQNTENKLEDELTEVGPRR WVITNSSKLKEHV*PH/GKETNGLEKRL DQ

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
9714	23615	A	9786	13	613	PGAGWARGHEKV*DPQGGHG\KRPSLLK IEKLGHGGRCLLSPAIGGGLKQGESLE TGGRDCSEPRILCHC\MPAWGNRNKTL SQ /QNKTR
9715	23616	A	9787	794	164	FSTLFCFFFLRNSLTSPSLESCSVTSP HCNLQLPGLSHSPATVS*VAGTIGTCHY TKLS*FF\FDDSL*APFLGVVDITETYP DPPSSKILLPHSQGHQHPALSRWL SC\VLPHLR/STSLGQ/RIV*LSRYE V*PROFTSPQNTPTNNGSLAPGRVD* SLILD*LG\CHDSSIQPQT*VLK\HPPT LASQAGITGISHHTRED
9716	23617	A	9788	256	380	YIFRAKIQGLPFCALFREAVGENTP*V FAC/PKINVLPYVHP*LFQ*I*YQLKIT F*NYEGMT/VFVRFLFETRSHLSRLE CSGTTITTHCSLELVGSTNSISAS*VDG NTGVHRNASC
9717	23618	A	9789	22	226	TKYNSKGNKELNVRAKITKLEENIDRN LCDILGLNCFLD*YCL*TKYNSKGNKE LNVRAKITKLEENIDRNLCDILGLNCF LDMTNAGT*TKGR\IDKLDFIKI*NFWL DT
9718	23619	A	9790	288	2	QVWQE*ASTESAHCWERRKAIQL*KM RMQFLKMTNV\ELPYGSAIPLVGTHGRE LER*ST*NIMPTALPLFVIGK/T*NLFKN PSPFQITWMSL
9719	23620	A	9791	142	361	FPOGKRRVFPVTFSPRIPSKAKSVSQ DCTTMTFTALFTIARNWRNRSKCPSP *IKKRNCTT/MECYSA
9720	23621	A	9792	305	346	TVEYTDYGGILE*LTTPYCHAVLITFL ICFLFL/YALFLITLITELTKTKTGDAQE IETV*TLPGIITLGLIALPSLRRLYTD DAPDASLTIKSIGHONY*TYEYTDYQGL ILNS
9721	23622	A	9793	2	317	SRDRPRVRDR*LFSTNHKIDGTRVILFF A*AGVLGTALSLIRAEIQGPONLOND HIYVIVITALAFVILFFIDLPILI\SSF G\SVYVILLILGVPCTAVFLHSS
9722	23623	A	9794	384	1182	RIGKYG/LCFLPV*WFLKFFFMEEFL PRLECNKI\HCNLLMGSSNSPSTASQ VAGITGMCF*F\VFLEIRFFPHVGAGLK LITGD/PPRPKVLGI
9723	23624	A	9795	205	1	GLQTRCWRHHFAFTKAITTYFFLRKKG GLNKKCW*GS/GTEIGLIHONWECGMV GLNKTADANAW
9724	23625	A	9796	307	348	QSAHL*RAVCDPSDLQKRNRTTALFKA VRQGHLSLQRIILSP\VCILYPAPRGAY EGRQASLSCGGHHPVRASRLLCPLKQAN AMVIGAPT*PASLPPCSSISHCCASNQRDS VGYPDSSP
9725	23626	A	9797	193	381	ILLI*THILLSMISSPFFFTGSHSS/V SRLECSGTASAHCSLDLPSCGOSPTSAF *VAGTTGA
9726	23627	A	9799	153	359	FQTYMCPADSYQLSYLFPVGTFSWLESE GV*WTCGSLQPPQPRVK*/FLPSLSLL SSWDYRCAPSC
9727	23628	A	9800	2	396	ARARARARELEELIKIFFFFFFFWGQIL ALMPKGGGGGILTYPNPPIPG*NNPFG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,151,26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
9728	23629	A	9801	256	347	LTPPRTGINGLGPGRVNFGLFKKGGFP PPGARGV*NGKPRGTPPPGFPGGR/DKA PHDGPL*TFEKVVRPPNPFQ
9729	23630	A	9802	109	401	LYILLNLNLSLK*LVKRLK*NVVVASIILIR YKVTTKRP* * PSKPAQSEELQLLTSAPG LNF*RYIISPPFWIQSFALVA*VGWQNC DQGSPPQLPPGFKRPS/CRSDYRHEPP R
9730	23631	A	9803	371	2	HLRRPCPTPPFALRTSGDQPLSPENRFD SGLLHSLTSPRGLNQQPFGSTLANFN P*ASIPASPPSQSQSQSQPPVASH PPDT*GDAQPPP\RQDQFQGPATVPRS QAGQWPSPLPSDFSKGAQWVPVPTTR/PP PSTSTQSRNT
9731	23632	A	9804	188	1	PGFPLSPFPFEGNPSKRTGD*TRCLF* DGKVMNECSPPKKKKTKKKKIVP/CV PVQTKCIVVRGGKTLVGDV*V*P*\GS FKEVVAHFPEK/DCLCTLYASFTKES RRVDGFCVCRVGT
9732	23633	A	9805	112	383	FLFFFFSRT*SQSVTHAGVQLEQSLPP G\SGNSRASASQVAGITSRKHSWILFV FFVETG
9733	23634	A	9806	599	237	VFINIRVPRFLTSPFPFKRGPNLSRVRK CNG*TKGHCIPLDGVRS*SPFSLILTNW DYRCAPPRPNKFFF/SFETGSHSVTA
9734	23635	A	9807	168	2	FRDRSLTLPLHCHCVCVITAHCSLKLLG SSELQASPLSSWDYRHSPPCLANFLFF VETRSHY/ASRNLQSNPT*/A/PKCN DMOV*ATAPSLATWFSSEKLIIRLLAL KVSDENICTNF
9735	23636	A	9808	225	3	PQDVFFFFFLTGYSVTKARVQWCHG SVQL*PPG*STDPPTSASQFATGTHRA
9736	23637	A	9809	541	3	GPLGYLPYPFPQLLSRG*NPSEFLKIS RVFYGT/HYKFFFLFFFTESRVA\ RLECSGVISAHCKLCLPGS
9737	23638	A	9810	213	1	RQLTNGISGRRCQFQPMNSVYFVYMDM IILTKKKNNKYWGCEKTELLIHCLEWE CRMVQLVNVKT*QFLNRSDIEFPHDGPI PPL/GYKRKKMKTKLCKLCLVLSB/RM FTAALFEVAK* * KQ/PQTPITR*INTWM RIYTIMEYSAIPRKTPLIHPID*LDTES II*TEKIQSQETTY
9738	23639	A	9811	54	388	FLCVDVFCVFNFAELKLALVGLFVCLLFG SVIQAGVQWQCNAL/GSL*PPPGLSDLPT SAP*VAGTTGVSHI
9739	23640	A	9812	429	24	PARPLRQ/NDERPIQQPPTKKKKRGRN LPTKKTKNTGQKNPAQLRQKTKNQK KPKTNPKKKGGAL*KKTGKPKTQGG K*KISPNKGGK*NPCKGLLEKNPFSQGE K
9740	23641	A	9813	149	350	RSKGARFPICPRSSKFSVLCQQRVTV FQHPFELGRSVAR/CRYSQILGRIRQ*SH LWNGRGSSEPRSCHCI PAWATRASSIF CNFQASSVEVRSARKKLFSDILKRHNT INNRVSGLLLVDSYFGRLATPVRTQ
						CHFPCTHTTL/CE*EGGEDVTGPGTKFK FPAPGRTDGHITHTHTHTHTHTHTISDPH ELCVWNTLIHFV

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						LILNLHFFCFVIRQOFSLEFF/ISFFFF FFHCNVTPELCDFSVCIHSDNSFRFLH LF/NF*HMTLCISRLR*TLKQSCYSYTK IC*FYVQLSFLTILY**CKS*QALSI ALONEFLSV\QYHKNNNYITLTIEFSRN KFLSVTFLLSIFSHNPGISASISIFIL HVYIKNNPIGFFK
9755	23656	A	9828	298	1	MRNCLTDDERKFFEMASTPGSDAVNTV EMTAKDLR/Y**YINLVKJASDFEMID SNFEKCSV/KMHLNSNACYRENPHER *GQSVQQTFFVNGRERV
9756	23657	A	9829	361	1	FLTGCTQWCK/DSPFNATW*DH/NTERRN LDLYLTPYYIKNLKQLTQPNLRAKTKL PEQNIGENMLCDL*LSRERYSTKSTRIR KL/DTLGFLIKIKKICISKDTIRK*ATD WEKIFANHVILKG
9757	23658	A	9830	402	2	RPHRRFSFVLQCFPAKVAFFPGANNPT NHYWAGVTFPWEKKNKIDSFLPPFSKNP ILGELKA*F*NFLP*GQIFF*SLFFCP FGGK*TPGVTSFFFFFLVFFETGSHSV P\RLKCSGTTTACHSLDLGSSN
9758	23659	A	9831	2749	3215	FCQ*IRMYVMCIQYINFRVYLICITYTL HTHTPTHTHKETPTQIPKDS/QCSLSD LKGHSL
9759	23660	A	9832	3	386	KLRLGQLNTSAMAAC*SERKS/R/THL TLNQKLEMIKLSBGMKAVIGOKLGLL YQ/TSGVYNMAKSELKDIRSATPVA*AM ICKQMSLVLQSKV*VV*ISDQ/TSHNI SLQSLIGN
9760	23661	A	9833	1	370	RRCRWFFDTSRTVGRQYKLVTHAFTVF QERGCFFPLTROAGSHHOGGAFAQVTS PKSISPCGRGGSEL*SQHGRPMQVDHL R/LGVQDQ/RWPCGQYGETPA/LKLP KISHAWMLAFVIPA
9761	23662	A	9834	125	409	GOENRSTKIVHLV*VLAT*HKRLNCF SHFI*CYOPTASOAHVHSDSDSTHV\ N*NSRNPGTVAHANPSILSG*GGWIT* GQSFETSLANN
9762	23663	A	9835	223	1	PKPQWMTF*PPNRS*MGPPHWRKMP FLKKRQHPFFFFFEMSRSVT/RLBC SGA/TISAHCMCLPGSSNS
9763	23664	A	9836	377	515	FILFLRQVLTLPLRLYSGATVACSL\ AF*G*SDPPASASV
9764	23665	A	9837	274	1	AGBWHDQICVFKIPLMKNGLHGARVQGE SWKERRHQV*DRQCKNLSDS*ICT*/R/ W/KCTVAHNY/PSTLGGQGWIT*GQ RSTSLANNWK
9765	23666	A	9838	553	114	QGVKTHFQHGKTLFFPKFFQKLPOV GGKTLPSPLSRLGRNSFHPGGKSNK QSSPPSPG/WGKKGGGLPQKKKKKK KKKKKNGVAPSRLPKYSN/WQATWG* RKLINDTTRVPTKSRMQLQDGKPVN GIFTETGRL
9766	23667	A	9839	36	434	LPFFQCVTFEITVLISWCYIREDACNL KHAITILNVCYICVCPCSTLVVYMY MLP/HLSDTLTLN*VTLVEMLSPOCL MFWYHGI*K*HRLDVVAHCNPSTWGG QGWIT*QORYCTSLANMVKPR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /possible nucleotide deletion, /possible nucleotide insertion)
9767	23668	A	9840	268	1	RFPFFCPLTILFMAFGVFSNPLGVRA PQPP*IFFPI*KKPSPLIFFFFFEKES RSVS\RLSEYSGTISAHCKLCVSGSQHSP ASAS
9768	23669	A	9841	463	86	LYMHFISGIFLLFCWSI\WSVLQYKN CPDDKVYGLDYGNSTQVFT*NSKLIK.Y TLTMYSLFCINQTTIKPSEMIQATKANIK DK*NYMKLENFCTAKETVNMKKRQLKKK EKVFSIHIPQEVNI
9769	23670	A	9842	37	400	VHSPPKFWSLIVSVLKPPFCSLPPFLL ALYSISFLQMQCHLV*AFF*KRGLASV TYRLCRGALSINCNCL/SQSSSDNWAS LPRKAEAGNSFT/CR*SQVAGNPISIS TRLNQRKTPES
9770	23671	A	9843	42	407	NCLSLYITFFPPFFLEKNVSPFCPPG/G RGQPFNPHQTLPPRG*GNPP*LPGRGE *RGAPPPDGYFPLPGKKRGFFL/GQGS KPPALKEPPPLGPPKG\NYKRNPPPP GNFF*LPPIQVV
9771	23672	A	9844	113	379	LGPVATSLRGRFLGYOLQSQSKH*NYP TVR*GOGEMRTSVHC*ECKTA*PL*KT VWQFLKKLNTGLPFDATPL/LAETPKE LKA
9772	23673	A	9845	284	528	PLPKTMEIMDKKQITQIFLPRKMGHK IAETTRINKAPGPGTANE\KCTAQMW KKFCKA*E\SLDEKKA*GHPSEVDIN
9773	23674	A	9846	888	1295	LEQGCNLFHRES*LGEVFFVCFRSP TLVAQAGVVRDLGSL/HKPSLSLPS SNDYRPPLPRLA/NPFFVLVEMGFTVL ARWVIS*PRDPPTSASQSGIIQVSHR AGPVAGILMPCRMNISNKPAGAVPKKK
9774	23675	A	9847	88	387	AYRMKIIDRISLSLYAALNVTLPLFL LFFFFKTEFCFAPQAGG/NGQFKLMDP NPPPPG*K\DFLVSHPEDLGIGAPPQC GQNFVFYKEGGWLLTAT
9775	23676	A	9848	298	438	KIPRGAPNFFGGGKISPLPLGGPIKTPR GALEKKTLF*VRGPWPGFVKESPRPKX LG*QIFWPPGKKPNPWG/SLDPPPL ILSRDPP*KKKKKKKKGGGPKLNP PGGKPPRGGGNFPPPPRGAYNTPOGS *EKNPFLGGGKKKQD
9776	23677	A	9849	251	498	ALIKMRSSKKPW*RHGEIGTIHCYWEF KMV*PFWKTV*QFLK/D/LRMGLPFD FQPDICLGLKTTVHTNCTQMFAAL F
9777	23678	A	9850	478	37	ESRNKISHANSINPOKELR*LRSGKPL NK*CRHSISTCKRKLDPVLTPIYKI KSKWTIDLVRAKTIKSLSENLEVNLD LG*GNDPI.DMTPKAQTTK*NID*LDLII I*NPCCSGKDTINKVRQST*EKIFANH VADKLE
9778	23679	A	9851	2	378	RLGLFLCALFCSIALCMFFFFFF* KRGPPFGQGDGPGNFRDLPLPPGIKO FWGP\PPRKAGTGGGPPGANLFGWK KRVPHGGQKGFPP/RNPRGSPRGP GVAFVPRKPPGLEQ
9779	23680	A	9852	229	3	PGPYKIFPKKGGAPCDLNPV/HOKL GLGFFFFF*DGVSILELLKCSAA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9780	23681	A	9853	108	420	ILAHYKPLPG*SDASASAS GPRVCVRILSRDDSDLLATEDSLAHTEG DPVTASSHSQAPSLSVHPGAALBGVCMG TGAIAGTPEPOKPPQLTPGGRPA\PIAP GLTWEPPEPSHPPO*RSPPPPP
9781	23682	A	9854	2	256	FFTFPLRYIYICARFQPLSPILYLQK*K MD*RRVFOERMEQAYFFVEV\SMACLI CQQLSVSKEYY*RCXYETNHGEND*F TEKMDNDNLWHTYQ
9782	23683	A	9855	323	3	ITQMANKHKKR\QSQ*VVRVQKKILIN IHRV\IOW\KTSKSDMKCCSGVGTETI FTHYLMECKLLHLLWVMVL\ILLKPT TDHPDPAIDLLGTYPAECGSHYDPA
9783	23684	A	9856	28	385	DGVTOAGTQSGKSKTAA*TA*YQGSITN AWSFSPFPVLKTPPPQK\YPPPKK KTPPKKK
9784	23685	A	9857	436	518	AANKLENTYRHLYDK\EHYRIVGRDD LFNKMCWVM\I\ASNKENTDSYLLDHT K/LNSR*IIQ\DVKD*IKLLENTLYLH DLGDRQKFLGRI/PVFTIKKIKGFDPH LKLSTFVHQKTP*RLNSA
9785	23686	A	9858	153	492	ELAGSDPGVADVSVQIQREQSEPCPSWK AVSQAESSSSSSAGVSLVLFRIADMMRP IPIKEENK\ASQSDINFNFIQKHCHRN TQNSV*PGVGPPGTGCFPRQSSP
9786	23687	A	9859	2	419	TGKQLQVSHKKSTYSHPSKKPTTKND MKRYGQPLAIREMQSKTIGVWRYHTP KYG\WKKCNLQCGEETTLIYQH*ECKGV QPLWAVMHFLK*LNIES/DIY*NY5* YISYSWRKTCITITDYPVILLGITYPREV KTH
9787	23688	A	9860	88	419	TTTTFFGFWPLKTKPLFVQLEFGRPY LG*WNPDPD*KNFS/GNPPGGGE*RA QPPPPGYFLFKKK\GVSPWGGGSKPP TPGNPPGPKIRVIRGQPPPPPGQRKHF
9788	23689	A	9861	301	401	KRA*GGGEPTKVCFPPYNRKVNGSGPPK KFKKGRRAAFGLRANKHGLFVKKKKI WVGKVGEPIT/DPFKFGR/LPEKDGP LV
9789	23690	A	9862	220	415	KINGGAQIFRGGGGFFFLLEGWERNFG VSFRNRKFFFGGVFLPPPP*HKIGNYFSS QRQYISLGGGGRKTPPPKKNFLLDOTPK LFFSHSPKKKKNPDPKRIWAPMI* PPPLPFFFFFPPFFFPFKK*/S FFFNFKKLSKFLSPPPKVPFPKKKK KKNPDISYRNPLAI
9790	23691	A	9863	116	366	GQFETSAMKCFETTESCSIA*AVVQNH DLSSLQPLPG\SGDSPASASRAAGELL EPRIRRLQSVEITPLHSLGNRVRLHL
9791	23692	A	9864	619	295	FFFMETFSLLPRLCNCATSAHENTRL PGSSDSPASAGLL*SOVAGITRLRHHD *LILY/FLVEMRPHRVG*AGLELLTSGD PPSSASOGAGITGMSSHSGHYGKIF
9792	23693	A	9865	12	432	IADRLFFTNHDKIGTLYLLFGA*QVLE STALSLLIRAEIGQPGNLLGNNDHYNGI GTAHAGIILLVIVIPILIGGFGN*LVTL IIGAPDMAFPRINNIISGLLPTSLLLLL TSALLERAGTC*TVYPLCA\GGYSHLG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						A
9793	23694	A	9866	30	380	LFSTNRRGIGPLLYLFGA*SGVLGPAITLLT*AEIGQPGVLLGDDHTYNDIDIAHAFVILILFTVPIIIGGFGD*LVPLIIGAPDMAFPRIN/NISF*LLPASILLLLASGIRBGRSK
9794	23695	A	9867	256	395	EVLARKSEKSFETVCINNRC/WFGKVAHACNPMTLGGRGGRIT*GQGF
9795	23696	A	9868	458	2	PKKRPTSQKPPRGFISAPLGKKNYIFPPVNRGPKLDFRGDPLEFFFFFFFFFFFRFFFLKLG*KF*NFHT*NRVTVLS/CSKKFPQFVLPTPTP*KVPKGVNFFWDFPIFFPKLPIFFPFCDRVSLCHPGWSAVARSLTASPRV
9796	23697	A	9869	144	423	TPLCSRTYSPGCP*PSLISSSCLSPFLSIPLCVLS*+T*+YLFFYISNREIYKTRTKGIYPGAGRNSLYTH\FSIEGVSTIKIERFWPGAVARACNPSTLGGRGQTWQQEFE
9797	23698	A	9870	138	401	DLRLKLNLSKNTIRLQQTVESSVLTKEMQIEKAKVRYNLI PVKIKR/SGNDRWN*GCGERTLIR*+ECKLVQPLMKTVNSFLKKKKK
9798	23699	A	9871	179	441	PSGKGIKGPDPDPKPIFNGFFFLKKKGVPDGPDPGPKPRPLETPPPNPKPGKYGGGP\WPPDPID*FFKGPFKKGGPPTNIGNP
9799	23700	A	9872	57	435	FTVMRKMLNNNSGNKK*GSITPLKDRHSNPAVDNPNBNFRIPOKEFK/SDY*VTOGDTRECKPT*VLKTLIDNDRCKEKMILMNQKSELLEKKDTFRELQNAESFNHRLDQVEERITTELE
9800	23701	A	9873	228	443	FSSKFTILSVPLFLPLETSGSVAGQVQL*DYSSLQPOS PG/SGNPPTISASQIATAGACILHALLTFVFFV
9801	23702	A	9874	349	2	KKPKKKKFLDPKNGGFFSPSP*KFFFFLKGFNFRGFPFNPPPKKFSQNSQLVFPLPPLKKKLP/CFTPVKFGP/SQRFILKGPPPLFFFFFLLDRVWLCPQNSAVARSIS
9802	23703	A	9875	405	2	KKASRNBNVRKKKKLEMTKLSEGMKLKAMGQKLSLLAKQVNVAKENILKEIRSAIPLNTQMTMRMONSLADNENIL/VVM/IEDPTNYNIPLSQSLIQSNALP\FNSMKTERGEEAA*EKFDALSG*FWTTKERS
9803	23704	A	9876	355	394	TRPYTSHQEQSP*F/LTGALSALLKISGLAM*GHFHSITLLGLLNTLTITQ*WRDVTIR*SAVQGHHTPVQKGLRYGILLFITSEVFFFGAGL*AFVHSLAPTPQLGCHWDPPTGITPLNPLEDPLINTSVLLASGVSTIT
9804	23705	A	9877	47	85	TIYIHI CVRIYACRCVCVAYITHIGVPAHLTEQNL/KPARTQSPAPQKNPELPVLDVSI SLDRAGQVLELNHYRLNGTCRTDVLPKVNTLCRL/NFFPCLPILKELQELP*LRNITPLEPQPIDYIYTVGRAYICV
9805	23706	A	9878	2	389	GRGQFPPEFFPYFHWGSGLVPSPTNKKPLGEVLGGGWSNRAPKNGGGGPPPIILAF

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9806	23707	A	9879	351	1	KPKGPGPKFVLKFSNVPLLEFPKMRG FLPKGGGLPFFFFFETKSRVTPGVQ WCNFGSL*PPP/TGSSNS
9807	23708	A	9880	123	387	FLGPKSNFNFPQKMPFAFFPKSHRAR VNEIFS/RLSVINF*GLTKPQLRFFSLL NFSS/PIPPPQFPRSRIKEIRFSTLPT ENSKIKKPLFFF*FFFF*DRVTLCCPGN SAVVQR
9808	23709	A	9881	341	659	SFLWKLRFSGAPTCMRCLLA/LLSGVSQ LOITGVMDPLEKAVCPFSQLQRHAGKT ALFRAVRQQCFEFAF*TELFPC/CSG RVGG
9809	23710	A	9882	216	1	SFLGRVOMHACKSOHFRRLRQVPHLRS GV*DLPGQHDTELGLKMP/KQLARHG GMCL*SQLRLRLRQENHLNLGRGCEL RSQHCTAWATEQDSISKTKTKK
9810	23711	A	9883	2	244	PKFVWVLRDQIFPKFGPGQGF/GGFG NPQGGKKPGFWGLG*KKGGFFFFF LRDGGSFCCPGNSIQW
9811	23712	A	9884	310	2	GRVGAVGRREGNFYKCEPLPPPPPEGR QQNLCKFLTGFSLPQDKEP/CFPV*KK KKKKKKKKKKKKKKKKKKKKKKKK
9812	23713	A	9885	242	358	IFLQTLPLPNTFNSLSEYCIIFSSYSFT **KQ/TNFISSLILYYI*PSGSIYNL *Y*ELFSQNLISYQHFLW*KKNGLGAVA HTYNPSTLGGQGRMLWSPG
9813	23714	A	9886	360	2	RTVWLNNI*MAKHRE*CSLPLVIREM *IKTPVTVH/VKMAAL*KKK*NITR/C W*ACRTAVVYCVNGFPTQPL*RTVWL YNNIE/IPCDAIPLGMYLKE*RPOTV AHTCNPR
9814	23715	A	9887	236	347	LLRLGFFFWAKGKKRLWEGPLKPP GGF/CQKLFSPGGGPKGSPSIIILPK *PVWVGPREVF*KKRFKLKKFPPTFS /Y/LFFFFETESHSA/RNCSGAILAH CNLCRLGSSD
9815	23716	A	9888	310	3	IKGFFFF*TESHSVT/RECTST/SAHC NLCLPGSSNP
9816	23717	A	9889	119	391	NFFFFFFGSCSVTQARVQNSDQ/BSLQ PRS PGL/SDPPTSAS*VAGNLKFLSLGLC SSL*SLIS*DTKKSQVQITDLDLCYTVV LCLFFEMESHVSUQGVQWH
9817	23718	A	9890	195	3	APAYWPHARDSPPFFFTNFPPFPQVG GQWPNSGSPQAPPG/SPPP/YSASAK ISGAPGAPFPFGPNFFFPSSPTFFSR DGVSPYEP
9818	23719	A	9891	3	378	DVSLLLPRLKNGTILHCHCLSPV/SW DTRL*RL/V*FFFLVEMGFHVAQA GLELLTSGDHP
9819	23720	A	9892	231	1	RDGERNNHAGTASAKAKRYSLSLSPR LECSGTIISHSLSNP/GLKMSCLAST SSWDFRPAPHELAKTKQ/HATEF*EG ESPYYVQAGFKLJASSSPAFSLPKWCD YKL/DRHAW
9820	23721	A	9893	2	347	PKPFPFKFFSP*N*KPFFQISPAIKQKI RVYQS/ILKTFSTFFFGHVSLLPRLE CNGTISAQCNLCGSSSDP
						APARQENVVCVVCVVCVVCVVLRRHC

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						EVLCFYHMLGKKRSTYAY*LVY*YIYIH MCVYIYI/YIYV/YMIYITVCIYTH
9821	23722	A	9894	28	382	TAHLEAGATGYRTFLPALGLLCLPWL DDGAGQTAQ*SMILLDHMLLAHRAHLEP I/DTYYEFETYIPKQKYSFLHDSQTS FCFSDS IATPSNMEETQQKSNLELLRIS LLLTESW
9822	23723	A	9895	93	386	FWKTSHTYKFKFSCSLISPSDLPLTC ICMHLKLLKQSSFTLGLLPLFWLVEET QSHSITKQPCPS**LSAA/CHLPGSSPP
9823	23724	A	9896	174	1	TLDMGPRKKNPFFFFPRTRSRVTAAGV Q*HNHGPLQPPAQ/SSDSP*TSASQADA W
9824	23725	A	9897	251	386	LQRLCSGTI/SAHCNLLCGSSNPLAS AS* IAGTTGTLLGDVST
9825	23726	A	9898	127	393	GHNGTLGASPAFLSLALFPMGGRISTQ LDGINKS/FSLPLYFLRHCSLSHLE* S GALITVCRLEKLLGSGDTPASASQETGTA GTCHT
9826	23727	A	9899	3	334	KLRLGQINTSAVAAKC*SERES/R/THL TLNQKLEMIKLREGMKAVIQKLLGLL YQ/TSQFVNAKEELLKDIKATPVTA*Y IGKQNSLNCLEKSCVLLIQDQTG/HNI FLS
9827	23728	A	9900	356	1	GRKPFPHLPKATLLPMIPVLGGRRALMG FDSRCPVPSCSLVLLTPLPLPLTARE SLCPCPPS*TPQPSVNP/H/GKLARSF CVVSGRQSLP*ASIVPLIAPPALGDRDS TPSQKKKK
9828	23729	A	9901	118	343	IPYAKEKKKEBNVLFTHVNLCSNAPF FETGSHFVTQ*VHVNCSLQ/PNHLQ GSGDPP*TSASRAAGATGVQH
9829	23730	A	9902	321	50	SLRTRV*RPSPAG*NPFCCLKPKITFGG GG/ESPLSQILKRVKQENSYN*GGKGFN *PKLPPCPLTWATKTPSPKKKKKKGNR TWETSVS
9830	23731	A	9903	317	8	NCYDPNSGIVTPLLGLLPEKRT*V*VRT KTCT*MLIVALCITTKNK*SKCLSTDK QVNKI*YIHIMEYYSPIKGRKY*HTLQH /WMNLENTS*KRLDIKKPHI
9831	23732	A	9904	287	3	RGALNGRGPGRGVSGFAPFKLQKPP GTFLNPK/Q*PFFPNPFP*KKGAFFHFF LLLP*SFRTFTFVVT/KLECGGALSAH CHLCSGSSRA
9832	23733	A	9905	2	406	FRVTSRSSRATLFFFTFFFPVFFWKGK ETWADPLKVC/TPKPKCYGQADPAG LPPPGVIVFVSLCRVVKKKKKKAPPGG VLGKKKKITP*TKGGFTPLTGGF*KKSL FGKKTILAVGGPLLJKNFF*EKPR
9833	23734	A	9906	1	296	IWVGATECFKFNNTWGGQRTHTPTCKD TYRLKV/KGKKIFPHTHINGNQ*AGI AIVISDKTDFSKTITR*KGHY/TMTNG SIQQGDILDWYKSNCSF
9834	23735	A	9907	474	41	PHRYTLTSLFTHVLQ*FTHCFVHLFIHS FFYALMKSLTQ*FTHLYSCF/ICIDLLI SSCIYSFTYALVKSLSNLSHFSHTPL Q*FVHLFTPLLTCSFTHSSIH*FHSLSL FTQLHLFPHALVSGFTVFIYLFCKINV

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						FLIDK
9835	23736	A	9908	286	84	LKPPPPPPPPFGANFLCFIRD/GPIHVIG QDGLPLLT*SASHGLPKCWDSCRCEALR PASPLISGPHQTT
9836	23737	A	9909	316	63	DQLVRSIGFEALMSPIFFQMEF/SLS LPKLECNAGISAHRNFCILGSSDPPASA AV*/PMANLLKLCASVSYCIELVLNELH WIK
9837	23738	A	9910	370	461	F*F*FLFSETESHSAV/QLECSAMISGR CNLRLLGSGDS PATREAGAQESLEPRRQ SEPGLCCHCTAW
9838	23739	A	9911	294	28	FGKSTVQKEFGKMFCEMKKPTGENAVN IV*PTTKLEY/NI/NIDKIVAGCETD SNFERSSTMGIML/SNSIAMYTEIPRGR KSOLMGI
9839	23740	A	9912	307	463	CKL*WLSNNDVIVGSLIVT/TCITLGV LIMGD/RLCMCGEKEYLGNLGTFLSLL
9840	23741	A	9913	377	28	REMLTVKPLAPSPFRSRAYRAIFFITP TWVSKSGKVTGLPFLHIFPPGP/CPGL PIFFFIKIKGTGRFFPGWFFFSRVSICC PG*MECNAGISAHHKLRLEPGSRYSASA SEFHR
9841	23742	A	9914	384	725	HLTAIRMVVIKDTENSKCERGC/KTLMH SCWEYERVQELWKIRN*P/LQQVE/LPS PCDPSIP/LLRMYPK*LATD/CXRMC/C IPTSIALFVFTK/SWKQ
9842	23743	A	9915	187	3	QPHXHLGLDNIYIYFFETGFCVSAQTGVQ *RDHGLQPRPP/GSRDPPTSGSRVAGR PROENG
9843	23744	A	9916	15	167	DGVSLPLPLECNAGIILAGCNLR/LPGL K*FSCCLRLPSGNDYRLPPPHDAHV
9844	23745	A	9917	345	477	YCSRTSLPL/TLKKGSA*FGAVAHYNP SLGGRGWIT*GQEPK
9845	23746	A	9918	460	42	HQRPKVDRTTKVGEKSRKTGNSKNGSA S/APPKERSSSPAMEQSWTENDFDELRLQ EGFR*SNYSLEKEEVRTGKEVGNLEKK LDENLTRI/SNAEKSLRDLMEITPKA*Q LPPERTNLSS*FNOLSERVSVMEDEINK MK
9846	23747	A	9919	282	21	AAGYLPSEFPWLISLGRRLGFLISVFFV

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						RGRQAMLSGDYHPVVRPSRLLCPLPTQA
9851	23752	A	9924	254	3	PGGFFPGFLPPLDQFPKGL*RLAPPC PATFFFLYQISKPPFFFGKYQNFPPF FFFFPEKSRSVT\RLCNGAISAHYNL
9852	23753	A	9925	309	1	YTPITMLLGYSNELKTINVMKT*+*MF TATLFLAETWKOPRCSLSSENI/QQLN YIQT/L/EYYSVVRNIK/LMKTW/MKLK YILQSEKTSSEKITYI*POLVDI
9853	23754	A	9926	237	2	RMPNPQLILKICFLKTKFFS*VSK*N FKYFLGPFPPFFFLRQGLTPVT\RLCEGG TISAQCNALPGSTVLRASQV
9854	23755	A	9927	244	1	KFOCLMK*+*WNTQRLDVEKPKLTH YWNKRKL*+*PLMKTVRLAR/NLKIELP YDPVILPMGNYSKEM*LCQREDSRA
9855	23756	A	9928	2	644	TVQVDQKTRINTHCLQETHFKCYTYRL KVNRR*+*VYHWNINQEKALVAIDGAYFR ARKITRDKERHY/IMMGSLQKD
9856	23757	A	9929	1	364	GTSQTRPINNTVTSKCSERKT/R/TH L/TANOKLEMLKSGGSLKTDMG*NLGL LHQTVSQVVNTKEMFLKETSATPLN* MIRHQNSLIAATGKVLVNIQ/TQHTNT LLSQRLNNKALT
9857	23758	A	9930	88	374	ILKACGCPGPNPHPWGL*GQGGGLNLP SKSPPHPHPRGDPDWGTPIGDYGFKEP KLPHGAGLPKKPCSGGQNM/PKISGF
9858	23759	A	9931	384	2	LCSPRFFYRKIMGGQGSRLLPFPWKP GGKDCFSPGVLDPPEGRGAPCP*KKI RWG*GAAPVVPPEG*/VGRALTEPKI PAPVSGPCSPALPBGQSETPFFLKKKK KEKSEAMIPPPGPRRA
9859	23760	A	9932	32	359	IFFLPPFF*/C*GGPFPFPQGGQPKT PPWPPINAKRTKPLSKKKKKKKRAGAP PPPKGGPPLKKGGEPPLKREFLKXNGG ENFKKKKINAGGGGNPREPPPPGQAR
9860	23761	A	9933	138	1	TOFFCCCS*SFALVAKGVNOMCLGSLQP PPPG\SDSPTYASCSC
9861	23762	A	9934	103	355	LQGACCS*STSANRQVNI\PGYANGR CDTITCILVFIIRNSWLITPILATMFCY HVG*VRPQEQAGNRVLSDDL\PPVTC
9862	23763	A	9935	29	363	AWSHNAPLFFFRBELAPVPGRENN FVSLKPPPPG*SPPSAPNPPKGGNKGP PPQQLIFFYF*/GEGFSPYNPBGPKPP TLGKPLGF*NTKKICPQPRGLKGGQHI W
9863	23764	A	9936	173	363	PKRKPILSLKRAPNSNPGD*QKFLKRGH PMSQFQKRGNYPYDRNLEKLCPGGNK GSG/YHYGL
9864	23765	A	9937	360	3	NQWRKNSKFTQICKQSGACP*PKKERS SSLAMQSWNMENVELAREGSR**NYS ELKEEVVTHGKEVKNLEK/NLDEMLSR S/N*EKSLKOLMELKPKAQELHGECPSL SSQFNQLARA
9865	23766	A	9938	194	370	VSNFFFFETETFCFSAQVGAQQGNR*L KAPP\NCCLEFPT*ASRVVGTGTGCHS WLI
9866	23767	A	9939	426	1	SQEFKVAVSYDLTHMISNLSNETLSOKE KTKQTKQKKPY*BGRIHLKRCPTPLI



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						IREIQIOTTVRYHPTHIRI/VLLPQKON KCWCHEKLLKPLVRC*WECETVQPLWIT VWV/FLKILNLIKLPFLDPTFVVCITYQME FSC
9667	23768	A	9940	255	16	RVYIYNIYIMYLCIYTPSKLLVEIGPHH VGQDGLDLTS*SIKLSLPR/CNDYRYE PPCVNIYIYIMYLYIYMSDGVKY
9668	23769	A	9941	206	355	FLQGHAIKNGRG/WPGVAHTCNPSTL GG*GGRII*QGEFKTSLDMVEP
9669	23770	A	9942	3	402	HEELNPRSATSSPALVLRVITIAHTIAF ABGCFQHD/FCFQSPENRHIPLVFTTASK VRNIFYLLCRGRGILRFFLVLCIKDIPAI PLMGIIYPR/KSLYHKOTYIHFIIAEFT VAKIRVQSEKPSYDD*IKKIV
9670	23771	A	9943	79	328	CIKLLKFLCGLCPLFPCLNPLQKSCS VARAGVON/SLQP*PRLKHTPTISAS*S AETRGTHHHAHLISYNFLAR*VSHVA
9671	23772	A	9944	321	414	VPSNAG/VVAHACNPSTLGRGGRIT*G OEFE
9672	23773	A	9945	142	480	QEAQSFDFSSITTEVMLDKKQIRVIFL FEFR/MGRKAETTCNIENAPAPGAAND *QMRWMLKFKCGEESLEDEECGRPSE VDDQLRAIIEADPLTTIQEVAKELSID H
9673	23774	A	9946	191	3	FFLPRGGGSDVPRKPKKKKKGPPIRPF CPGFPLAT/INFPQIFFFFF*DGVS LCHPGWRV
9674	23775	A	9947	451	461	K*INK*KVKGW/RKEHIANINQKRVDT IFISDNMNFREKNKIIGDREGRYIIIKQ PIHQENLAI LNVYVPSNRVAKYK*KLI ELKKEIHKFTILVGDENTILSTIDRTR *KVS
9675	23776	A	9948	186	405	NHFLKISLF*PYKP*ALLKGLYKRRKR LVC*RDICALMITELVTAELMNQPKC PSTDK/WKMYICIMEYYS
9676	23777	A	9949	18	412	PEFRITITLPEKIDILL*LTN*VSFRSGY NINI*TSVAFF/YSNKIKSETGIKIVPF TILSNRMKYLGM/TLTOMKDLHETNYK MLRKENEEYQMNMGSNILKINIVKISI LHKVIYRVKFLSNFNAILLKK
9677	23778	A	9950	1	396	LAFDGRAERLKTGPHRWQDGLLELTS* SVRLGLLKCNDYWREP/PVPLWD
9678	23779	A	9951	307	405	GIVRR*POGLRPPNDALVFKKMWNP PTN/PRNGGKGWEPQGPQDPPQAP GFLPETWRGPNWSLPTGAWPPNSNLPP WPPAPSRHPAQRAPGSTAAPPPGGGGE GWDPGRV
9679	23780	A	9952	2	402	YGRPKGGSLRFVVLITTPGPKGETPFFL KTOKITGGGGGGP*PPLPRVRQENSFY SRGGGFN*PKRAPCALTWGKKQKFFLKK KIVFPQKPKLPGCRIQT*TKQ/SSSLF MGTFPKQ
9680	23781	A	9953	249	1070	SSFISRFYFICILYPLTTHSHSVTKARV CCDYN*LOPPQGAQILLPLQPP*SAG/ ITGVAPNTPOLIIFYFVE/SGGSHVAP RLAINSAQNIAL/RLPKVLYFTF
9681	23782	A	9954	75	396	GFGRKRGILPLPLNQKLTNLNLSKGLS KANTGQKGLL/RPVSQVWNPNGKFLRE

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9882	23783	A	9955	181	458	IKSAF/PIEK*VI*QNSLIIDMEVILG V/WKTKKYSHNILPLGLSLTQKRVILTF RLWNDGLYNTFDLKLQ/S THV*SLLLLF ILEPESHVS\RLBCSGAVTTCOSLIP GWSDSPPQAFQVAGTTGVCNNAVPSAFL
9883	23784	A	9956	67	430	LAPRLITYSPIKQWSPMSVRQIQVQSLA IGNFHNPRIPILTCHCYAFHRIILLPQMV RNFIYISISANKQBSKILKYLLIY NLRNWLGTVNIRYN/PS*LGVS*GORTS* AHEFETSQQN
9884	23785	A	9957	77	422	LPLALANASCRPQLCLDTDFINGPPTSGA ASQFLCPQTQPPFCSSRLNHL*FALV LDRITSNVVCRSP/SPFFLLPLPZA PLP\PPFFFFFDRVLLCHPGSAVARFQ LTAAS
9885	23786	A	9958	3	422	LHESLVTQODTSIKKKKKKTKPLGRTKK GGPSLGGFFGPGPPFKIVKKRQALIG PPFPCKKKKKPKPLFPKPLGKPPRKKG F*IGEPWKT/EGPGFKPLNFVFPSPWG GNFLFPQKPGKVGKILQLQPKKPPGK G
9886	23787	A	9959	370	2	PFSSWVANFREGDGRKCSVLQGIKCFMF CRYINVTPLVHFFPPIKSGTSFPFLYFF SPEVM/HFP*LPY*FGWALLSRF*/MSL L*LFFSKFFFPSSFFFF*RFPHSSPRLK CNGAISAHCNLCPL
9887	23788	A	9960	256	2	AWHEETAPLHSHCLGNQARPNWHRHAP\ PLILVFVFSVETGPHVQAVALRLASS DPPTRFNLLSSNDYRGLSPQPMRSKSAQ EG
9888	23789	A	9961	269	3	HQACQGVRSPTQCNWACKIAQBSLQIV RSSLEG*I*SPYDVPVILNVIYPRELKT \SLHTKTCI*RTAALFIARRWKQLKC PSIDE
9889	23790	A	9962	268	324	SGTILSH/WIFS*VGIEITIMLKVDPDQTK KISLRSAEAAIKYPLTQATASIIIRRAI LFNNRLSEQSSITNTINQYSSLIIDMAI AIKVGMAPPHF*VPEVTCGSPVTSGLLIV L
9890	23791	A	9963	341	2	ITFLPKTIHQSNFKRGRRKTDSNDLNR HFKREDTQMANKYM*PI*IKQI/KTMR YYFISKRTTISRKTSNIQC*DTWSPGTF INCLLECKMVRLLWMTWQFLTEVHHL VY
9891	23792	A	9964	250	2	YHPVNLYFKYISPIDV*RGCFYIYFDYP LCSCFSLHPILVLQ*L/LFFFFPARESHC VARLSCGVVSAHCHNLFGSSDPSAS
9892	23793	A	9965	3	334	FTLRHHLLDSEVF*HLGCVHLLATIN SAAINIPC/HSKV*THP*YS*MYRGRTA GSYAT/SMMLNLRNSTLLHNCTCF*PF YH/WE*VPISQSQKLDFFIPLIIAIS EG
9893	23794	A	9966	179	352	NQR*TEILNRNPSNQIESVILKLPTRKS HRHPRFTALRYQTY\ILKLKQKVBGBG LL
9894	23795	A	9967	2	350	THPSINSFIHVFTHASMSLIHLPTHSF SIYLPKSFHILFHFFSFLFLRPSFT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PVATYSPTHTPTYSSTH*PIYPCVYSCTD <sup>B</sup> ETHSTPHTAQHLPIN*II/IFIYSFISLFF
9895	23796	A	9968	228	558	CHQLKQELATPSTFVLQLFSGHLDVVMQAWAQRPD KYEYDNK*FISIKKIQTPLISKRMK/YVGLNLTR*VKDLNENYKILMKETIEDTSEWKD <sup>I</sup> SCSWNGRINSVKT
9896	23797	A	9969	196	2	DRKVFFRPLFLIIQGLKKIKPLFPWFFS/IRGRG*IFFFFFFFFETES <sup>S</sup> PLRLECSBTISCHCTP
9897	23798	A	9970	245	1	TQDMCVFIYTHIYISHCYMYIYIHTETHTGILFTPKREKNSNTCTCATKDNP/CMTLC*/HKRQTHITHTIHTIHTHTHT
9898	23799	A	9971	163	380	NHRKFKNGR/HNGNKIKYIVTKMINSNPPTIRNLNVGLKTPTKRQKLSDSIKKQYPSIYCL*/KT/YLKKYD
9899	23800	A	9972	328	1	AKCGVLKKLIELFNSTPHGSCKT*VTQMFAALYIISKKYKQSPSPSNE*WSEINHILTIYGSAAVKISWG/RMNNLENLRLSGRGRGHILQSDVDMKSP*AIPO
9900	23801	A	9973	200	3	MAKCSSEKRSKR/SITHNQKLEMIKLSBEGMSKAKIG*KLGFLOQ/VLHVVIKAGKPLKEIKSATP
9901	23802	A	9974	111	517	NLEQPLTKRTIANKPIKINPTITLITINVNGLNLTK/RQRMSD*IFKNQDPTXI/C*KKN/HCKYKDTNLTILKIG*KNLYDANMLTQIKKKAGVAILI/DKIDFRA/TDI TRAKBGHFTIMIGSVHQYVITLNVSAHAS
9902	23803	A	9975	342	3	PLATKKIFFFFFVFPQGGPPPLVAPFFWAFGGGPPKMAKKKKFFGRGPPFENFFP*GFFFFKTGGFFFLRPSKKVYFFFFFS <sup>T</sup> ETESCSVA/RL <sup>E</sup> CSGTSIAYCNCLPGSR
9903	23804	A	9976	13	326	TLDHNRKPSSTLKT <sup>P</sup> NAKRDVEQKQFL/LCCW*ECKIVNVLGR/L/WQLTKNLNL*PYDPEILLGLIGYQKELKTCTHTVACT*MFIEALFVIAKT*KKPYSSVG
9904	23805	A	9977	74	396	LAPRTQPLKCSAPLRCRCHTQSLPFFFLRLRIFYFFCFLKTRAHSAQAQAQ*RDHGSLOT*TPTLACTPASA/VARTTGRHHAWLIVFFL/ISKVSHSLVCDKT
9905	23806	A	9978	287	2	QPHNSSYQIPTFKTIKT <sup>P</sup> PNLKNNTTPIKKKTQ*FP/PSIND/SYPSTHPTHLFIYPLTHISPPPSPT <sup>R</sup> IRIHPPTILYSIHPSTHPSIHPPSR
9906	23807	A	9979	97	332	GNNDLFIYFFFFLETGSHSAQAQWQNC <sup>D</sup> HSSL*PQPPGSGGPISTC/RLGLQACMCHUAWL <sup>I</sup> PNFFCKGRISLPLGLLR
9907	23808	A	9980	168	2	STWRWUYWKTFPFTSKS/WPSTVALTYNPTLGGQRHTY*QSEKTS <sup>L</sup> ANIVKSLKRSK*RRAN/SKTSRKSITIKIRAEITATENRKLPIK/SNKTC*FEKTDK/I <sup>D</sup> NPLERLRLKKERD*ITKVRNGREDIL* <sup>N</sup> NDLTKVKKD
9909	23810	A	9982	230	412	CHTYLC/D*PTDGV*CHTYIYFGHGHHTHTYTHTHTHTHPTC*VSKILLKKKRR <sup>T</sup> CSVCA

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9910	23811	A	9983	229	415	SYVFCHEIRFCPLDSINKEIVA/SQVQWC VSVVSTT*VAZAGSGLEPRSLRPDWASQ RDPISKX
9911	23812	A	9984	2	288	RGYDSTSSAYTVGHPT*EDKATITRLSG KENVKHAGGETLRLRLDVP*QRIIDS VGNLNSA\SAMM\GPPRLPKVLGLQAWT TMPGP*KYIHIFP
9912	23813	A	9985	246	3	FLIDYQYCALCCHCFLFNFANQGHFNIL LGGVKHTKFPKYS*KFSVL/NLDAVAHS CNSSTLSGLGWITRGQSFETSLANDVK
9913	23814	A	9986	342	1	FLNFGLTVGFPPKGGPPKPLRLDGLALPLD PPQFLGVFKRGAPFLGTQ*PHF\LEGPK FWFVEPRAFFFFF/CCETLSAICNLCLP GSSDSASASWLAGITGAHHYARLSRRL RQON
9914	23815	A	9987	330	1	NRFLNIAVAASKCSSEKRGYTSFVLBRK /LRKMIKLSSESMITVTTG*KLGLICQT /VQVNTKEKFLMBIKSATPNKGTVTKS NITLADREKV*VIWIKNKTNHKILPSQ
9915	23816	A	9988	209	2	IKGSHFFPLY*YRKILIIFFGVKRGKGF YSY\LFFFFKEGYHSVTQLKCSGMILAP CNLCLPGS*DSPTS
9916	23817	A	9989	256	357	QHRNNTNTEMLNYLC*IIYVHF/HTHTHT HTHTHTHTHTHTHT
9917	23818	A	9990	263	1	IQTRVFENSHLPSYVHFPHGHSYLFCS L**AFFRH\G*FVLSVHFLKIFLNLKKI FPETG\SHSVAQACSNGISAHCNLCILG SSDR
9918	23819	A	9991	3	368	SLDPRSRLELAKIVPPRSSLGDRAPC LLKKLELFFETGFCVQPGVRWCSHG LQPRIPG\SSNPLTSAT*VAG\IAGMCY HROLQALF
9919	23820	A	9992	294	391	SETVAHANSSTLGGRGWIT*GQ/ESQ TSLTHW
9920	23821	A	9993	317	3	TDKELLARDQRKCFVMEFSPGHKAMS NVDMTKDEYSINLVDAVLELRADSN FERSSTLGHMLNSISCYKEIFLERKSQ LM*QIPLLM/FKXLPQPP*PSA
9921	23822	A	9994	193	395	IPWITCCSSLSVLAASFCTFMLNRQLLS LNLMMQ*DHSLSQSLIQSKSATLFSVT AERGDSEAREKLEASRSMFMRFSRCL HNIKVQGEARTDR/EAPASYPENLR/V KDEGGYTK*RIFFVDEIAFCWKTMPSKT FIAREKSIPGFKVSKDRMTARGRSCL
9922	23823	A	9995	82	420	SPLANKLCPRGAAATVRCUSA/LLEDYSQ LGYTQVRDPIERAVSPFSELKRCRETT AVFTAVRQGHLSLQK/FLLPVQLCPAH RGGV*RQ*ALLCCGGLSPVQAPLPLCLP TQ
9923	23824	A	9996	376	1	CGRTDAPASTSPYATVTRFLRPQPCVL DGLHCPARAPQQRSHVTKRGPRQ TA/PATAAPPRLPGSPNWCPEH*+CR NSLQOPLSAAVARGRDNALAGLPATVS ARFQEQQONTV
9924	23825	A	9997	495	982	VQKFLRPNLAPKKHQRKLADNSLQGRLR SLSPSTVVICMAPPYTVGLSSLLGLVTA VCLNRMHSHQQRHN*ASFKKTHD*TG LAEP\SCARKQCSIGRTYSNAVISPLNETT

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						RIMRVSHTFPVVDCTAACCDLSSCDLAW /WFEGRCYLVSCPHKKNCEPKRMG
9925	23826	A	9998	401	341	LASKCSTERV/SRSHTLQKLERKFL*RGKM/SKNEIQOK*ALLYQ/VSQVNAKEKFLKEIKVD/LMAQMIK*NSLTADVKKVLVVKIDQTL/PLGHSVIQSKALTLFSSMKAQ*GEAA*EKS
9926	23827	A	9999	30	393	DTTILKRLQITGAVATKRWSEKSLTSLNLNAQKLGITIKLTSEGMLEKAKGQKRGGLSCQTVGQVMN/SEEKFLKEIKHAIPGNT*MIK*NSL/ITADMIRKVLG/WSKVI*F*DOTSHNIP*SQN
9927	23828	A	10000	133	1420	EGRRLLVPTPGVASLQTLCCFLPRRGCSHG*ESAATHPPGPELVLLAQH*AGYLQ/DPS/PRATKSPQ/PAGVQPCPLVPQLSRAAAG*PDYT*GALFSYHCKALRA TANRHCPGCG*WPG\PAGSPPTSRPLSHPSPPSPPTGVSSFLNLNLVCL*ASDAQGHACYPGPVPALAGQGHDSAGRLGDPGHHMQQAALHQ/DQQPGHQHAQTPQS AQGLGC*ATHPOBGG*VGQQLPAG*GRSHPRFPVIVTRPMGRSCPVATVRPGPGSQGQTFFGLV\PRGAGQNTPGGAAPGLSCI QEVTRGWWW*GKKPLGHTVPCGAVRCPSS*PHPDTPKOTGRBGLPPTSPVGVGTQMS\BGRPCPWTLTMSPWGR*SPRASCAMLHPCPGSRVGGYHOCPLPHHMPQSTAGQAGQPHYTDIKAS
9928	23829	A	10001	1818	6682	IKFPEABEESIQEVLYLLFVRVABEKENP SRVNSQRIYEQVYVSI CNQLYRYENL/RHVKKDERGYTBELLAYSRDIEMLYP YRLLDINWGFSTTPFSXYTGIMENIMN SGNHNTAADCLRLGLGRNQYIDLMTQC RSSKKFFRRKTAGDLLPKPVLAIKAW MVVQAGYITEDDIIKCTWPEKCATDKTV DSGPQLSGSLDYNVVHSLYKGFYILDV PMSDDSCIAVAPLEGFVNRVL/NFYDF ETLLYKIFVSVDEHTNVAELANVLEIDL SLVKNAVSHYCRLGFAHKGQVINLDQL HSSWKNVPSINRLKSLDP*KMLLSWGG GESRRPVQERASSATDITDINSQERPADTA SVRSLSLSAGHTKHIAFLFDSLTATFLM MGNLSPVQSTGEAGQRYFDHALTLRNT ILFLRENKDLVAQTAQPDQPNYGFPLDL LRCBSLLGLDPAICSRVINTNITLLVSH APLNLELPSVSCPTQHIGAPLBSVGV WFKLYLYIVITQCGPPSLLSKGTRLAKL PDIPQSY\DRLLITSSGHPDQGVPTSH VITMLNDALTHSAVLICQHGHLGIGRTV HVPPFFDETELQEDSC\NMGVHKAQLIL RNRVDLQHLGCVITMLNASSQLANRKLSDASDERGKPDPLASGSDV\NGSTESFEMV IBEATIDSATKQTSQATTEADHWPLELC FGILPLFSSRLNRKVKYRKIATHGL*EKR AFKNLLHSSRKLSLQVLNLFVHSFOGRSLTLDHTEPSSSLSQSSFADMGVPLPA KKFN/SLKIVSY
9929	23830	A	10002	439	1135	MAVDFFNFVTLKVTVGYLRLSFLAYKF

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						FSFPFLDLSI/LLSPRLCSGVIPASLQ PLLPGFKRFL/CLSLPSS*GYRRAPPFC PALLYF*VETGFHVGAGLELLTSGKL TRLGLPKWDYR
9930	23831	A	10003	216	572	LTLSVIFPTAKQSVLPTICMLNMRKWL NDSAP/PII*KVLEPKIFFFFFF*KG VLFPPGGRKGQAQGLTKPS*SKLKI FPLNPPGGWKRRVPFAGYFCFTIKRVS LWRLGN
9931	23832	A	10004	3	354	YSNNPKDKRGETGINNEKTNMVDLSS TSVITLNF*ML*/D/KIN*KVFKSP*K KPTLCLLETYPKYIGGLKVKRWKKI*H ANTIGKTLVAILITRQTSLS*YPNKE KSYLLKE
9932	23833	A	10005	187	455	ASIHSLGVRICYYIPGCIHPKBSQK NTGGRKSTQKPLVN/HR*LGHRCKM* NBSGKTFTRVQSL/ACHKRVYTERKSYK C
9933	23834	A	10006	134	456	INNLPTGKPKCAWKQVTSIDLSPDAFTN AAIHSLSPFFPPFFBTKFLV/PQVQGGP HNLN*LLKLPPKL/SDPLVA*VSKVGT ITGPPHHPLVINGFKKGGSPMLPR
9934	23835	A	10007	210	451	CYTTTQTTPQANDSMGLKPHVSLTL NVNMLNTPPKRLGVADWK/TQDPAPCC LQETSILTCNRTHRFKVG*/WKKLYH
9935	23836	A	10008	169	462	YPCWVTMAKNTSYNKCWQSGSIRILPH CRWEYKMASPLWK/SQFLNK*NMELP*D LPILPLDIDPKEWKTGVQTKTCR/RMFI AALFPTSRS
9936	23837	A	10009	490	724	EMPT*FMEKNFLAPGGVTPPPGVNTRV NPKTADPDKSSSPFLEKSKRGLIEGL THLKTLLMPLKKRSGRPVFL
9937	23838	A	10010	306	588	KQFTRAFTESSMLTPVPLWHDTKAG SGIRDQPSQHGKTPSLLLKIKLAGHGA GL*/SQLERLRQENHLNPGGGCSEPR SCYCLAAVTE
9938	23839	A	10011	473	53	ISLQDSDTISTINPRMAPLSSSKRKS HMSFLNQK/L/EMIRLS/BEAC*KPRS QKLGLLSQ*PSCSKFLKSTKSA TPVN TQMI*K*NSLITNK\LKSVLMVNIKQDI KHTISLRQSVI*CKALPLFNSMKAERGE BSAKC
9939	23840	A	10012	184	455	FWLSLTKRPLSSVTQKRINRET\LLTT KKKKDCNPLGGLLIGGSCRLVYRHY ATLYSVFCVDSKSERGSVDPTQVFVET *DKCFDY
9940	23841	A	10013	203	453	KRLYSIRERSSTSLLLNQSK*LKL SEQAMPNANGDRLKARPLSPNSHLIKT KQKFLKEV/KCATP
9941	23842	A	10014	237	483	TLIRYTLIQGLFSYIPPPFPETEERSVA QNGVM*CLASLPGSRPCLASAGVAG TTGPHV/HAMLI/CLCATGS
9942	23843	A	10015	157	875	DDFVGRGRGESSANPSGRNRNVSSSV GSMAGITTTIENVKRTQVLQHQADRAE *AHLQ*EAKGKRWANEQAGAEVASVNG RIQLVREKLDCAQECALATQKLEAGK AADESDRTKVIEIWAJKD/E/EXMRLO EQQKBAKHIADEADGKREEVACKLVI

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						EGDNGCTEERAEIAESRC*EMD@QTRLM DQNLKCLSAAEKYSQKEA*CEKERKIL TDNLNKSPPMR
9943	23844	A	10016	579	30	CGISTKKNKGMKQNSSEISTCVHNQIT LHKIMATQMG\KNSFNNK*C/W/EN*V ST/CKKIKLSPSVTCTI*KQYLKIKYL NIKI*QTS*IS\NGOKYDGLGTNELLQ KTKNLMFS* L* NQMEKQILIEKWDYIK LQNFCTSKERFSGV\KSPKKN/DEIFEN HLFORS*FSQ\INNV*NSIKSE
9944	23845	A	10017	44	228	EFVCRVGLW\CVVLQSLQLWEAAGG SLEPKSLRLQ*AMW\DCPTPW
9945	23846	A	10018	471	40	PGEGRFQQTIRPPFLPQKGGPFFKK PKKKKKKKMIKLS*KPRQANQ*LGILCQ /TSQVNVNAKEKFLKEKQATPVNTQVR KLNSLIADIE*VLV\GTEDQTSNIPFG QSPIQINILAVFHSMKAEQSKATEEF EARS
9946	23847	A	10019	217	486	EKIS*PVYLSLYLSIYLSVCLSVYLLSI YLSIYLSIYLCYLSIYVYLSIYLPV YLSINLLSI/CLSPIYLTLYLSSYLLS YLPYTLTP
9947	23848	A	10020	327	1245	TENQQGVLAALAALKRNNPTRLKWFILN IDYTKCEAPHVFKRRKKKLNKIKQ KMLPTKRIYLAFTYSTQ*QNTH*PFL SADETHGKIS/HVLGPKTRNNKFR
9948	23849	A	10021	329	490	GESPTRNHCSPKQSEKVTITTFETES RSVTPAKV*MCNLGSLQPPPVGTS YRVLEVLGYLMLIRFVLLZCSGQRAQ FREOSRCTACRHPAHTLHAQVSRKV SSAKR*RETPKKRSARKSAKPAPQSE TKPKKAAGKDKSSTSS*FSSSSSLKAEK GGKEKQAEVADQETKDLAE
9950	23851	A	10023	448	477	SQVFETSLAS*MSKNLL/WAGTGATCN PSTLRQGGQIT*SQVFETSLAS
9951	23852	A	10024	198	455	SLKTRRRETPEDFHGQCGKLHVSEKPR VMSGQTESKYASYLSFIKVLIRRGVRA S/TRNLIMLFQTEQCLWFPE*GTLDDL KDW
9952	23853	A	10025	469	26	PPRAVQPPFLPSSSLHCTVPLCRVFS TSRPSLLPALQVSAKMSPLV*SSLLLP SLGQGFPMASDAPRL/PHRSLRSCVAA AHSRAELDRHEAFLQCSLGQWPRNDFL SFFRDRLVLLCHPGNSTAA*S*LTAASNS GAQVNEFQ
9953	23854	A	10026	222	489	KKKKKKKFPCFIARVKSNGAISAPCNLC LGSNIFPASTSLVSGNTGACFARVNF FY*ML\FVLMVGFHIGESI
9954	23855	A	10027	313	2	QDWEISKLYSYCHS*VREL/IFLKIRLS LYYILQHSNKNITG*LQFESCYIKLAG DKLAFRFLTKNTNHQLGLVAHYNSTL GGRDGNIT*QGEFKPSLANM
9955	23856	A	10028	49	388	TPKTRGVFPFKGWLGVGAFPPFQKDI FYFPRTPMGRILVSPGKKKKKEV*RVLY GLKKAKKI*FVLKVKFSHKGFFGEIQFK KLFWK/HLKRNPPPKKKR
9956	23857	A	10029	394	231	GRQIASAQEFKTSWGNMAKLCFTI*RD VSPCCPSWS*IPELKQSCNLSLPKY*DY

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						RC/RNTTTPGL*HLLFRCLLTITPSYL*FCKSFLLLYNDI
9957	23858	A	10030	265	2	HDNMRGSDYFPASNGLAVPFKRQVFTIA SNFLEKSPRLAFT*LOVD*ERKWAG/P VAHTCNPSTLGQGGWITRGQEFKTSIA NMPKP
9958	23859	A	10031	235	413	KGRGLFFFTETFRKKRKGSGGSLPKP HLFGRPGGNHRVIRIL*KRGPYKGRVVR LKS LFCDSPPPLASQKGVSRKSPPPRP CPF*RLFP*KKAFRLFIPIKV*ALN/ SLPFI GEGKTLFFFF*DRALLCRPGNNA VAPSGKLSSCLSLLS*DYKRVPPCLIA NP*RF/CRN
9959	23860	A	10032	167	424	GRVETLRKSHVTKPLSFFFPFSETHS LSVQTACQVW*DTALSASWTPVTSDSP VSASRVAG/IGTIGVREHTQLILFL
9960	23861	A	10033	252	3	VEECLSSGVQIQPEQSHTFSLQKKITFF \*LAGHSGMCL*SQLGRLRKWDHSSPG G*SCSEP*SCHCSAMATE*DPISKKKK
9961	23862	A	10034	175	492	CPTCPFVVIPLCSRFQVQLYMNVAHTH THHTHTHTHTHA/HLLFSLFSFLRQG LSLSPTLMRSGMI/CGSTQSQSPRLKQF CSPRYRG*GWRGA*/DPGGRGCSE
9962	23863	A	10035	200	448	LYLHLVQLSLPDPPTPLFRVCEPVLSL CLSTS*FP*VCFPIVSLGLF*GRVLIC RPGNSAVVQSQLTAD/SDFPVLKHSCL
9963	23864	A	10036	229	463	MILGTSKTSFSLATLANFPPTLNLPIF LDTGS CSVAQADVQWHRNQGSL*/SELLG SSDPPTSAS
9964	23865	A	10037	164	422	GLSSQLTDGHLALLRVGGSEVGSRRES EREAGRERERGERDRSGG*RETEREES GARERERKKEKRE/EROREK
9965	23866	A	10038	1	490	PNQIQNVLHMTSFLCSVSVTFPKSEI YNGQPKFSFFFF*DESCSVAQGVQ/W CG/LQSQQPRPPG\SSNP\PTSASVAG ST
9966	23867	A	10039	255	446	FPLRQSCYVAQARVQ/VATHRCSSHITQ LPALASSNPALLAPRVATAGMQHNNQ L*YFFRIHS
9967	23868	A	10040	157	390	DHTCPPPSTADYRLS*FLYFLLLFRS LALPMLCSCGSAHCTLCVQETRETD AAHFAARTIRAPHPAQLTIAFQVQTHV YQDGH/DGSNWCDLRTTHPPRS
9968	23869	A	10041	290	30	TLKREKRFSSVLCPRGYLVLLLVHQL FFQTGS CSVTQAGMQ/W/CDQSSLP*TP G\SNPNPVASQVAGPTGMHHGLFTE YESRGGP
9969	23870	A	10042	190	929	NHRYISYLTRLVKIKNFANKSWLESLS TLKHS*/W*CK*V*SLWKTVMHYLVNLA KDDLTDPALPFLMIYLTBMCAQVHPEI YARMEIAYLFEIPKHQ\NNPNKLYHT RESYKTKIKS
9970	23871	A	10043	457	724	HEGRPRQVDCSSGVQKPGQHGZVQSV LEKL/KGLAGHOGAHL*SQLWLRLRHNH LNLGGRGCSEPRWCHPTPAWITQDSV* NNNNNN
9971	23872	A	10044	111	429	KPEDTITGRENYPVFFNTTNDANLSKTR CMYPCISVH/HVNMVKGKIPEMPT*Y*



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						*LFLSFFFFYEMESGSVPRLCEGVSIAH CNLSLPASSNPFPPGFR
9972	23873	A	10045	30	220	LGVLKKNSVFNKCYMDN\*ISIWGM\G LDPLYTPHTKINFKNWIKULNIITKLIC CSMMKTKA
9973	23874	A	10046	203	361	TYKLAVIPIVIDHF/LPSFLSFFPRDRV SFLLPRLCEGSAISTHRNL\*LPGSSD
9974	23875	A	10047	198	358	TQRKCTPTFFFFPEV\*SCFVQARVQYG SPG\SSNFFFSASEVSKTIGVVILFS
9975	23876	A	10048	270	272	RKNQRFKIAKRLNMQTRISFLSTII LNVSGLNFFLKRYRLAMTKKK\DPFI CCL/QKTHFAG/RDIYRLKNGWKKIPH TWGSC\QRSEFF
9976	23877	A	10050	256	1	GVTINLYFWKNPLNPPFLVKKCENGYN KVFP\*KDPILKKTLPFSKKKPCGV/HPT EKFPFFPPFESLAI\*SRLQCNGTILACHN LR
9977	23878	A	10051	112	359	SKVSEPTENEVEHNKLV\*SFLPLQRY SM\*OKKNIHII\ISFYKK\ELTWPGMV AIACNFGRGLGTAGRSFBOQEFETSLA
9978	23879	A	10052	346	2	EVSSTYTLITLNLRNLVALKRYERLNGF PFLKKP\*PN\ICCKQTNLIYKSTSLK VKGWNIH\HANGLKQAEVAT\LFISD KKDFSKIVKRDKEGHVMTKGSQQ\*D RTIL
9979	23880	A	10053	376	6	TRPSQHDFILNKLCLFEATPFLVICY SGHRKLRFPVAPPIRGSKSQIIEMFPAVL PRMHLSCLSFRIPSSFF\*LRLPRLCKSR /SANGPVSPhLPQFLFFQATISFFPFL\*D GILLCHPGWNAVA
9980	23881	A	10054	102	347	FLSFFVQKCLLEAKITWLAFAVFTVR VLLLLSTL/ROVELNIYLCSSVHITH LYFVCLTGLAYLTQMSLY\*HL\*YHSNV
9981	23882	A	10055	251	51	YSLVNLFTILENKKDLFLSFYTKTNR /NQ\*DLNVKNGTKVLEEN\*GTIYVMVG WKRPIACQPKS
9982	23883	A	10056	169	342	SQKQYSTQNVCFVFLFLETRSHLV\TT LECSGAIMAYCRLD\*LPG\*RHPPTSAS\*V DG
9983	23884	A	10057	1	586	AAARPAQGKARPOLLRRGRVVELRAGF LTAKGAFRWMLSQKHVMYFPQSGRCG GGMGAGPFLSLTVHQELGAYSPDGTTE ALPLASWPRAPEPAKAYD\*TAKLPAL IGCGRRPPGVNPGASSLKFGACVSEGA GPTGTLESAGSRPPTFLPPV/CCPGFP ARADH\*FCHVTPQCR\* /PPRPSP
9984	23885	A	10058	393	43	HARPGACERPEAGEAARADAFSGRHAC PHSLYRL\*RGFFVIRKLHINKA/RLTKR RKANDIKCWQXGAPGILMHC\*WDYETH GLLEQTVFSFEIRSHCAAQAGVQRNNG SLOEF
9985	23886	A	10059	228	466	GLLHEFPIYDLPEVSTFTSLYHPFIVP *ASPLGPSAILLTPFHSPPA\*PLFSPP HSLVSGSSGRSLPT/SPHLP\*TLPH
9986	23887	A	10060	293	9	DILQFTYTFSPIQ\*CPVYTLHL\*YISLQ L\*FHQYILGIYFIETWSCSVARLECSG RITPRCNLNFPGPTTYPTTSASGVAGITG VCDPLGLPWSR

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9987	23888	A	10061	199	428	TATCRTLPLKKSNPTISGSPFFFLFTGTP RSVPG* RAGG / DLMHCSFDLPGRSDSP ASPRQVVGATGPCHHPWLIFS
9988	23889	A	10062	191	2281	LQTRGKLPFKYKEGICTKLHRSYITIGK QWKEAVCPPTGQAQSQGLDPKSRRLR GGHGFVPGGVCGHQEL* LHSDGLKAVH PAGSEPSDPGGVQRAACQDAJTGTPLIQ PMPETARGC / TATASSREAGPGMD / RE A / GPEAWQLGKARSSWGSSSTSGSPANV FIRDTPSNWGLPGTVSPGAPGRCPPPTR PQWEQLSGSRPG* MQTTABETNAAPRAG QERTPSRPGSADPGVQHVLSHRSSCPK CERRSVPRNG / AGFTLTLHPSGASVS ALTEPL* GDVVRGPGYQ / CGYIKPGRTH QHNWLDLRLPAASRTCRKMLRLPRV* F LLELPELAETYSSTPPACAQRPRGTGGG / PPQRCLVMSGSHQGGAS* KGRDAPSLG SGLERPREGGPGWLS / RQPSPHAVQPC HMLCLGPAP* RGRGARGVPVVRASHFP FHGAANNPGDHMSQP* NQMLSRPARGHR PSHQVRRQCTVLGALKPGLPDLKCPGPT AFLPG* GVS / EENGQIPNVSTQLYLQNL PLPREQN* RRFPRDSSGAGPGTG* CG GGGGHALSPTPSRRLRAKSKDNWAQPL COWMPPAASGC / PGIGCNVPPVAAS* QA AA* TP PMSGSLPAG* QP SAHRCVTRV PGKRI PHLLAQAVPPDRAFPNCQASGQ LLOVHSRPSLSAASCROPLAVSGIGCNQ VDPVAAS
9989	23890	A	10063	65	453	ISREFLFLBTKSLYIMLKGSTQQBDITF VNIYTLNTGAPRY / IK* ILLELKRQTES DTVIPEDDNTPLSALNRPQRK / VDLIC TIEQMDLIDYRTFHPTASEYLFFSAHG SFSKKYYMLGHKICLETFLN
9990	23891	A	10064	100	466	LGLPLQSRSPSGGGQCTPLFPFVSLP LPVRGCFHLHCWCLFYSGALGSPCHTGL VCMHIPC* CGGVSP* R / SCLEVHLVTH THHTHTHTHTRFVLM* MRTLRLRGKQK VMRLCGGGGRA
9991	23892	A	10065	226	377	GLAGSPCTISGVS FCSGCITY / RGHGIMF ICNDCKVFR* CKSK* NCFKHNH
9992	23893	A	10066	292	458	KVSSICLKMSFLFLFFFRIGSHCH* KVS SICLKMSFLFLFPFRIGSH / SSFRLACS GMITAIKSLKLDSSDLTBSAS* VAG
9993	23894	A	10067	252	36	TGFFNPLHETTYTTFYF / TSSKSSCSHAQ AGVQCDDHSLKQDP / PSSSHPTTAP* VAGSRNAHQANSTAMPVMS
9994	23895	A	10068	56	481	GILKNCNHLMTKLRMRSCVLMGRQK / WIY* DESTPGERT / NTVKITINDLEVFI NLVEKTV / GVRTVDNFERGPTVGM / IVCYREI / THEKSSPSMQQL / YF* KFPQP LQPSAATLVS* QPS / SKQDPLSARLQ FTAGSD
9995	23896	A	10069	263	435	HFSLSLFFF* KTESHSVI / RVEGRGGIS VDCKLCRPGSRDSFASASRVPGT / GISQ GRG
9996	23897	A	10070	116	474	RGAGARKVSGRSSPPLSALPIQPPPHLS TPPPLETP / PPVLH* PLKDLGGWGAALLA

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9997	23898	A	10071	139	377	Q*RLPG*HSPKKKKKKKAPRPYPYK*GP PKTPVDFPDGPFLLDPLPWPFPP\VF LPGRRPFL
9998	23899	A	10072	180	473	KSHMPLTLNOKLEMIKLSBE/GLMSTAE IGQKL/GLLLPNSQVNAKEKFLKMKNS TSPGNT*TIKMPGAVADA
9999	23900	A	10073	98	440	AIETQLLSRPLCLMPGRRFPDAQVANIR VRVAV*GNPLR*VGPAKPGQRPSPMGF PSIS/WDISPTWSSSSPPGLSADCKPT CHYRCRALVCLDCCG
10000	23901	A	10074	358	404	GQLNKLSPYPYENVGTYLPLVNLPAQF VYSTIFAGTLITALSH*FFT*VGLBI NMLAFIPVLTK\INPSTBAIKYFLT QATASTILLHAILFNILSGQKKKKKGR PP
10001	23902	A	10076	3	419	PCLYTVHLSNSNST*SLRARSIMETVTV SNLHRTVPHSYTPTQLGINLVMAHLG AGAMVSISSPMKINNALVHFLPQGSPTPL IPILVIETISLLIQ\PRPLAVRLTONI TAGHLLMHLIGSATLSTINLASTLII FTILILIT
10002	23903	A	10077	335	414	KWRKRWCLQKMEYSS*KGKRLSHVT IWMDEEVMLS/EIS/SVTEGQILFNST YV
10003	23904	A	10078	279	1	DKSPF/D*RFFLPNNGFLVKMPFSVK RLPFFFFIPSPFFFFFETESRSVT\RLC SOTGLAHNCNLRLPGRSDS
10004	23905	A	10079	397	3	KDTQLPFIQFFETGSCSVPEAGVQWCD HSSLQPPPP\GSSGSSPLSL*VAGTIGM LIPKIPRNPLNFFFFLRLSLALSFDWS AVARSWPT
10005	23906	A	10080	281	1	KSSSLFQNHLLWNSSTVSHLPTLGYLL NHGNQFDPDTL/RDK*NEFTTIVCHY ELPSLBQW/VLSGLSNVDTLLPLDLCK RQKMGKIPYAQDPMILVQNLITICOT/P QNPFPKPKSSKVELDIDDPH
10006	23907	A	10081	207	35	IPLWGEWPPFPFKKSPFKIPQWVFPF PPYRKIKFFFLPR*NMA/HPKIPFKRP PFFFFFFFFFFGKENCFLLPKPKHI TQAPAWGAG
10007	23908	A	10082	2	408	OENRRC*RGGRGS/GTLHGWREQCOTVQ PLWKTVMQLKRLNTEFFYDLAILLGE FH
10008	23909	A	10083	195	2	IAPLHSSLGDRARLRLKKKKKKGRPL LALFFKNQNSFKKNSHSFYGALMEP\P PPHIPPFF*FWKVQPLPFFPGTLEFPGR IGTCKLQTLGSPG*WDFPKPLPHQS GGLTPGRKGRDPPSPRGLP ECKQRPLEHVSFRRSGHSEFFFTGPR SVAGAGQWHL/DLSGLKPPAP\SGDL TSAS*VAGTI
10009	23910	A	10084	219	1	BLKTLKLTITTTTTDSGICSPKSKL* H/LKIQNMWLDKLAHAYNPSTSGGRGQ IT*GQKFKTSLGNMVPK
10010	23911	A	10085	364	413	KKKGGKGGKPLKKER*KINGOPLVHNF /RLPGLKYFF/CPPPSKMGLRAPPKPK GDFFFFFFFLVFLVETGPHHVGQAGLS LLTS*PIPLGPKCWYDRRE

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10011	23912	A	10086	200	3	INFITIAITFVLDITFTSTGSCIAQATVQWRDHOTLQPOPLGLKQAILP/ASAP*VPRTIDVHHHARLN
10012	23913	A	10087	154	329	FSLSDFKTYTKAAGHGRGSL*YQHFGKP\RRTDPLRPADVQDPDQGRGTSPSLKKKKK
10013	23914	A	10088	157	390	NSSSFPPSPGQAQ/KSEVKSSSGPHSSSSG*RG/CLPLVSGSGMHFLAYGSLTPVSAQVFT*PFSNLCVYIQISVS
10014	23915	A	10089	305	1	KKRAQSLPGQKGRGSPQVTAQDRSFRPKIRKEALGLQGLTDLCRTTPPTATG*TFPSSAPFPQ/YPPV*PTKKKNTNLN*FTRIKISIRIPSGHKK
10015	23916	A	10090	329	2	RFPFQPLQPDQFPLSNLQSPKNNLLKASLHGHGCTVPFPQAGLPPTFPFPFPPRPFP/CFPTPSLGFPSNPPGFPFPFPPFLSRVSLCHIGWSAVA*SNLSAAS
10016	23917	A	10091	84	408	EKKRGKFLKFGWLLGTFLIGGYRFLKICLVGYFTPIYIGENR/FSILJLGL*CNGTCSVHHNPLPGWAGSPASTSGGGITGMRRHPRLY*TYLGRWSFALVARAVMQWHVLGSPQSPAWCKRPSCLNLRGWWYRHAPAPPSLLNIQKILIGFWLAPVY
10017	23918	A	10092	184	359	FQINSSVTRRSFVLAQAGVQNRDLGSLPLPPP/GSSDSPASAS*VAGITGLHVLGSHK
10018	23919	A	10093	298	386	KLCEK**ITPIRMAII*KKREGENS/KCW*GQGEIGTIVYCL*EYR/VQPLANKIVNQFLKILGIEL
10019	23920	A	10094	310	1	ICMNEMLDYKQDFGRTIIRKIVITYFWIFN*FGH*IRLY*NLRLYKICML*RG**INLPQKSPKMLR*KL*W/HGTVAHAYNINYSQGRGRI*DFEFTS
10020	23921	A	10095	40	407	SHHTTACEPGGI*TRPDV*WVLSLW*HGTITCDW/TLGEGTQGGQGLIIIFPFPQ/TQSLFVPRNGVHCGRDLSAR*KLCLPGPP/LSPT*AS*VAETIGACVCTWFENNFFLRLPLHCY
10021	23922	A	10096	189	2	PPFFFFSNLFFKSFYQGLALSPRLKCRGIITA/HCS/L*TPG/YK*SSCLSLP/SSWDDRCAPPRV
10022	23923	A	10097	260	401	DHLRSGVD*IGQHGETSSLLKVQKLDGROGLQLIP/RLINHENHNL
10023	23924	A	10098	187	464	WYMTKRGSLGSPSSAIESHHPFPQOLMNP/PSPPSSAAIESHHPFPQOLMNP/PLLS*IPSPSSAIESHPGRVGRPEFTGGAHGYLHLSPP
10024	23925	A	10099	397	1	FFGGACDPPPRRGKTPPPRKLFPDFFFPRKPLPKKNC*NGNPLGPKKKNRPPGRFFFKKBP*NPPIAPITNFWSEKKKKASDFKGFPPFGKGRKDPFFFFFPFFFFFTKDPVRRVRRV
10025	23926	A	10100	253	3	NATNRNRKQ*TKTSKWKYADIDHATIKQKQRKCOVL/NRCCGETIKVACWBCOBRQAPAVEN/N*HPLRNKIQLPYDPAIHE
10026	23927	A	10101	121	404	VLASVVS/FFFFFHWKGLLFSPLRLEGG/LIILG*LKPPISGLSPGSLCLTPGEWR

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						LKPPPPDPGPPPPF*GKTGPRGGQSGLNFLTWEPPLAL
10027	23928	A	10102	468	1829	IRDTTYTONPDKAKGYFSCIPFRIETTM SRKQKQKSSGFIPIQLQNTVLAQGGAP ENMKKEKINAVRAIVPNKSNNEILLVLQH FDNCDKXTVQAPMBSGASEVLKWTVIG KKKKKKKKKPKPAATSNQIPDS SKSV SIQEQSAPSSKEGGMNGHYVNGAINDT ESVQSLSEGLETLSDARELEDPEASML DMLDRTPKSLQGVSDPFTKSLTWHSIH NSQQPNAAKSLSRPTTTRTPSNMAMRD V/RPHQ*KS*VFIFEKSVDELQRCVTS LARYRVVVKEEMDAIKMKKQAFLELT LINGSRKALLAEMDKVKAEMEPILSR OKKAEILLKQTHVAVQMSQQLVELRAD IKHVFSEKRYDEDLGRVAPFTCDVETLK KSIDSPQGVSHPNYSYSTRCSVTSV SLSRPDSASASSSTCASPPSHTSANKK NPAQGVY
10028	23929	A	10103	254	2	KKIDPPLTLPLGFGGLKIQLFFLOKKKN FYPPP*IFPKIFFFFFPGTQSCPVT\ RLECSDRIPAHYMLHLQSSSHSRASVSH E
10029	23930	A	10104	256	419	KVIELHTGR/CAVGQHVGRFRKYDCLSS GIGQDFPGRGEPHLY*KKQSSQAWM FPGRGEPHLY*KKQSSQAWM
10030	23931	A	10105	153	439	TTVTSGLCTTYTYTFFLLSTHAYHYI THIVY*KLT/KTQPOAGPSEOP*KKEF* RRV/VVGTVAHTCNPSTLRQGGWMT*G QEFETSLANMVKL
10031	23932	A	10106	424	157	SSHLLGRPRWVHLSFGVDPDQWGRFTP SL/LKLAGGACL*SQLIGRM/RLSSGR GCSEF*SHHCIPVWETEDFISIGNQTI PRMFIN
10032	23933	A	10107	213	3	NYKCPPTPNLNLKALYFKRLILSPRA* AIKEKID*/IIKIKHFPYASNIINRMKRO LTEWKKIPANHSVSDKG
10033	23934	A	10108	300	1	*PQGRGKRGKPREKFPFVNLGKTLF/Y EV*FNPDLK*QKKKNPQGFFFFLIGOT VYHOFTSK*ERGVTVAHTCNPSTLGG RGGWIT*DOEFETSLG
10034	23935	A	10109	120	421	KKIKKRNHNNIISDAE*AFDKTQHR FMKLTINKLGPBGRHI/KIMEATYGRGG QDQGLHAKA/BPLPLRNNKISGKP
10035	23936	A	10110	102	418	TLWVCVVCVVCVSLSVLSLSLCLSL QGVQVQCDISLQGRSGVSGDPTIAS VVGIGYVHCHWETTYLEIIRLKLML L*TSSEHALTMQGVSHGLEFN
10036	23937	A	10111	382	2	VNNATMPKSCSTKRSSESLATSNOKLDM KISKMGMLKAKIGIKLGLJ/CQVSQVN AKKKP*REI*NPTPVNIR/DMQKVL/V KTEDQTSNINPLNLIQNKSLTLFNSI KARRSERAA*EKCEDSRG
10037	23938	A	10112	61	427	ENTTYOVQCSIKREYIQRITLKYASLFQ KHICGLAPLHLL*PKLYSRSNASDNI IQLFSPQPNVKEISKHIGW*RGHACN /RQHFERPRKHDLRLGVRDHPCQHGCT PSLLSLLKIH
10038	23939	A	10113	71	399	NVLGKEARSVGRVAVRGQISRVSTQMKW

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10039	23940	A	10114	362	1	KGLIKGKIKMEKSKQACICTYFFPFETE TNFIAQAGQGGQCHDLGFMFPSPG\*SDS PA*APHEQGQL/TGMHNPRTVTFV
10040	23941	A	10115	314	3	SKKKSWGSHSGSKCHTSFLSYPTKQKQS YLSLFYKCNLQSLTFKELLDFRPVCLP TIY*NNWP/RDLPLKPSFKTLML*NGT L/WPGVVAAACNPSILGGQGGWITRGGE LKTIKANTVK
10041	23942	A	10116	44	394	WRERKCGAHLMRGACSNMHDKPSRLNL *KPKMAT/RNTDHDNF*GHGETELNH YMWYKIM*PLMKTI*QPFMFNTKLPY VSYIQLLGITYPRNLKINHTKT
10042	23943	A	10117	398	3	PGFQRVSQGLDLDTSSAHLGLPKCND YRHELRAPAGIYSTPAVLFSYSTRASN IT*MLMTFKPTISQVSPFLSFRFSSFSY LRDISAYMSLSCLKNVFGSKPIIFLSP LMLLV
10043	23944	A	10118	104	386	MECCPMGIRFVLKEEVLKICRTM*TY LHY*SLHLRVMVMVTLSCVYHN*TI KSSSVFLYAGNKOL*I*ILKNYIYVMI PFTITSRNMKNRLTKGDKMSTETYKTQ LKEITD\*NKWRDITFMHGN
10044	23945	A	10119	258	401	KVPVWATCGVMKRLAGHGGRWLRRLP WRLRRDNLRLSSGSRGA\AAAILPLCHCT PTWVTEHDSITYKY*KGAPCWRASS* C TLSGHALFFFA
10045	23946	A	10120	310	384	YNYPFLLTCVMKEKIQAGQJAHACNPSTP GGRGG*\TRGQHLETSPTNMV
10046	23947	A	10121	245	479	GVFFFLTFLYGGIKGGPPPPRFLLF*FA FLFFFF/ETGSHSVAQNCSGSVSAHRS FHLPGGPPTSAS*VTGTGICHS
10047	23948	A	10122	268	469	TSSLYRKQKRLVHLALEVLKICNTYF MNTERRFLKLPQSPS/RLI*FPFPL FKIYHYFLDRV*LCBOWSAV
10048	23949	A	10123	221	423	NSVFWLGVWAH/A*WVPSLTGGRGWNI TRQLETTTPANILPP
10049	23950	A	10124	73	183	GQNGVAHACNPNPALGRPREDSLRPGV GDQPGQHSKTPSL/LKSDNF*KNMGLGP WAMNLTPIIPALM
10050	23951	A	10125	342	2	AGGQWALNTVINTP\PPSTPTFFCLSY SCTISTASAFRFPG\STSTAVLTHVRL KSTPADAPHPPLKIPRARNIQRDHTLSS NLFFYNNQLNVTBELTYDYLT\INPTAT IHAIHTMPLFLHNLNCISI
10051	23952	A	10126	85	442	PNLSPCPPPPGTGKGGPPPPFPSPST\IG PPNFFSP*RP*FF*MLKSLGV/SPTGP IPKFPFFPPGFENYSPPL\PKGPILLKPP RALFFFFFNNRHRVLL\CPGWSPTAGLK RSSC
10052	23953	A	10127	180	484	KKVINIKCW*RVWRTGSLTHCSWG*KMM PHMRAWQSGFR/SLSMYLSYEPALPLPG SFPRALRTTCVCTHSRCFSLLELPQA/W NH
10053	23954	A	10128	376	1	KSFFFFSGSAQIKVLPAP*NEHFFGVK RSCSLSLRKGGRWVPPPPPPFFFFFL IKVMRSHYAAQAGLKLASS\VPSPSG IPRTLDSYDP
						WSPGAQLLFISCLYNNLSLHRTGRTPAK

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						PE*GWTLQKTTPLSCPAP*LEPPLPSFL QQIDLKELVFTAPACSL/PHSPNSFPW PQRNPSPVS/P/PAVHAAPRLPPPPVC ARPLNLPRAPLLGIPPH
10054	23955	A	10129	140	454	CLIRSSINSVHNHVIYHSTPDRHLGCFQ FLVVTKNAASRLAYVF**I*IPYDHI HTHTPAGYIPRHGIAGSQLTNIFNPS* LSSNSFQVCGTSYFLPSHI
10055	23956	A	10130	340	473	AGARHSVLRFRPFLAGSSCPSS/CGGHC VALGVSCPGGGCRACVPGCCCLLGLP SDVCVC/SVWGGSHGSLGGNAPGP* GNSREGPNCSORAGLAGLGPAPMA EQAPDILCCGPGPHVAGAPQVPLAPPL SPPPCLVGLVSDRGDL
10056	23957	A	10131	280	2	DSIALLEFLELVNGVNVHCKLSSWIR SSHLSLPLKHLDPYRSMH/LPGLLEI*YS YCK*CLLTSPYEFFLNLSLEDISSCFIP IRVMPKCRMK
10057	23958	A	10132	244	3	IISTDLISHSWTLYLISLVLVFLKQHS LAVLEPRLDCSGMILAH/CLQTPGLK/ FL/CLSLPST*DYRHTPNRANFYFYF
10058	23959	A	10133	272	3	VGRPRVFPYRIAPNFGVTSITGPHIKK YHFCRGGKHKCF*KAFFFFF/FNETG FCSVPRLECSGTILALCSNLQSCSNP TSVSQV
10059	23960	A	10134	217	3	FFRFRPLVSPALTLGQF/HPLTRGL*K KKPPFPLFFFFSITESCSIA/RLMGSG ISACNCLCPGSSRTG
10060	23961	A	10135	229	3	KSDYLKQWQGTETQMLGSDML/LI OP/LNKILWQFLKLKAWELLNPTPL GIY*ENNVVYHTQTCLCIDAN
10061	23962	A	10136	84	352	RREFKGLATQNLVSTFKYKTYRHYL TSTRMDIKGR*QVCM/RKC/GDRGTL LDC/MMRMLVQPIWKIV*VMKFCRK*KL NLFFFFPPQ
10062	23963	A	10137	280	2	KCVVVPERILREKSHGKIKQGBRLN AVVLQPGQGHETLSLQKI/QLAGHGA PLRQLHRRMRREDHLSPGVRSRSEP* LSLHWVTBQ
10063	23964	A	10138	2	386	HIQEKQLPNRDTLNPYFLTSLKRRKD EKIQMPSKHKMKRCSLIV/REMQIKRS HFPH*VGKILKSANIKK*MKRKG\TL ITCM*TYK*TYLKVTF*RIILQHPLLK THQSYYPALPHLKTA
10064	23965	A	10139	229	1	TRSYHSLTILATNHLNCSPPFQAITE *SRFPYSNRA/MLGSVAETHNPSTLGR GRNA*GQEFKTSLGSLK
10065	23966	A	10140	261	429	LSHLFVALI*LGSLV/SFVVF*PETGS LPRLECSGVITPACSLDLLGLSGLPTSA F
10066	23967	A	10141	377	34	WVFGSSGPPPPPGFKKFPSPFPKIKR GPPPPPIIFFFKCKKGVSPLELP*GGGP /HPLSPPPPGVKPENKFDGGGGFP* T KTSRPPPPGQKQNFVKKKKKKKEHQ IKR
10067	23968	A	10142	208	424	FFSLFMOTFHIRFIYFFLAGGGGAGVD RVS/LLSPRECRDTISVHCYIHLPGSK QFSCLSLSEN*NYRHAP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
10068	23969	A	10143	1	297	PTSPQVSNLNKHSFTSPYLEIDLLSVC LSGVSYVFTSLTLRLRSCGAIITHL LLSS*GHRHAPQV\FVETRFHNVSQ SGIELLSSSHLPTFA
10069	23970	A	10144	185	488	SGFFRGTELGAVCVVCVACVVCVIR LGYI*NHKRIYI*LLYIYSTYI*PNLSL *LSVY\SYVNRNRM*DRSQSI*IFILPK LKTCLNTHTLKNTHGG
10070	23971	A	10145	283	3	LQWPGRKADSGKLTIDYGRLDKLVSP/ I*SAISDMASTKAVLQAQRDQYSVLDD AHAFHSIR\NQSQSFIRDSPQYAFILP SSEHANGLDGQ
10071	23972	A	10146	146	380	CPLWDRNFFFFIFTEKKGSCSIAQAGMT Q/WVGIIISYCSLKLMSGRDPPTLSCVA GTTXMHEDAVYIYFFLE*QQGL
10072	23973	A	10147	275	3	YKQMLKATG*KLCLLCJ/TQSVENAKE EPLKEIKSATPVMT/RMIRKKNCLDAM EKV*VTLLDQTHNIPLSQLPQSKCLT LFNSKKAER
10073	23974	A	10148	281	2	KIFLPQPPQEMVSGQAPRG*IFPLV* *KQPPPLPLGRFVK/LPGQIPFFFFF FFFFFETESHAI\RLKCSGTISAHCHL RLSGSSDPTPT
10074	23975	A	10149	413	139	SLRWVPIFGLLQNKKKFFNIFLFS/IR PLFFGRERGGTLPFPFFLRNPGKKS PPG*PPPLPKIQFGYFFTSRPAFFFF LPCQPPGKNLNYGLGPGPKIFPPFP FFFFF*DRVSLCRSGWSKVAR*LTWKG AFFTWVS
10075	23976	A	10150	100	431	GPRITDHLRSGVFNHPQGHETSFLLI/ HNYSGG*GRKIANRLNPKGGCSEPKSC HCTPSGKKKRNVPKSKKKKRE
10076	23977	A	10151	134	417	GLAAPLVH/KQENPPFP*FEG*GSEKTON GPHDKILFLKKLLFFFF*KGLSFP GGREAHFWLKKTTPSRKIEILPPPPP RGQGGPPPPPL
10077	23978	A	10152	403	2	LAPFYLQVFPQCNLLISLRMYSSGTS KLFLPLASQPHSLLYHLTARAPNILEE LQSPNTALLKYL*EALKKKGR*HITS SL*KVDLSFFLETKPRSA/RLKCSGTI SAHCSRLRLGPGNSCATASVAG
10078	23979	A	10153	382	297	GLN*EWSGSEKRT/LDHWCKRPVQL WRMV*RL
10079	23980	A	10154	209	15	SSPKF*FPFLSPKKIPLPFF*PIFFPTK TP/HFFF/SFFFFVCVSGSHVPRLECS QAITAHCSTST
10080	23981	A	10155	153	422	RTSKGNRQRIILVMT/TNWLSPFFPF PLKTGPHFV/QAGGQGRAHGSQA*IFG \SGDLLALVSLQAGTAGPHHHAQSFFF KKTGLF
10081	23982	A	10156	257	3	RRLQSKKDCCLFFPLSAPRGATACQPE LS*CMRCLSALHAGVSGSQTMGVDRD HVK*PLABELK*AGRSSAPFAVRQGL S
10082	23983	A	10157	37	386	DATRPRINSVGTAEGLDRIEINPDLO*Y INLVGTAVRRPDRIENPESSTVGKKLS NNIVCYRS*FFCRESQLTQOTSMLYYFK KLPLQPSAIIITH/SRQPPSSRRRLQ



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10083	23984	A	10158	407	272	LGQ HKGGKRRERKRKKKKKKGGREKQERRK ERE/RRKKGRKREMKKVNRYSKCTQ* LLSN
10084	23985	A	10159	248	478	VKVVHRLLLDPSVSDP\KKSLKQPLQ* /RL*IFFF*MSGLLCHPSRAVAQSRFT GVSTSOQAAILPSFSLPSSWDR
10085	23986	A	10160	458	129	GFSVLNRLEDEDLQENLLMPAV*DPQG QHSKTPISTKNNMPAGHGGVYP*SQLL RTVRPEDHLY/SNKPSCYLAPANATET LSLKNAPSCCSNHYSFQTSFHRILMF
10086	23987	A	10161	82	291	YSLKTSLFFAGHGGTCIYSOLFRRQVQ RQEDHANPGV*GCS/DTMIMPNNSHCTP RMAA*DPVSKKKK
10087	23988	A	10162	6	409	LKRNILPPEPTSLSLTADAVFPMWTNYS SCDTPSLASWTLPLPLSTSLAPNSL FLAPSLFQISKQQLYLSPVLLLTSSCYF LNPFCRNHILANLGRPROANTLRSGV*D QPCQRGETPSL/LKNTKITNPNW
10088	23989	A	10163	249	415	APPECSLPLVALLLLALLFLRWEDHL GPGG*GCSBPKSYHCTSAWVTR/GDPVS
10089	23990	A	10164	1	405	RSEWLROPEROSRTVKKKKKGFFFFSR CGGOGKIFGLMEPSPGGLQGFFLTPLLE NGGYRPPPLGGPFFFFFFGGGFPCLGPG GFEPFALGTPLLFPKOLNFRGGETPPA RFFFFWGPVPSVFSPKN*NDPVFRGNKR KMRPPKKKKGPRG/WGPRKFNPNQNKR GGVPRAGNSKDPGQPRGNPFLKKKKKG VPKGGGR*PPFSRGVNKNCPKPEGGGS INPKIFPPPPPREKKKKKFFFLTVSLC RSCWNLISL
10090	23991	A	10165	175	404	AIRWNTQVPSQCLHGVFLPRSVCV KTP*NKRRQGVVAHGNPSTLGGRGW I/RQGFETSLTNMVKP
10091	23992	A	10166	317	2	FFHHSPLLNESTRIHLEPTCNVANS PFLK*HKSLFF*EMESCSVT/RLECSVT IIAHCCLLKLGTSNPPTASAWARMIIG MRHCDAPKVCASHASAHAS
10092	23993	A	10167	325	2	KMOERQGHFKETREKANKHIERCSRL AIREM*IKATVTI/RHQTKC*QG*RES GSLVHG*KHIVHPLWKILSVSYKTKH SIIIIQYSSVLLGTVLVHSGSDAN
10093	23994	A	10168	245	3	GEPLFLCFPIKTKPVFFCPTFPIQAVFPL ETHRGFFBFFFLF*KKKKK/LGMVAHT YNPSTLGSRGQIA*AQSFKT/LGNIS
10094	23995	A	10169	164	1	MKMSQYTPPYKN*QWGV/SVAHPYNS TLGGQAQMIT*AKEFETSLSNMAKPC
10095	23996	A	10170	214	419	LS*PPPPFPFGKFRNR/LRFYKSKKGGP /FMFVALPQKGGPYQNTPPVLEPPFP PITLRVSFFFG*QGVNLCHPGWNAVA*S QLTSSSTRWH
10096	23997	A	10171	168	1	VTWMLPFGSITNNYSCSFSSLHLAW/ LGTVAIACNPSTLGG*GARGQSFETSLT
10097	23998	A	10172	139	3	PAI/CKST*PGLKISSYVLSFG*DYR/ HTPPH/QLIFVFWVMGPHQA/SA/FP CK*DYRS/DHKKWPT*HLK/SFHF1KK* N*IKRYLACSRILWYLFCLIRCTV* NLD DLSTIYLNHMKQFIFITLFFEMES

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/015,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10098	23999	A	10173	253	2	PPLK\ONTLPPQIPSTORGLLSLPPTIF LLSLILLRPPFFFF*TESHSVPECSGMI SAHCSLRLPGSSDSCASAS\QVAGKTCAR
10099	24000	A	10174	300	3	GRAFFPFGSLVKWVFLTPHPIFPLKNFL KRVFFLAPSEKCVFFKNNPP+LSFLIPG EKNFFFFFFFPEMESCSVA\RLCNGM ISAHCNCLPGSSDSP
10100	24001	A	10175	117	381	ELLRYIVSIRIKRNLDFQGBELRNLIK NLSLSLAWVRLP\EGSCVITAPTAVS APQPT*SSHPLSPSSNKKRRAPALQDP FLIETRSHHVAQAGQVFFVYVSFPLLLK FKLSPSDPYRNINISQDLAIGPTNMVPL QPIYVLCACTKNKNIIDLDSEQSST
10101	24002	A	10176	194	412	TLKNLLSLHCLSPFDLYQPELSKRP PRPAKYKFLIL\WLGVAHACNPSTLG GRGGWIT*AREFDNLTK
10102	24003	A	10177	100	339	VPVKSLLLCVCCVILL\PTISDELPTLY ANLG*CFPSYLVISYS\NSTYCLQRLH LAIQKQ/CSFLRQ/HLWGWLKKKHYH THTHTHTHTHKSNTHTHTHKSKDLTGTO NTTEPLLK
10103	24004	A	10178	229	2	KKYIKSKLHFEARENGSL*SQHGRGP RLMDCL\VDQPGKSGENFIYQKNTKIS QAWMLVPVVPVYSHRASKTLS
10104	24005	A	10179	368	2	SGSSPSTSPQGRPDFLGLFSAKIVLGQL ATPLPLCLPLKIFPLTLPILLLGGSE FNLSPOQDSLSLPLFCYRYGPTYAF FVY*ASVPEKI\FFFFFF*DTVSLCHPG WTTVAQSLRTA
10105	24006	A	10180	398	1	QNTLNTINTNTNFIQQLKXKTIGWSEF FBNKWC*ENMIFCTCKRNLHPLYLPTK TNSKNISELNL\KSLKVNRRGNLHDFQ GNGLGDTKSKTK\AKISKLEPIKIKNF CVLNDIIKKVKRLLEWKYLY
10106	24007	A	10181	252	419	GARPKGSNFTSGGGQGIFFPGSPKLIS RPVP*HRGEGKTPGVTQNLNRLHGLFA
10107	24008	A	10182	101	380	FCWYNSMLIGYLPFFPTLNLILACGG SCL*SOYFGRQQAHLSPGVRDQPGQY GETPS/LTKISWAMHVPVVPATQRAEV GGSLPREVK
10108	24009	A	10183	2	377	PGVDCFSSGVQDQPDQYGEILLPLLKIQ KLGGHGG/IR*EDHLSLGGQCKEPRLY HCTPAWVTBQYLVSKKKKKKKK
10109	24010	A	10184	140	3	DGVLLSLHLECNGLAISAHNR\SSRCS PASASQACCTC*SQL
10110	24011	A	10185	364	3	SVCPRLGGVSQSGDHWDRDFPERAV*P LAKLERCAGRSATFPATIR*AHLSLLK\ FTRNHPPPHVPCPRMSR*PGLLPFPQR CPAQREIWRERSLAALVSSCGRLQVR TCWQLCLHR
10111	24012	A	10186	2	249	SVRLNKNKENTQIRNKKGDTINLTETK IIKEYSEQLFANKIAJ\SLDENKFLER* NPLRPGAEARLVS*RFWRATAIDHRP
10112	24013	A	10187	270	2	PWAGRGCVFTNQKIFPGFFETPHLD*P CVFQRPFS\F*VRLIFIGGGFKPFFFFF FEMKSCSVARLECSSTISAHCNLRLPGSS DSPASA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=-possible nucleotide deletion, =possible nucleotide insertion)
10113	24014	A	10188	428	28	PIFDKG/E*GN*WGKKSITNNKQWCKCTC/KELRDSLSYSY/TRINLKWIKDLNVRTK/STKLSEENIDIV/IYDLGLGIGFLD MTLKARATK/AKIEKLDDKIKIGNFYASKDPKRMKK*FIEFIEQGKIF*NAVSDDTSI
10114	24015	A	10189	85	243	DRVS/LLSPRLCSCGMISAHCSFDLPG*SDPFTSVPKSSWNYRCPAPKRLSPT
10115	24016	A	10190	96	440	LQSNHINTLVNRLSSMKRFLSDIEIF/KIGHPALCCL*EMYKDKGTCTLKIIGWENIYHANNNNKT/GWLLSGKIRLESN/TVIRVKEG*LV1/ENGRLL/QEDLLLFLLNVIAP
10116	24017	A	10191	137	423	AKDLRQFSKEDIHMTNRMKTC/SGRQLRSTQIKTIVRYPLTPDLRLSKDKKS**YDQKGTPAHC**ECKVQPLQKII*TFPKLLKINL
10117	24018	A	10192	221	72	AKVK*VVVFPCFLFF*DGVS/HVVVAQECSGAISHCNCLCPGSSDSVRVG
10118	24019	A	10193	460	121	SDTKTYW*RCRATKILTHF*DESKLP/L L*RTI*CYLAKLKHIVFDSALPL*DTYFR/E*FCICAPKTYSNMVLEALFVBANQTSKKKNK*LSCPQIVNFLNTHLMKYHLE
10119	24020	A	10194	393	2	ATMPSYQRLITAVHELESPE*MDQFLD TYNLPREFNQREIRLNINSPIMSNEIQSVIKCLPFGPNPGNGFIIEFYHTYKEE/LPILL*LPQKIRG/ILPNSFHEVSIITLRKTDKDAT*ETHKPISLMNTDA
10120	24021	A	10195	3	353	EAAPHVKVFFQLLEPSGPPGLSMKSLGDCNGYACFSVSLHQAQSIDQ/SIYQSAIHLITV/VSIIY*SI\YLLL*SLI*PMYVP1YPLSCLSIYLSNPLSLCLSPNNLSITRHSGMCL
10121	24022	A	10196	118	395	DFNAGLLPSYQVLSIYFCF*NGV/CHCTP/RLGDRPLR/PPKKKKKTPPPPLGGSPPGGEPYTPRPGVGP PPPFSEHPRENPGCFHP PPKWAP
10122	24023	A	10197	437	160	FQYPRVFP/LALLKRPGLFWMGNKJN YSSPARGSKICFFKRGPPFFFFFYFFF*QTESCFAVPVGVMCHGSLQPQPG\SGGPPPGTS
10123	24024	A	10198	259	3	RQGNHVTHVYSRILQLILSPASLAWFTQKIYVNLCTYIHVNLVA*MCICVCICYTCIL/ICITYGLVAVARTYNPT/LGAKLGGS
10124	24025	A	10199	1	416	II SAHCNHLFPSSWDYSRTPPYPANFCIFSRDRVSPCWSGV*HHLQHSRMLSKK*NKIDMGGMCL*S*LLK/RAE*DVLRQENCLNPGRGRCGPGSRHCTPAXATRAKTLBSKASVASSSSSPKKKSSPS
10125	24026	A	10200	369	3	TAPFFFFCFRDLATSLITFPSEATPYS LVTSGSLPLNAGAGRGLSLRVLDLVQDGPCPSQAWAALGGPGHWAFLCFPETASC5VAQEGMQ*CNLGSQPPSPG\SSD SPASVVLNTSK
10126	24027	A	10201	314	2	LHMRPEV*FTPSKLGVTGYWVNSISTYPWRCAHK*SQVTVSLRHKHFLPLEMESG

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						SEVQLDTNRCISANCNFCLPGSSNSPT SAS*EAGTTDSRQPDADADAN
10127	24028	A	10202	68	413	KIGILLKTH*PSIC/VSI TNF*YNDTGE LKVXG*KNIIYANINQK/KAGVMFVLD ETDFRKK/DYQGH*IMIEVSVHE/E/ LVILNLVYASNKRVTKYMK*KDIDIKGEI DKSTTIVGDL
10128	24029	A	10203	351	1	PKFPPPLNPAWGTITKIFFPKKNAGNMP PRKEKALQKIKKG/RLLAKEISFLOGF *TDYKINPQSDSIRTLGKKKKIRPGTV AYAYNPSTFGG*GRNIT*GQELKTSIAN MVGRV
10129	24030	A	10204	2	392	FLEGVLLLLPRLECGAIPAHNNLHLP PRKRLSCLSLPSSHDRHAPTRPANFV FLVGVGFHHVQDGLLTL*SPCLQLP KCMYRH/DHAGQSPF
10130	24031	A	10205	264	2	PLSLNLPPLPLNLTPLTK*E*TH GKLIHMYRKV/LV*TSPPSPQC*HLR*V *HNIQNMKMLGLGVAHRSNPSTLGRG GWIT
10131	24032	A	10206	281	2	ISPPPLFFLSPPKIFFSQKHIFLGPPL FYPPPLFFSPPP/PHFLWGFPRVNPMP KIDPQIWAENKDKGNFPPPPFFILPPK ENIFFTKTYFFGPPPLPPPPFFSPPK KK/SYPPFLKNSPNPPPS*K*AAISLP PPFFYFFFFFSSFFLENTWADAN
10132	24033	A	10207	340	1	STKGLVQKLGHTQCWGCATGFLIHC RNECKLVQPLWK/SAWQILRLQ*NFML PYNPTIQQQS YSRE\QHYCPYKDLVA ALFTIARNC*QAKFLSTGE*INKLWCIH ITB
10133	24034	A	10208	136	3	IRNGPPPSGKGFPPPL/FFFFFF*DRV \YPSHGHSAWVPSQT
10134	24035	A	10209	327	2	IRKKVYEQLYA*FQNDIETVGFGRYN LPKLTQEKANNINRPSVLRSTKSTINL PKRVDPDQDGTGELVQTFKEEITP/PS TEAKGILNPSFCEVTIIVRLFLRLQ
10135	24036	A	10210	89	485	EIVPLLRPLPLVGFIASTPTFTTYGFSG EKSQYKKREKCDKTEQSRSLGOMIST CGIALHPKREOCQCTLCACFY*FFLKS HSAARAGVQVHNILSSQLPP*PSSNS
10136	24037	A	10211	361	462	TOQTGSNTGNI PAMELACKRNSKYNRL AGWNP*VFAC/PKNVLVYHP*LFQ*I *IYQLKITP*NYEGMVP/FVPRFLFETR SLLSPRLCSGTITTHCSLRLVGSINS ISARAEFLQGANL
10137	24038	A	10212	62	469	SLWLKSSSGASTSLRLCSA\LLGLVVSQ SGYTVGRDPLKEAVCLLSRLERGAGRT ALFRAVRQGRSLSKK/LLPFVQICPAP GGIYR/QO*ALLSGGLCPV*AS*/M CLPC/EA*TLKKPPPS
10138	24039	A	10213	197	1	VVTFPRKCVTKKASGQRCCKKIKT/ NPMVAVTCNPSTLQGRDGHIT*QQFK TSLANMVKPH
10139	24040	A	10214	31	213	HASLDRGFHHVQDGLNLLAS*STICDL PKCNDYRHKP/PAPNWKFLSSKAFKR *LGCY
10140	24041	A	10215	442	29	PTINPTMAKCKLSKRSKSTSPFLNQLE

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						TIKLSRGMLKARAG*KIDHVR/QVSQT VNAKEKFLKEIKSATSLNI*MIRKQKRF IVNME/KKVLMEFWTEQTSINIPLSQSL IRKRP*LFLNSLKAERSEEAPEKLEASSG G
10141	24042	A	10216	195	533	LWVFWLRV*YGAAKMESSTTTIGRLSW GWRLHF*KMRAHL*GYWNEASVPLMKLS SCHGTG/SIRVKDPRERLRKQLQCFYDL VLEVTYWHFYCILFIRSKLSLPAHIQSK RI
10142	24043	A	10217	274	494	CVLKGFLFALP*FFFFFF*DKVSPSPRLR CSVAL/SAHCSNLNLGSSDPPASASQIA GPFLQLR
10143	24044	A	10218	142	480	VYIK*KLHPHDTTFLKRGQSSRLKLLV SY*QQKVTSTPSHVI*FTVISTQPKKTV TTRSGAVARTCNPTLGGREGQI/T/RG QRFRTSMNTNPK
10144	24045	A	10219	163	464	AVYPSWVRVCEHDLASTYFENSGRRDNK FVFLVLQAQGPAMRGVRVHKHLLPCVYH FAFVVLTAQPPSPF*DG/QSHSLAR/LE CGVISAHCNLYLPGSSNS
10145	24046	A	10220	379	469	V*KVQM/WFGNVAHTCHSTPLGG*GGWI T*DQRFETSLADVAKPC
10146	24047	A	10221	211	473	VTWLLFFPSFRASSLSIDSVSYVIAFQ FYFYLI*TYFYLI*IFETRSQVA*AGAQQ CDLCSQPPPPRGS/SREKSTLQMTSGSS NL
10147	24048	A	10222	142	394	GVCQSLGSLCQLGGTGVRDQLEAVCP LAELRFAWRTLLRLICCSLQSQQAGIF /RFP*SYIHICPPQVLLSSRMGLVIR P
10148	24049	A	10224	77	396	KRTKYSFWTSGQLRPP*LPCKKKFTN SRGQGGQFGRGSGRGGGSTRGGGGY MGVFGMGQ*MTGDQGLARGGFV/FVFL GRTTIGIKGALKLFA/NNEHDLR
10149	24050	A	10225	155	443	GQARNTTLKSGFFPFGWFLTLPGGV FSPKFFFFFFFTRV/CAVAQAQVQNCNI DSSNSCASS*IAKITGAHHH/TELIFV F*ISPPSQ
10150	24051	A	10226	290	485	KRGKGPVQKKKFFFFFFFSTCVAAQAG VQWHLSSL*PPPPG/SSDSPAEFPR
10151	24052	A	10227	228	424	KLYQNLDHTLFGFELSHYREYH*KMLKG SSWRFVMIHS/VSNKCILICSAKKKKKK KKKKKKKKKKK
10152	24053	A	10228	269	454	DLFAASQGHQALLEENATLLSDTHHT HTHHTHTPWSLF*SR/SALSVC
10153	24054	A	10229	255	1	FYI*SKFLYVWLVN/SHLDSHICFCIQSV IISCPGVFYIIYY*F*HQSCSVVHTGV QWCDRSSMQPQLQGQNDPPTSASQVAGS A
10154	24055	A	10230	18	472	GPFRGTRRRDRRKRRTDRSRVRVER RRRR*/KQRRRRRRRRR
10155	24056	A	10231	52	361	WKHYVFOIKITVILRWYDFQGLATFK CH*G*KEIGRAHCHWRCOM/WIQPLTK R/VNQFLKLNMLLPNPAVELLDIYPN ELKTHVCTKALYKAGRGSRSL
10156	24057	A	10232	3	402	APRLPLGQWISFSSSPKAMGLNRRATGIM GSFFFPFLKKKSPGLQGBRGQNLG*G

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US951,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NFGPRG*THFPG*TP*KAGNNGGPFPR GNFGFLKKGVPQKQGSXFP/RDPRGT ERLGPFGGLE*RGCGPPFPAPQK
10157	24058	A	10233	48	470	PGRRTTAGLGRQBPAAASQPRAFPAQT FLKREAAAPSLRHLPEGA*APRSSARS LLTPAASLRSPERRRTCRRLRHFGIITR PFQPGVRLPDSGQGLA/RWACAAVPAAS RALPALRRPL*RRPGHGAPSSKSGHRSR SP
10158	24059	A	10234	169	446	CPPGFPAPSHLLDRDDFQAGRQSSFPYAG WMDRWREKTLFLRLRQSLTSLPTTFFFF \FEABSHSVTHSGMPGVISAH*NLRLCG SNRPPTSAS
10159	24060	A	10235	264	2	KLKPTFKWFLIKIMESYIMEVFFETET GSRSVTQAGVRHHDLSLQ*PF/GSSD PPTSVSQVGKMKHTWEAEIYVSRDEATP RAKL
10160	24061	A	10236	306	3	SQDMVFSEPKKFP*TV*GLTEI*KTRAL VFNKKFFSFFFPFETGSGCSVA/RLE CSOTTIAHNLQLLGSNPFASASRVIN SIKKLFANFIVSANRFT
10161	24062	A	10237	20	469	QCGALPRRGDHLKRSV*DDQPGQHGTPS LLKTIQLKLSRHDPH/CRRLSHKGNLPGG RGCSRLRSCHCTPAWATR/GNSVSKKKK S
10162	24063	A	10238	313	3	TRPRPTQGFPHSGRACRLTSPFHGFPO TRLSTPVSFVRPLGQVLLSARHGFL CQHGMF\PSLPTMSNITLWGAVAHTCN FNTLGGRGWIT*GGEFTS
10163	24064	A	10239	274	49	KGNFFFFVTGSHSLAQDGVMGNHSSL Q*PP\G\SSDPPTASRVAGTTGV/CFC EDKLSHLRLRCYAVPVLG
10164	24065	A	10240	144	454	VCKIKITLYLVLLRDYIN*FVFSST*YK S*K/LIQMMALISLPECLNSVCLGKV G*KRCQQGTVAHTCNFSLGRGGGMIP R
10165	24066	A	10241	289	178	FNYSIKNNITDGWWMCLLPVTPALMEV EATSEF/CSRDRIPLSCPGWSPVFLKLR FYCINLF*CWYRQRAFFPAISIIFDA TVIELFS
10166	24067	A	10242	352	294	PPRTTRNNV*DDPGQHVAVTILQRMQRL VERGGKHPQSLC/REDH*SMGGGCGSE PRP*PCTPAWVTERDHVSKIK*NKIK
10167	24068	A	10243	293	1	VSLCRESSNSPIWQCPVSHILALCPOR EKRLDLF/S*NVGK*EIPFLVPLFLP HNPELLLMK/YM*IFFGNRVSLCHPGWS AVAQSLTAAVSFRR
10168	24069	A	10244	218	3	LSRHIPVRPIITCDYKQWVRP/HPIRLPL HN*FLFSFSPFFFPFETGSGYSVT/RLE CSOTTIAHNLGVHLL
10169	24070	A	10245	185	1	KKQPGTKRLSNVKKCKQQLFFPFL T*SRVQAQGVQWCDLGSLLQFPFPG\SS DPPPS
10170	24071	A	10246	2	265	AHKKKPAKHIASTPTLYCTEARSMPK AAQLKCGRAGTILFVFKTESCSVAQDAV LWCHNGSLQ*PPG\SSDPRDSACRVAR TTSI
10171	24072	A	10247	2	430	BAGGRALDGCGLTGREGSVORRRDSMG

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						CQGTACGCTRACKGPGWPEILSRRPFA SSVLLSWAHLAWVGS*TGSLCDLEAP GPTLSPWCSWSPEILQLAV/HHHTHTHT HTHS/HPNTHDTQSLCHQPSFSVSPRA RTVL
10172	24073	A	10248	201	16	TPPGGVFFLGGFFLFFFFETESCCVAQA GVQWCDLGSPPHPPASRRPGNRSSI/AAA *GYHFK
10173	24074	A	10249	167	2	GFDFPEGMLSYLEKEET/WGOTRAHTCN PSSLEG*GGWIT*GREFTSLTMEKF
10174	24075	A	10250	92	389	FQPGQHGELLSYBIRKI*/ELAGCIDN CLWSY/LLRLLQSDSCST*VQCSBP* CLSCIPSVTTEODPSGQI*KKKKISL GRGGIPLFLKLIWVFFL
10175	24076	A	10251	221	415	KKKKRGRGRFGSNPTSPKWRGNIPFPGP PKLNSRAGV*QRDD/WEKGGGQFNCFG SNPFFPPGGK
10176	24077	A	10252	94	383	GKLNRCGIIWLLGRCORESPVSNALWLR VAPDEBAGEAWAGTSLQLSCSKITPN KIVY*KKNKT/WLGTVAHVCSSTLGRGR GGWII*GREFETSL
10177	24078	A	10253	249	2	YPTMIFKCSKKRSPSTSLNQKLEMMK LSEBMSKALS*KLGILH/QVSQVNA KEFLKEIKSATPANTGIRKRNGLIA
10178	24079	A	10254	132	414	NTYFQGIKIFILNSQVKGMLICSWRECK *VEPLAKVAVRFLK/DLQNSKEYKL* TWNQPRYPVAVDWIKKNWYIYPMEYHA/A IKKNEINFFAA
10179	24080	A	10255	359	3	YSLRHNLEKRPVSNPTASKSCHEERSV LSLTLANGRELIGQASKEGTAKANKPKA KLFTVVRQVVAKELKEAKSAFLN\ RMIRKONS/ADTEQV*VINIEY*TSHS IPLQSL
10180	24081	A	10256	283	2	SLQPKWLVAVPLPKYATYPPGTLPKT HPFHKLPSKAGSDLSIYAMTYGHRHI TIFFETESHVSVTRLECSGAI\SAH*NLH LPGSSNSPATK
10181	24082	A	10257	216	386	PSKNPPFLINPPFFETUSCSFA*AGVQ WRNLSLOTPPP/GSNNSCASAS/RIAG I
10182	24083	A	10258	263	1	FSOMLILSPLSYSPLFROGPALLPRL ECSGEITA\SSAS*VAITGACHAEF LNFVSRMEF/HNVQAALKDGLSSRPPTP ATK
10183	24084	A	10259	248	47	IPKSRVIRENRLNPGGKGCN*PRSPPCS PPWVAKQNSLKK/KNVKIYQNIHTBTQ TVHGDIRGQEK
10184	24085	A	10260	159	2	KRMSSSLKLEY*KKE/RINPGAVAHITS LSTLGRGRWITGQBFESLTDNWK
10185	24086	A	10261	190	405	ASLHNWIKFFETFPQITFFVPPQAENQ WNLGKRNPDPGLRDP/PASPPKEAGF RQIHI*POLPLAT*GE
10186	24087	A	10262	39	293	PSSTSRIVYEDTPLITQKYIKKILPIV ALFIPPKHWKLCCKPHIG/E*IKLQCIV TWRYVAVQKNKEINYLMYNDYQELIV SD
10187	24088	A	10263	282	3	AFYNRFPLKIFPFRGRPRGKKGKGGKK KKWGKKKKKKFFPSGQIFLGGVFFF

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						FLFFFAESRSVT*AGVQNCQDQ/SSSQP RPRLKPFQ
10188	24089	A	10264	196	376	KKGGGHIINFPDRKGYKPFERKKFFFF FFRMESCVA/RL*CSGM/ SQAHNC/L LPGSSN
10189	24090	A	10265	514	157	GLTSLFRLEYSGMMSL*P*LPG/FR*PS RLSLPSSWVFLMYYHYAQQSPCIFPV BTGFHRV/QAGLKVGLRQSAHGLGPC WDRYCEPL*/LTKLICPTYGLR*RSKPP FVQGIQLF
10190	24091	A	10266	57	378	RERW*DSVLLCS*LVSV/VDQSYFY*V TEILQIKLGSKINCPILQLHFLCPL CGSFVGST/IFIFSRNIMGTVAHACNP STLGGRRNIT*DQEPFCLASMVK
10191	24092	A	10267	1	212	LQKDTNIVYIKSL*/IPNKH/KKISS IVSHYQIMKIMR/YHTRMAIKRTDKC LYECRETRTLMHCN*GC
10192	24093	A	10268	3	399	MANKHIKIPASLIRMBT*IRATNRB/H *FIP/IKWLVLKSRERBNCKWQCGRTGI VIHFQRECKVILL*/KTV*QFLKLNIR LGVAHSCNPSTLGCRLRVRVQDQPGQG KTLSLILEIQKLAWHGLHLSPS
10193	24094	A	10269	190	386	FSPFLPLVTLLSCDKAICRRGKSFDFFL LGSPFYFFKLLA/FIFY*BRVLCGPG WSTVAQSWLTA
10194	24095	A	10270	166	327	KTNKTAERVCPLSVITLINDGLNSPIKR QR*TD*/NP/ICCLQETHRFKEGTN
10195	24096	A	10271	180	1	IFLFEVETCSVA*AGVQNDLGSQPP PP/GSSDPQLIFAFLVETGI*IMVPS CKT
10196	24097	A	10272	273	3	FLGLFSGNPLKANKPVCHLPTLQRI FFFESEFHS/VAQAGVQCDLGLKPPP PG/SSDPGRRR*Q*AMITPLHSSRGDR VRLRLKKK
10197	24098	A	10273	399	27	YHVPVTRMALLRRKN*/Q*/TGEINL VYCNWCK/LV*LLRKIVNQFLK/DVKQ NYHVPVILLISYRI*/FDCLFLCKSHVE M*LSGVRVGMWVEIGSRNFILMSGFTI SSCHQDCEFSQDLIV
10198	24099	A	10274	275	462	KTNLVQLDFFPVEMSESVTQAGVQNC HLSSPPPPP/GSSGDSRASDS*VAGIT SVHQHGL
10199	24100	A	10275	2	379	RGPGRGLSGSGTCFHEGRGGEPIVYQHL P*FFGP/PMNYILLPGGLISH/IVTY YSGKKRPFGYIGMA*AMISIGLFGIV* AMHITPVGLVDVTRAVPTPPYHTFESPG YILSRHRKTKGFLF
10200	24101	A	10276	2	407	FFGSGFPFGVLSLS/HLGLPLTHW FLDSGTCKNHSQAKAGYALVPSIL EATA/PAPPTTC*QASLIALTRATIAK GLCINIYTD/SHLLHSHVWG*K/G/LT TQSSIIIDVSLIETLLKAFLLPKRAGA
10201	24102	A	10277	203	545	FLWRGQSLALLRLKESSTLL/AHNL GPHRFKRFSLPQPP*LSNN/DYRREPP CPANFCTPSRDGFTTLGAGLQLLTSSD LPTLASPKCN/DYRHEPLVIGLTNRSP NFFF
10202	24103	A	10278	250	3	AKWPLEMKSTFGEDANNTIEM/TRDLDY



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10203	24104	A	10279	333	3	DINLVDRVAVAGPGRIDSNFERSCTVVVKM VSNSTCYRELPHERKSRLMCOM*LSYF SLTLLEFOSMNHVVRVTFIDQFCVCSN YSTDWLFPHLSPISLRTPYSLRYNIKIR PINHPTMMWMSKCSSEBSRISLTLNQK /LETIKL/SEBGMKAQIG*KLGILICH
10204	24105	A	10280	251	3	ITSKVIDSNPTTSLITLNLNGLNLSF*R QRLL/DWASSPK*DSIIICYLQEMNPKYK IFKKIGRIYYANSIQKKVGVAVLTPDK V
10205	24106	A	10281	22	226	TKINSRGNKELNVRAKTIKLLSEINIDRN LCDLGLGNCFLD*YCL*TKINSKGNKE LNVRAKTIKLLSEINIDRNLCDLGLGNCF LWTPNAQTTKGR\IDKLDFTKI*FWL DT
10206	24107	A	10282	238	383	DAKRKVSSTEGSEGVANERRSAHLAK PCPAEVE/AKPQAAKEG*SEE
10207	24108	A	10283	127	377	RTPGGSALGRETRCGVKGQAEIGKIE MSOPTOREVVGIGSQKARQVDHLRSG VODQPGQYGETPTLLKH*LAGHG/GRC L
10208	24109	A	10284	328	370	VGPGPGF*SSGRVSSCCPGWS/PSELK* SAHISLPKCDVRCQPLRPATFFPKTAS HYVAQAKVQWCNYSLLQGLTLRLKCCIF KKIQVQVV
10209	24110	A	10285	341	1	KVVCV/VAPLSRRFSVCLPFLSPFFYFQ HSDIEIKPINYPVASKCSNERRSHTSL TLN*KLETIKLIEBGMSEAETGRKLSL L/QSVSQVVAKEKFLKIRISTPVT* MI
10210	24111	A	10286	199	329	LFPSFLNCLSPHRIEES*KEIKSAPPY TPGIPRK*TSLSAGKVPVNDKQDTHN NIP/LSQSKIITLPSMRAETVEAEERK L/ERCGFMRPKERTHLANTKMKPGVVA HTCNPTLGGQGRQIT
10211	24112	A	10287	358	387	YTNALLLV*DOPHLMGKCSLFPKAC* KNEYSHAKKQNN\*P*PSLTKTNSKWS KDLNVRAPKIKLEK
10212	24113	A	10288	111	373	SAQQCPDQHGKPTPLRLRQKLAGPDDAC L*SQLLR\*GCGEPSSRCHTPAWAT/EG KTPSQKKKK
10213	24114	A	10289	197	375	TRIGLCKFTI*PLETKLHTVARVECSSA ISAYGTLSLVDGSDPASAS/RVVGTTG
10214	24115	A	10290	118	371	QCLNWSPLKKT*MTGRLEGRNRLNPG GCGCEPRSCNCTPAWATK/GNSAGKNQ T\INKQOQQQN
10215	24116	A	10291	214	368	CGYHQNKKTNPENSRCWQCGCEIGTLM HYWKDHQV/Q/PL*TVQQFLETRI
10216	24117	A	10292	2	376	PPFLNAQRPTHLVPLSASSGTSLMPS LLMLPWLKHAHAVPTVPLSKLFDHTKPY AVSKNNIGALST*SY*VTPVPPRSR/S FRKQKTS
10217	24118	A	10293	1	379	NILBLDFPKHTLLEPOSSRLQRAVLAP LHPSLGINIVRRCPKKKSGWQMLTPVIS ALWEADVAGSLFPEKSETTLGNMMRPCLN FKKKKKKAF/LGAPGFFFFMGKILPGI AAPF*SSGRVSSCCPGWS/PFELK*SGH ISLPKC*DYRCQPLRPATFFFKTASHYV

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						AQAKVQMCNYSSLQPGTTLRLKCCIFKKII QVVQDI
10218	24119	A	10294	201	384	GEERLSVQCSAFK*LR*HINLSLQTFPP LRRRSHSVA\RLRSCGVSIAHCNCLCLFG SSSDSPA
10219	24120	A	10295	161	400	VCVIESVKANHLVDEHALKSTLSFHL SLL FGV*GVVCVVCVCVYMCFCVCIIYVC
10220	24121	A	10296	1	433	GBGGGCGSGVSGVETAGSRPAPGABQDL IAPALGRWQGLNGVCY*PAM*QPNRRQP LALLCAAGLGPQGRLECSGNIMAHSLD LPSGDPFMSAG\SLMGTITCTCHHAWVE FHHVQSSLLELLSGSNFPTVTLGLQW*A TTPGH
10221	24122	A	10297	209	1	LTFELLVHHYTLFFP*ESGSCVAQARM QWCDLGLLQPKALG\SGDPFASAS*DA* STGVDIYSNHTCI
10222	24123	A	10298	225	1	RFGNPLSALPCGTHAPARQPHSAACSGP KCPVQSGSPQAVGWTV*VCPPLSPCLC /FCVPQFPHGGLPLECPV
10223	24124	A	10299	212	367	VTAGSGHCVITWCERLBQSL*KTIVRF LK*LKVELRDPDPAVLLI\STYPED
10224	24125	A	10300	97	406	LHRCTFAMVTERGCLTKTNGNGHVE GEACSSKPTTIC\EEKIHLVCAITTED *RLAETITANTTDIPISAYRILIKLKLK PGLKTC\YVARQLSPQLQTK
10225	24126	A	10301	3	422	YRSSSTKFLTIIRRGFTPSSTFLLAHLST TLSLSHFQKGVKLVFFFFFKGFPFPF PFGGGGRKAP*P/HGNVFPFG*KNFPAL PRQGGKKG\GPPPPGQFWFFKKGVSF WGGAKTFELGNFPFGPFKGGITGGP PP
10226	24127	A	10302	330	1421	RKRGKPLLLALPVLALLPLHAFPSAPP GPSLSSTEDLKNLTLSPAQSRLQDQS LHRAGVXDLQWGRAGARLTAAC\WDAP PRPETA\VLQGLPC/QBGRILLESINGF ALVVSAGTIFYASATIVDYLGFHQTDV MEQNIYDIHVDDRDQFCRQLHWAMDPP QVVPQGPPLLETGDDAILGRLLRAQEWG TGTPTREYSAFLTKFCICRVCLLDSTSG FLTMQPOGKLKFLFGQKKAPSGAMLPP RLISLFCIAAPVLLPSAARMKRSALLRA KPRADTAATAD\SKMRS*LTLSSES*LPN *FEINDSAAAGTLPSLFPFGAFDQGHIF CHTRALRGSTRTRQCIAAALGASFRN HVEL
10227	24128	A	10303	172	383	KLBKNGVQVYHETETLVYCNWCECKM\QL LMKTVVWV\KILKLGPP*\DSIIPLLGI NQGTETKFCIKKYSNT
10228	24129	A	10304	205	2	NFYPA*KIUFFLVGSLFIYFP*ASHDIT \RLRCSGT\VTCHSLDLGSCNPFAS HVSGTAGAHHCIL
10229	24130	A	10305	423	30	LLEGKLTNRKDRITKTPSVRLHQSFKV DRTAKMGKKQSRKSGSKNQSAYPFPPE HSSSPAMEQSWMDELREBGRQSS/M SKLKEEVRVNGK*VKTREKRLAKSLTRI TNAEKYLKDLMLKTSVLRPL
10230	24131	A	10306	211	387	ITFFFF*IKACSACAGGGGRHLGSLQPP PPGLKQDSC/SPSGVGTITGMTYHAQFI

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						FFGF
10231	24132	A	10307	229	382	BRVVQVQ*HGET/PSLRKL*KLRCGG MCLYSKLLRLRL*EDHLNPRSWG
10232	24133	A	10308	168	417	GSYCFVRRNLLIVKVRSSVHLLFIMLL YRGD*WYVTIQTYNFCLQCKELIYRIA /HVRNPSSLRGGGG*IT*GREFKTSLAN
10233	24134	A	10309	253	402	KGGGQVVRTPARGNPPPPKGGGRGG PPPTQTGGFF/CFFFKGTTRPPGKGTGE RAKPNRI PADGKKRFFLPKPPKEGRIKG /PRPPGQINF*FLKKTGFKGGGGGSKP RPGGTTPPGPQGGGNGGGPPPPKGGP FGGKKKKNNPPR
10234	24135	A	10310	182	400	LHVNIILFWYGLKRNMLNPTTF/CYIF SVASHTKLVKV/MLGVAHLCVHTLG G*DGWIT*GQEFKTRLAM
10235	24136	A	10311	371	400	FTWNGI*ASNKHKEFT/STSLAFKKTV K\TTMYLSPPPTIRMT/I/I*KSYSKK CW*GCEIRSLHCKMQPI*KT/WQFP KIINIQLYNPALALLGNTRG
10236	24137	A	10312	113	404	QRGKGIGTFTHCWNEVYVQPLWRTDNN LLORINIELPCDLATPLNLYPREMKT SYICT*MFPLAALFII/AKWRQP/KCSSA DE/IGKNWHICIMK
10237	24138	A	10313	146	1	FLTQKFFFFFETESRS*AVVQNLDSGL QPPSP/GSSDSASAF*VAG
10238	24139	A	10314	157	434	FFFSIEFFFGGVFSPPPFFIGGPGIIF FCPLKCKILPPPRGKRPFFFKGIP/HPP FFFFF*BGVSILLPRLECNGLAYCK IHLPGSSDLP
10239	24140	A	10315	277	2	PFPTAFFLGVFVSPFFPRFFKPGRGFF LGP*KGNFFPPPRGK/IKFFFLKGGPSP FFFFF*BGVSILLPRLECNGLATLAYCN IHLPGSSP
10240	24141	A	10316	1	388	KTTTHREVITCEIWLKLYLLYPNQCITY VRMHICVVCVCHISI*MDHIVSYKCIHI \LCIY
10241	24142	A	10317	134	399	LGLPGGDTGGGTENPPFERALNSQNG GK\NPLLGPKTRPLGNLCSTPKPWEKP RVRVVDLN*TTCPLEKRAVWLKAKKTPA PEIRI
10242	24143	A	10318	233	3	EFLFSLTCAICL*CALKQFSSCFCLAL IELLGSMLLPH/SSLTFQFFFLQIFF /SFFPLFPGANITYNKPEYSLI
10243	24144	A	10319	221	8	CDQKSPPLSGVOMGDILV/VFFFLFL AF*R*GSHCVAQAGLELPGSSDP/POAT SQVAGTGMHCTWLVF*F
10244	24145	A	10320	1	407	RSTPDVYLGTSSGGCKTERAGCFPLN KLHTKGAPARCQPELGGMR\*R*PLGG V/SQSRVWAVKDSLEAGCPLELRCA GRYSYLFKGRGLDMLRLRCPOTTLCP GALSQDSSTFKPLTGLALLSWM
10245	24146	A	10321	115	398	ADRELLLNKQIKYLESESTPKQDVN TVMTKSEYSI/NLKA/VGPERIDSNF ERLSAVQML*NSTTCYKETPI/RKSQ MSQTSLLSYFKLP
10246	24147	A	10322	137	454	FFSLYFCGFFFFFLGKFFSPGGGI CPKPPFGPPPPPGKGSPPPPPGKAKK GPPPPPP/GPLFF*KKGGG/LGGFFFF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10247	24148	A	10323	246	372	LGKGIFFSPAGKGGQKPPFP ISIRSYQLW\LGWVAYCNSSTLGRSK WIT*QOKPKTSMANN
10248	24149	A	10324	415	1	INGAPRVFPFPPF*NPPEKNFWGPKKK KKFPFPPPG*KIFFFKGPPPLFFFFF SETSCSVT\RLGCSGGISAHCNLRLEA SSNSPPPSLRLMPSTFVLRPHGDLSPQ LSAMVLSWPLPLSLLPDLDFVQ
10249	24150	A	10325	3	559	GDGITGLSPITSKFLFVPSISLSPL GSSGAIMAHCSLTSRREPPCPSINFFVS VITLNVNRLNKGIRMDFF*MM*YTIQ ICNLQNTICRP/KDTCFKNRKRKEIHH ANSNQRKGVALLIPKIDPKFNVTFR HRLVRS/ISQSDVITNTY
10250	24151	A	10326	24	387	NQGLGANKQKSRVFLGVPFFBSSCS VQAGVNH*DHSSV/PGSSAPASATVV VGTGTGNNHPWL/FVFVETGSH
10251	24152	A	10327	145	396	CDYGRMFSYALMLIYLCDPAIPLEFY VPYRNENTDLSKMLNDAHSSPIMNSKL ETKCPGTDEWI*MTKSDYCKGW*GYRV TGTLYYEGECKIV*LLGNV*LF*LLN IYLCDPAIPLLPYVPYB\MKTRIHSKT *PMPIALAFLIAPNNK/PKCPGTDEWLN TL*HTHAVQYHVAVER
10252	24153	A	10328	94	639	ASISSIKWNNISFLVGLGELNETRNI CKAVNMKQALNKWLLILLFVINNNVSA SSNNPKIFYAYYAKAVLLIITEHITLS IVLILKKQNTAVTKC\RGGREKETL IWLGV*ECKLVQPLNRRVWRFLIKVIE LPIYPT/LLGIYISKERSVYRK\NICT PWFVAAFLPTZAKTWH
10253	24154	A	10329	143	3	SAWFFQDQVLL*/SPRLCTVSISNHC NLRVPGSSNVCLSLISINDR
10254	24155	A	10330	153	389	RQGLTLFPLGLVSNPLWLSLHLKPKC WGVCYHAWPS*CF*NRSI/WSGTVTHA YDPTSLGGQKGPIT*QGFETSLA
10255	24156	A	10331	382	422	RYKLDL*KLNTLPYDPTVFLGNYPKY *T*AF\SKTCT*MPFIAYSQPPKGRSK SSPNE*INKMPIYIMR/YYSALIK
10256	24157	A	10332	194	1	CKRQCKNDRNT/CSK*NPFTLFTTK RKQ/WLVAVAHACNLSTLGG*GGRAS*A QEFKTRANN
10257	24158	A	10333	348	1	NSGQSWIMYFLKRGVGRVSPDPDIVN SISMWCGRLFSNERFASLLTIKKKLA GHGGTCLQSLPLGRRLRREDRLQGGQG/ C*GYSS*LCCRCIFANAEGDLWSNSPN SVAY
10258	24159	A	10334	388	2	IPGSPKRGQGGSKKTFPHYFL/LRAAPP LPR*IFFPPKNPPLKGGGGFFPPPPKGL KTPRLKKKKKKNC*CPWKKFFKKQTPQ RGREFFFFLRQSFAVAGVQWCDLGS LQSPSP/G*SYHARTTG
10259	24160	A	10335	3	396	LLRPPCSLRNDISIMPHNMTASKCS SKKSCYSLTSLQKLDVILSGKMKLKA KTQGNL/GLGHLYRTVTHAVNVKKECLK ETKNAALNTQMTK*NSLIADTEKH*V V*IQE*AS/HSMPLRNLQNK
10260	24161	A	10336	165	442	GOMELLYLARNPGLLHFNLSIYYRRLF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
						FSIPRYLFTPIYLYLYLPIYFESVAHSD AQVECSGTINALT*KNKSLP/ASAPRA AGATG
10261	24162	A	10337	33	430	TGTHASANFCVSLVFTQLTSRSSGQGL ARLQRLCLPCCILPFSFSLVIYRLHSY LRLPMRRICLQVPSGC*NSFPCNFRIG GSLLL*/MOOM
10262	24163	A	10338	284	3	SOHPRPRWVDHLRSGVRDQPGHQGETL SRETP*SLLKIQKLSGHGSACL*SQLP RLRQENCLNPRGGGCSBRQHQCTPV*V TQDSVPKKK
10263	24164	A	10339	414	2	BRAGPPSRKRIFFSPPLAKKVKYPPFP RARAKRIPSRVVKRGRSCLPWP FFPSLM*KQ*GPSLRLRFPV/SWIGFP SKP*GPPGRPRKVPCTG/LPGRPGPG FFFFFPGDRVSLCSKRSVAQAQSLTAR
10264	24165	A	10340	211	422	ASLNGGRRPSPSLAALQFDT*TRAGLI FALFGAARQDLSL*RLLLSP/VCLCPA PRGGAYRGRQALPSWGLHPDRASRLFC LPQAWAMAGAPFPALLPCLSLSYCRA SNQDSSGGIGSEPSAGYKLLVFGFLIP ARK*RTIYGVTRFRGP
10265	24166	A	10341	116	432	SRORMPSTYHVQSGDITGTRBKPCANEN KCGSSILRSCLHRKRPS*SLKALVVC GGACLEAQLRLRLRQEAHLSQGVPCNE L*PGYCTPAWATEP/DSVSKKK
10266	24167	A	10342	103	458	SLNVCLTTLTSPSSCSPTSLPLRGP PYSL RARNLEIRPINPTWASKCSKRS*MS LTIANQLA*WNLHBECLKARTG*NLG LLHQIVDQVNAKKFLKKIKSAIPVNT OMVRKN
10267	24168	A	10343	53	408	SPQFFCSVFSPSLMFTYLLVDDGDEVOM GPWCGYPFCLLVFLLTDTKTLSCRSVGP CRVRQCA/LLGGASQLG/SRGSQVDRP LEBAVCLISDLQLAGRTITLF*AVRQG HLSLQRL
10268	24169	A	10344	265	421	NNFPSPSRGGGNGPFPFPPRFFFFFLK NPLGPP*VIYLL/YPTLTPSCLWCYT ISVYCGGVPFFFFFFFFFFEKIFFFP RVEPKRIPVYPKILFPG*NNFPSPPR GGNGPFPFPFPFPFPFPFPFPFPFP KKGAKFPDLINPPWP
10269	24170	A	10345	207	420	WQKGPVTFMELGVVGLYPCFLHLNIQ PTSHRYIHL/WLGHVVHTCNPTLGGQ GGWIN*GQETSTLTD
10270	24171	A	10346	115	3	APRAVKRR/RPWMAATHVCKPSTLGG RGA*IT*GOEY
10271	24172	A	10347	41	421	FTYVGVVHKLPLSLFFETSVPG SPLAPKRGCGGSGPWPDPPLGRSP PPPPORTGKGYPFPFPFPFPFPFP RGV/PPL*HPGPGQSV*GTTPPGPPKF WGAQSGGVPVGNPLP
10272	24173	A	10348	228	1	SKQVEEKYDSFLKIQKAT*NTFTFRV TKKHVEITKK/WAGHMAHYNASTLGGQ GGWITLQGEFETSLANMKP
10273	24174	A	10349	405	1	GGFLERGPFFFFFLRQGLSLLPRLECSG MTVAHCSPTILDSNLSRRSNDSYSHA QLIFLVSE*VLGSHSVAQASVELLAS/P

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						KCWDYRIEPL/WFSQSQNINSFFLDGFS LLLSRLCECNAISAHCNRLRLGSS
10274	24175	A	10350	301	546	RHIFWNLPPFHNLVKIFHCRGKTLFLDI SNPYLKKQVSSSKPNCK/HLKBI*LPLE AKDYMLGVVPHAYNPSTLGGQGRSITG
10275	24176	A	10351	873	1258	FCYQCYFHLHLHLHRRPSRLEPPPPG AALPPVPEGRIIPLPCPSSGPRQTGTGK KGRHPAPHRTPAASASLPAARRTLPA PW*PLSPONTTPGSA\PGGNGQPASGAG GNSRT
10276	24177	A	10352	184	576	GLSPLSHLKPAASSSEISEMKGVESPK VPGGRGHSBAETGPFQVLAVGPDQPEA PQPGHNTAAPVDSPGPKCLAPETITP AQ\POKQPRPOTSA*QAGNQRPRTAPK THAQETVSKPEUSKERATD
10277	24178	A	10353	110	384	VFGSPKRTKSPQOMERVLPAPKAKGCP RPGDHRSLR\CNCRDTRARIKWADSVBRP PWAG\PMVAICNPNTLGGRGGMIT*GQK FKTSLVM
10278	24179	A	10354	123	422	RKQIANDSKSLFIINLYNVLNVELNSPIK /RERLAGWIRKEKHDPSICHL*KTHLT\ KDTNLSLMKMG*KKIYHANNY/QKAGVA ILISDKIDPFKFKKVVREK
10279	24180	A	10355	36	426	PPERPOYSARVVCVYPTTCRGLAPKPE CRGAI\IAHCLLNVLGQ*SSNLRVNSS* DYTQILFKLVQV\TGSCHIAQAQFELL/S SKDPPTLA/FPKHWDYH\DHSM
10280	24181	A	10356	193	3	FQTRIFKISFFFESFLKFKFFFFFLI* ESSSLAQGVQMRDLGSLQPPPP\GSSS PPASASLY
10281	24182	A	10357	205	377	SBVVPQFYRLTIPYQKC*LKVCI*VY *FFKLILYPAILLNSIININPTSDPL* FSSHITG*LSLKIQNVWPGMLAHA\*N PSTLGG/RGBNIT*GOEPETSLANNVKP
10282	24183	A	10358	51	376	LCRPFOLCHGDRITDMCCPFPEELQDRCS CRSTSMRVAKGTTCPFLKVLQNIYTV*M FCRTFRKHGTVPLATRLV\IYNSGPFV TLQGRGITYLSCHHGKAGVCRATQHAA GVVVTKQACI
10283	24184	A	10359	295	376	ASELTSQSGSLFENQKGRCTAFLPC* KCNSLILVHCWNGCKH\NKIVN*FLKTL /RLELVYDPASPLAIYPRCI
10284	24185	A	10360	451	1	CODIKTILRNDEVLVI\PSVTRYKQVGK SPFSRRYILWSGCULCYA\PTVEASKTWHH FPYRSPGFWGHSGGGRQFDS*PKSQADFR APOGFPPTBPEGAARRREPEIAPPIDAP SKYKT/HSPFSGAPPSAPPFLLGRAER GW\AQGRWRP
10285	24186	A	10361	2	776	FFFLRSLALSRLLESQASAHCKRLRL AGSRHSPASASRVAGTTGARVHARL/L /YLFVETGPHVSGDGLNLLTS*SACL GLPK\C\WLYRREPFPAYFIFFLRBSL ATSPRECVQWCDIRSIQAVPIG\LHHS PASASLVAGTTGAHHHRLVILL\FFY FLRNSVTLSCRL\AGVQMHNLGSLQAP PPGTPFSCLSLPSWDYRCPPLCANF LYP*RRGFTMLARMVSI*PRDPPPSA SQSAHDLFIYVGQ

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,511,266	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
10286	24187	A	10362	188	365	CPQLHTQSNLNNMDASQRYQFELKIQAL /WAGTVAHACNPSTLGSRRGWIT*GLEY ATSL
10287	24188	A	10363	146	1036	GWAVYQTQAAWLGPRTESSGVSTPHGRPS LPHPHPQPTLHWAPAPLQPEPCVPLRE DPFMPESN*LPPSIPAEQVSP*ECDFSR RMMGKGSVPVTVAPPLQPAPEPFCVTAG CAPMHTPTHTQ\PHHCISFLPKISFKSK HFY*LLFCCKLSSSVFSLPESLLLLIV ESVQCFGERCLALNMGWDGKSGRRMAT KSGQVNDIATQTEA/VESFV/FAISCP AGVSGGK
10288	24189	A	10364	229	1	PLENAKSYIAGKGRLLKNNARLPTVA*SNQPPQSLMVDMLKK\WNRWVTYTESCA AI*R/DEIVSCAGTWMELEAMY
10289	24190	A	10365	186	449	RFFFFFPKFFFWVGLKSPFFFFG/RLGI *EKDGGFFFFFPPFEMASGSA\RLCE SGAVSAHCNLPQPGSSGLPSAPRVA
10290	24191	A	10366	445	3	RVDNGVRGRYRGRGRGR*TRWQGHF QRMQDQRDRRERPRETGRERAAGRRRETE AAETGRRRRRRGRSDNRN/RGRPREM IEAGRDAGRER*ARQESWTEKKTARQE EGD RD/RQGHQETRAHKGWGN* D*GRQ AERSENRRMY
10291	24192	A	10367	1	491	NTAPFPPTSLESAPVVAQDRVS/LLSP GPECNGAT\LTGCC/LRTPG/FKPLSHL S/LPS/SWDYRHVPPPLNLLICDRVS QSGKLILASNPILTSAPST/YDYRRET PQPRASP*QWOPCPMP/RS*SQ*TWI A/R*QSNWGSQ*VLINRELAPGTMFPQG RPKAFF
10292	24193	A	10368	572	40	LHSFQHFSNTYPOCTPGTP*VTCGLAA RPAGLPEPTASGSGAGAVTPPRTD\PP SVRWSGKKGLDPLVRGGAPRSPANPAP APQGPAPRGTECVPTASKTFRPGGRWE FAAPPHAHPGKDLQPPSTLVKECPARC PRALTGDLPSSGENRNLGSAFQGGRRPA QKSGENCEN
10293	24194	A	10370	36	517	PFLPSDIDFLSPYFLSFFFF*KRGLIL PP/GPRGGQGNK*WPLHPRG*REPNNL TPQTRNGKGNRQTGPVIEGLRNGFPF FGQGGFKPPGLREPPGLALQRGNNQN PYP/P/PKGFF*RTKRGESPPQPYNNK NKKFNAPMSEESSFKGRGPPSLN
10294	24195	A	10371	60	403	DYBQKLSVPLCKKPSALITICHA LQYNSKELTQSNWGLSPFSSGSVQ AGW\CDHGSLOT/PTDSTSQAGATDP ASAP\QAAGTIGACHTCLIFVFL*RWG LAKP
10295	24196	A	10372	358	33	DSLGVPGAPILSPGVTPHKQWFFRPYTO IKKLGFPPQIFPGFKV*KAPFFWNGN LKKKGQFFFFFSSSEMAGSVA\RLCS GAISAHNCNLPFGSSSLPSAPRVA
10296	24197	A	10373	264	3	RQTSVSSSNDGSSWPDITDI\KYVIG NRLITQQ*LIKLSQMITHNTKGT *SLILVSLIIFLATTNLGLLPHSETPT THCI
10297	24198	A	10374	298	384	TLVY*KDGVHITPHHQHATVPGPXTNML

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
10298	24199	A	10375	84	518	HKAPLLHVSRRDPSPFAQSSNCTNRSIK QEPVDFLTQAEFVPRDAGKMGKTPLSEV SQNGGPS/HK*GQYSGGV
10299	24200	A	10376	70	363	IMKLROKSRSSILKIMRSKLQHTRAS/GT QLR/PMLGQNFIALN/AHIKKLGRTQIN NLTSQLELEKQD/RNPIARGRQBIT/K I*BELKETET*KKEIQKIYEFV/WFLE NINKP/PASRLIQRMIERINTIRNDKGNV TSAPPDV
10300	24201	A	10377	299	2	YIPVAGRGNR*GCGAHLGVCGAAMPQLGA TISVSVSLTISLCAEPGRGGLPSPAP HTPPPPPP/P*ASSPSPRGHMLVPPCMQ PGLPPLPPRRLSPV
10301	24202	A	10378	302	3	WPTVATTCSCEKRSHTSLT*NOLESTQ LSEBGMKASIGQKPOLCHOT/VQVWNA KKLLKEIKNATPVNTQITRK/QNSLIA DT/EKV*VIQIEDQTSV
10302	24203	A	10379	125	375	NEYVFLERSKLKLRGVGSCLLGRQRPVD HLSSGAQD*PGQRGKTPSLQNTQKLSRH GGMCP/RRLRWSDHLS/RRG*GCSSTR ST
10303	24204	A	10380	458	3	ITITSTICKATSPERAPRASRPFPDEWV SQAGPAPLRGWN*GTRRRDDWFEASLK DPRRSGBPEAPL/PLRLML*SRLPPLR WRRRP PPPDSHTPSPGNGKSPRVPTGS KKKPSALP*FAGSPLEANVPFVQHG GGSVRSRGSYLAT
10304	24205	A	10381	327	2	LSAPKFFPFQKSLFLGANFRSPFFGRF PTNRFSDLNWN/PLTKIYTSKSSNPPT FFFFFETGSGSVT*SGVENRHHNSLRP ESPG/SGDRP*V*HTGAPYHTNLV
10305	24206	A	10382	754	1	NTALETDTTFSGGGGGHQLCVRSRVSGG G*LIMPDHNNHPLQOTSQRNRLOQSVT DPSPGMSGGAQTGPKAPRPSPALRHS SLQGQP*FAHLYCGTIFPCYQTAPLPR APPPPTPGH*CPGEA/PQDELVPVCGCSP NPRPPGQAQGRNKH*FSGQRSSRDTTA CSPCSQSKQSPSRPPCVNDS/PGQGGP KAPAGPPPALPRASLGSVHCS*VGWMT PTRPGHFLVPKVTLEQAPGGGASGGVP P
10306	24207	A	10383	39	433	SHOQTYTEELLFMDQRKNFLMESTP GDAVNVVETYNLSEYCIINLVDSTVA/ QVSNFRSTVQGLMSLTVCGKKE/R *XR/SGSNMQTSLLFNKLGQPP*PSTP TILISQQPSMMWRQPPSEEL
10307	24208	A	10384	283	1	NVFSCKPTSSCLISFDSPTDPRRFSAD TYRNFAPLREHHTHHT/MTHTVHVC TQICLHLRPH/ITHGSL/TCAPPVL*R PSFKPLHPTPV
10308	24209	A	10385	12	471	SPFWTHGFRYNEPTPPRFVPHDALGO FHTALFRLTRFPOLLSSCINISPTCLP PCLGLCVGGLPEAVCMAR/CP*RGWV SGWKASPLG/CPPTLLPEC



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10309	24210	A	10386	287	1	SFCVRSREAPITSGRTEFFAAPPFFPAAPP FFAATTPTSTADGVPG*G/PAPANCSP HSSQSGSAAMGIPLEQAS/PPAPTAPP SP*SLPTFFPAMY
10310	24211	A	10387	336	3	LIEGKLTNRKD IRSKTASVRHHQSPKV DKPTKMGRRNQSRKAEN\KIKSASSPK ECSSSPATESEWENDELREGEF*LV TNFSELKECTGKLNPAALVGRSEDEQTT
10311	24212	A	10388	15	470	ATSPDVGK\PTEDKATITSLKCKNV EJAGGETLVKLG/VVPPVQKIFDSGNL SSASIMNPVGVVKGKELTSLVDALK HLLDLKGTFAQLSEIACDKLHVDPEFK LLVNVLTVTVAIHQKEPTPEVQAYLHK MVTVVANSLRYK
10312	24213	A	10389	3	438	OTOREPTVLSPADTKTNVKAAGKVGAK AGEYGAELERMFAPFTT*KITYPHFDL SHGSAQVKGHGK*VADALNNAVAHVDM ENTLSDLNLSHAHKLNVDPVFKLLNHC LLETLDGHLDSAEFT*AVNLSLEQPTAF EITWLT
10313	24214	A	10390	2	444	TMSPTTLATCLDCLCSLQPTRSIFGVP SSPLPGNPPTPMTSSSVYMSNQEVK SPFLFDLKPNLNLSHSSPGSGPCDEL LTPFVRDGVV/SGALPFAAQPGC
10314	24215	A	10391	405	3	KMILTCLALPAQCCHPSSACPTTAAQPL PLSINKGAASMSDKLGYKRVADIGLATWGH KALDIVEN/EMFGLGNGELYASRPLK GACIADCLQITVETALLIETLPSLQVGE QKSSCSIFSTOEHNVAVPAEAGNP
10315	24216	A	10392	248	5	RLNKGGHGNGYERHLYNKLBTIGYNYK FLDIYNLPNLSLEEIR*NLNRPITTSNKF ESVIGHFPTTKIKSLGLDGPTEFLTN
10316	24217	A	10393	252	3	LPRDRQAGRSQGPVVPQAVGSRKMPFF ISYQVYSKNIFRIECSVTQAGVQGNRI SSMHPPFF\GSSDSFASQAQPGIPGAH HHA
10317	24218	A	10394	287	410	ALEGGSSRLITMLGANLTPVIRK/LWEAK AGRSSEVRS
10318	24219	A	10395	175	1	GGREVVDDRIPLVRESTIPIHPFFPFETE SHSVAQAGGQWRDLGSLPS\PPG/SCH SPA
10319	24220	A	10396	661	963	STLIAFIVISTLFLPLDMTRIFPSLLDE IVDTLGEAGAGKGVVKIDHKGAGRHVAV KIVKIVORYCRAARSEIQVLEHLNTDTP NSTP*CVQ\MLEWFEBH
10320	24221	A	10397	1	268	PQTIRATWLSLADWTVYAGWGKGGGA PAGSDCAALERMLSPFTKTYTFPFP LSHGSAQDKSHGKKVADALTN\AVAHVD DMENAL
10321	24222	A	10398	33	302	SRGATLIIVDNNENGEPGRVVAZDGLKL RSGPSTKALDGRSQVSTPRPGQTDPAPP ALPKATRKASGIVNRATEESV\KTKGHL VQEHF
10322	24223	A	10399	16	233	PTDYFNITTYRECGPRRPEFSTSLDLL SOPCRAYVM\VGKNDIPFELRIVDLIT GKSLIGGEPKSEQGDR
10323	24224	A	10400	177	1	KLLDLGQPSPALAACLEYSGALAM\C NLCLGSSNPPTSASRIARTIGVHHARP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
						YA
10324	24225	A	10401	185	419	HVNKDTLRSHVWKLSALLGRKESVTPGPSCHPEPSDKIVEL/WQGAVALACHLSTLGGQGGWITLAQEFETSLDNIV
10325	24226	A	10402	104	3	GIILLPKPGRDITTKENF/RPLPIIDAKILNKILAN
10326	24227	A	10403	3	344	SQVMVAVGAPAGAGARPRLDLQFLQRFLLQILKVLFPSSWSSQNALMPLTLLC/LTLL EQFGNYQVGLLPNQYGVGLGNKDLBGFXTLTFLAVNMLVLNSTRVRSPLSVSLVLS SPV
10327	24228	A	10404	3	404	ARAQRGRDLSATGRNHSPLPPAGLPAIVLRHSGSLMAATCELSNIFSNYPAMYRS\EDYTLASVPPAATFGADDLVLTLSNPQTSLEGTENKAWGLEGSCFWPKTQGLD WISQPAEKNYEASAIQEPKDX
10328	24229	A	10405	254	443	NQLSSIMVWPKTKRSPEDPNDPEKYVVGSGDKVAG\RLIVEVCEDTRVKAVRILACGVAKELRM
10329	24230	A	10406	26	461	GEVARRSCCGMAGTALRRLMARYKQLTLNPPGIVAGPMEENFEWEALIMGPEDTCEFGVFPALLSPFLDPLSPPMRFTCEMFHPNITYDGRVCISILHAPGD/DPHGLREQ\PERWSPVQSVKILLSVVSMLAEPNDES
10330	24231	A	10407	1	463	QQAARVARNSGRAGKSSG/T/PARGRR C/PARQVIAGFNRLRQERGLSKAARLEMELEHSLVIDTLKBVDETRKYRMVGVULVERTVKEVLPALENNKBIQKIETLTQQLQAKGKELNPFREKHNIRLMSDEKPAKENSEGAGAKASSP
10331	24232	A	10408	180	446	KKAASVAAASGSHLSNPALPSPESNGSMYRHSSSPFVRVPSDKPFLNSLRSPSKPTLGYPSNSRAIPNAL/KNLQD/KIRRLNL
10332	24233	A	10409	1	417	BAGLVNTEIGTIGERAGDETPALSVSRPQTGLSPLGPEPDEDLEDLYSRP/KKIQQELEFLEVQREYIKDEQNNKKEFLHAQEEVKRIQSIPLVIGQPLEAVDQNTAIVGSTTGSNYVYRILSTIDRELLKPNASVALY
10333	24234	A	10410	305	53	LEAQPHAPPLIGHHLPWRTPSHLGTCRRPRAMRVQGSSEEGVA/GOAPPLPWVHRGSLPLVRRRPAKPTGGNAREEKGKVEG
10334	24235	A	10411	419	2	NNSRKPGNGTLLKLEVEITYPLISESTPDKSEILLTPQDKKHAPLPSAVNPSPA/CPDLRPHITPASPV\PAKIVETRPSAPQGFLPGVRRPGRFSVRAASQTSGRPSAPRPPGPALREATDAPRAATPPAALANGHS
10335	24236	A	10412	74	322	MDMMATTG\SKRLDRLIAPAKVDLSSNPFICDYLHRLPVRANPLPGHARETIQKMLDGDRTDQKTS\YDEPAVISM
10336	24237	A	10415	1	415	PQTHREPTWVASADKTVNAAGKVGALHAGEYGAELERMFLTPPTTKTYFPILDLSHGSQVKGHGKMDALTNVAHVDDMPNALYALSDINAKHMLDP/VNFMLLSHCLLVTLVAHLDPRTFAVFACLDKLL
10337	24238	A	10416	19	454	APSPNANGHCTREDKATITSLGHWNVSE

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						DAGRETIIGRLVVYPATQRFFDSFGN/LSSDSAIDMGNPKVKAHKKVLTISIGYAIMHLDDLGKGTFAQLSELCKDLHVDPENFKLLGNVLTVLAIHFGIEFTPEVQASWPKKMNVA
10338	24239	A	10417	2	395	ALSSSQPSAPMHPFFYTRAAIMIGELAAVVSFISKFLRTKGLTSEKQLQTFPSQSLQELAAHYKHMMFPKCKGSGYSMIGVNP/KMISLILQACIEGGI
10339	24240	A	10418	2	374	LSTPHAFGKNGTFFLSLLFSSAYSRGVRFDAHKEAAHRIKDLGEEDFTALVVIAPAQHQQWPFEDH/VOLANDVTRFATTCADDESSNCDOSHLIFGLDLCRSATLDESICVQGRF
10340	24241	A	10419	48	347	DFKQFLPEPLRDLQGLTANAKQSR/TSLL/LAFALLCLCPFKAGPPNPLSLRFLDHAHLQARRKTTAIDTYQEFENLYPKD/QQYS/FIMTPTSSALDSIPTPS
10341	24242	A	10420	166	1	NFLKKGKPFQKQFQRLPLITTTTTFF/FETKPHSVSL/LECGGTVSAHNCILPLV
10342	24243	A	10421	2	251	LGCTOHRSQELVAATSHTQCTQASEVDKEI/FARARNGKYRPLKISITENGQIMIGSY/SSQPSDSWNDYDSVFLPLLEDKQLCY
10343	24244	A	10422	251	1271	KEDLSRAPMSGTQSTITDRFPLKPTRHGSLANRESPTDKKQVERIASHDPDPTDSSSKRTKSSSESRSEIYGLV/QRCVI IQDDNGFGLTVSGDNP/VFVQSVKEDGAMRA/GVQTGDR I I KVNGLTVTHSNHLEVVKLKSGSYVALTVQGRPPGSPQIPLADEVSPSVIGHMSPINTSPKSGASGNMERITSPVLMERNVPRVQVLLARM LQKBOERLOLLQEDYRNPQAOLKKEIOBAKHGIPQLQELSKATGSAQDGAIVTTPSRPLGDTLTVSEARTDPQDVLGRTDCSSGDASRPSSDNADSPKSPKERTYLENPEEQKKG
10344	24245	A	10423	198	569	QRNVGQRLVEPRRIKPGFINVKSTGNDWEHQGFPLCFFFFLWLSLALSPRLCSGAISTHCNLCPLGFKQFSCLSLPSSMDYRHAHCKQLIFVFLVRMG/FHEVQNGQGFPSLEKSLTII
10345	24246	A	10424	2	343	POTOREPTMVLSPADGTVAAWKG/VGAHAGEYGAELERMFLSPFTTKTYFPHFDLSHGSAQVKGHGKNVS/DALTNAAVHVDMPNALSALSDLAHAKLIVDPN/FKLLSHC
10346	24247	A	10425	31	342	RAAVMPREDRATWKSNYFLKIQLLDDYPKCTIVGADNRSSQKQQRMSLRGCAVVLAKRNTMKAAT/AGHLENNPALEKGLPHIRGNVQFETIKED/TEIG
10347	24248	A	10426	196	2	KNLIYSQYKVICPNHFLVFPKRVFFFPPFFETESRS/VSPRIECSA/STIAHYNLCLPLGSDSS
10348	24249	A	10427	1	405	RLECKWLEPPHAGLQGLAKWVSCSVSTGPTMQALV/LLLCIGALLGHMSQNPASPPEEGYDPDPSTRALEDDEDDPIFIDPENKLPKAGSNFGDYLRLAIRANSPTSNVLLP

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10349	24250	A	10428	223	361	PLNVAITDILMDLSLEAQLTESIT EGPTERNMAKVFES/IGKPGLLAVAG/ GPVNSALYNVDVGHRAVIFE
10350	24251	A	10430	3	359	LTQREPTMALSPGDMITNVKAMGRVCAH AGDYGAELERMFLYFPT\KTYFFPHFD LSHGFAQVKGHGKVVVDALINAVAHVDD MPNALAALSDLHAHKLVRDVPVNFKLLSH CLLVTLA
10351	24252	A	10431	273	1	NHKGKRGKSGKTERSKNSQASPPPKERS SSPATBQSNTENDFDEPREBFI\RQSN YSELKSEIRTHGKEVKNKLEKLLDRLTR ITNAQK
10352	24253	A	10432	211	3	SFLMKFLCRLGIPSHVSQQA/LLAGAS QAGYSGVRDPLEEAVCLFSDLKLHAGRT TTLFNAVRCQHLSLQ
10353	24254	A	10433	281	2	TVQSEKQDDPKIKESGKEDTITDITVIT IRDYYS/HTYTNKLM/LEVDKFLDTY YLPFRNQREIENMQPITSNETSLSVIKS LQTKSGPGPMAS
10354	24255	A	10434	219	1	SFLMKFLCRLGAPGCMRCQA/LLQGVSH LGYSGVDRDPLEEAVCPYSDINLCARIT TLFRAVREGCLSLQKF
10355	24256	A	10435	133	2	FPKPPGNFFFFFTESHVPT\RLCSGA ISAHCNHLPGSSDSA
10356	24257	A	10436	248	376	EGGVFFFFFFFFFFESCSITQTAQMHT \YGLQPRPP
10357	24258	A	10437	250	1	KGTRKSLTFIEQLLSAKYWAAGQMHYFR GGGKYSGYPVFVFPVFISETESCS\VA QAGGQWCDLVSLQPPPP\GSSDSPGASF
10358	24259	A	10438	354	2	KRGLKKNPFPNPNMGEPLKLGPNPKR IFIONKI FIOGLKKKVLGFIYNSKNLKR GKIANPFIIFFFFFFFFLETGSYIA \RLKCSNGTINTAHCSPELPGSRDLPGS TQVAG
10359	24260	A	10439	126	1	GMTCVCLCFATLKEGRERERERERK RERQRKER/ERERDKRKRERK
10360	24261	A	10440	29	347	IQKPTADTKKFPKKKLKTYTREHSHARK EORKEGKKSEKTKTKOHGSSKSLINKTL NINGLSKPIKTHRVAE/NNKNDPMLYC IQETPETYKDTHRL/RIQGMKKIFH
10361	24262	A	10442	405	1	IFFPHPPFFFKSFRLSQVFIQGITLGF WKLFPFGPNFNS/CPNLNINLGFPGLLP RPSYFRIFCKKKGF/H/RVYPEGFPFL ALGFFPLFPFKSWGFGQDPDSWGPPFFF FFVVLVAGKTLSEGCRLIRGRWKNLVP
10362	24263	A	10443	122	372	LYNDPISIVQVTLRYRVFFWLYSANWS LRWKANFLFSPFFKMSDPVACAGVQC DLDSLQPPF\GL\SDTPTLASOVSETT G
10363	24264	A	10444	171	3	RHPTMGSSSEPLGSGFCRLTVFVLF TESCSVT/RECSGAI SAHCYLSLPGSSN LP
10364	24265	A	10445	173	3	CMNVVCFSI FIFLKFNFLETESHVSQ AGVQW/LITVHCSTKMGSSDPPSSASQ V
10365	24266	A	10446	187	329	SFLMKFLCRLGVGHVRCQA/LLGVASQ LGYGRVMDPLBEAVCPFSDL
10366	24267	A	10447	27	226	YSYVPVYLHLHLFLWKCISLFIYTVZEM

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						ESCSFAQAGNKWCDLQPLPPG\SSDSLA PASQVAGVDA
10367	24268	A	10448	119	296	SPTHYILVITICPIHVIILLITFSEVGS HSVAPAGV\SGAIIAHCHNKLGGSSSP VSVS
10368	24269	A	10449	111	363	SLKKLVFFFS IYTHNFFPFPDPTLKNST RHLVLSLSLSLPLSHSV\SRLECGGT I IAHCSLNLPGSSDPHTSMQV\AGFTGS C
10369	24270	A	10450	218	1	QRFWGPGPNLVFNKLGSAFFLGRQKLF LEIKGFFFFFLVFFLRQSHSTAAQAGV WCD\LSNLQPLPRPK
10370	24271	A	10451	179	3	GPRLITLPMOKKALGRKCHFFPFETE SCTVAPAGLQWRDLQSLPPPP\GSSDS PAS
10371	24272	A	10452	71	232	SSPLSLLNENIVLEVLAKDIMGVEV\TK LILITGKDEVMKGLIVDKI\LLVKNKH
10372	24273	A	10453	153	3	ARGELYFLTEGGGFFFLVFFLRQSHS LAQAGVWCD\LSNLQPLPRPK
10373	24274	A	10454	338	221	MOFLHVGQASLKLITCTCP\LGPLKCAD YRHEPPRPVIPS
10374	24275	A	10455	214	366	YNYKYLHYSYLFETIFF\NIYHYIF FILFFYLTSPFLSYFFFFITLF
10375	24276	A	10456	155	2	DRVSLLLPRLECNAGATLAHCNLCILGSR HS\PRVAGITVAHHHARLTCIF
10376	24277	A	10457	870	1249	EGPRWADHLRPGVDHGH\QHGETJST\ QKIQGLARRGGTC/LCOSQLGLRISQEN CLNLGDGCGSEPRLHHCITPWQDE\GDS FKKKKE
10377	24278	A	10458	222	404	KRPGRAQMLIPVIPKLEKAEIQR\MLE ARTLEPAWAT
10378	24279	A	10459	122	362	LSSEGLNCTPQRLLHFTPLPVITRVQMS HYLCOQSCILPHFF\SEFFLYFMSSSG T\RLKCTGMTSAHNLVLPSSQSSG
10379	24280	A	10460	3	102	AASTLALSRLCNSATLAHCKLR\LEA FTTPSCL
10380	24281	A	10461	133	339	KLSKFGQSKRPETKANSLLALFYHNYT TRQCFSTYSNFGDRVSLSPRLCNGV ILAHCNL\RTPGFK
10381	24282	A	10462	3	193	ASNMMTELSQSPILITLVNVLNAPLER HRVAGWINDPTICYLQETFT\CONNR LTAK
10382	24283	A	10463	126	314	RLGGSTIRVORDLSRDKPGRFLYTSN SSVVRKGKKNKACPIERV\PVNDII
10383	24284	A	10464	1	332	KRNFLFSRDLCLSSLFSSKSPPATLGGP RGTWPKTRF\IGKAPFFKKSLSLGRKY HFGLKVPV\CPPFLSKTRFLPGVPPFFF FFFETESHSAV\RLCSG\AISAHCKLR L
10384	24285	A	10465	173	365	RFVCSITIKVRLDLSRDSRNPGRFLSLQI PP\LRKDKRNKAYFTK/RPSVPVNDIIST
10385	24286	A	10466	335	3	PFKFFYKLSITRALLSEPVFGKKIRVPP QRLSPINAPLFRKPGPNQVIVPLFF FFFTVRHGLALSSGVCSGTRLCSGAL /STAHCHLCHLDASHPPTSASRVARPTG T
10386	24287	A	10467	818	1008	VHTDVLADTILEGINNAEKQCT/RRCFLS \WLQGHCPFLTVMNQHGLCGVLEGLLPG

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10387	24288	A	10468	111	1	PGDFCKRPR MVSFGPRPADAHKV\GVRRDQPGCHGETP SLLKGIIRI
10388	24289	A	10469	204	1	LWGPILKTFQCLTKTICGNFRGPTFFFI FFFBMSQSVTQARMQWCDLSLQPLP GS\SNRSASAS
10389	24290	A	10470	190	330	ERIKKQDLSICCLQVTHPTKDSQKLKV KGWKK\IFHTNMQKRIMT
10390	24291	A	10471	162	2	IKGPKRAPANKGRAPPPPPFFETESC SCLQAQVQWHDLSPPQPTP\GSSDS
10391	24292	A	10472	120	3	SWGFFFFF\EVESYSVAQGVQWCDLS SLQAPHVIMLVK
10392	24293	A	10473	298	1	RRALPCPANNFLYFFFLSILLFFETESHS \VAQAGVRNHIELGSLQTPPG\SSDS PA SGETSANVTGETSANVTGETSANVTGEY SVNVTGETSANVTGEY
10393	24294	A	10474	1	380	AVTGRAGSWAPR\PLRLVLVFPQKLR SHAGNFQSGSHYLQRLDGHDLINEROK DLKVLSEEREYWKLRFFTKVIGALCEHL KLKQPGTATATATVFRFYARHSLSKSIDP VLMAPTCVCLASTAN
10394	24295	A	10475	289	2	TGQPPPTNNSPYALYPKQIPPFSDKLF RVKGFPGPVTHYGVKDFNKGVPPIFF FEMASGSAQAGVQWNRNLSLQPPPI\PG SSSLTTSAPRVAS
10395	24296	A	10476	138	402	ITGRAPPKPPFLKRGVLSGGLTNIGFSF SFSFFETESRSVTQAGVQWNRNLSGSRNWL EST/SPDSGNS/PAPASRAAIT
10396	24297	A	10477	2	336	ARETNDITOTRLPANNMTSRSDPYIS LTLNVLNGLNTEIKR\KRVASWNRNCGLN GCCLQETHLSHETHNDTHKLKIKTYMRK TYQWNGKQKARVW\TLISDKTDFKP
10397	24298	A	10478	51	250	RKVSLEFKWNRNTPCKK\LSLDTYRF AKTFEITDLNVRKNT/IKLLKGNIKE NTCDLGLQKDF
10398	24299	A	10479	216	2	GPTRKALSGPFTGWNFVNDPNSKLFPK KNFSERFFFFFETESHSVT\RLCESG PDSAHCNLHLPGSSLV
10399	24300	A	10480	191	3	FSTDGRVNCVLKYSIYIYIYFFFLIIF FEMKCS/VSPRLCNGALSACIKCLIP GSCHSAPA
10400	24301	A	10481	135	768	LGGQVLSCASQPVSLFPLEFFFLISFLSC LLAFLSACFASTFSCVLGSPETSPCL HPPPKVLSSHP\PPCSR/CPQPPKG/P PLPKHACPP
10401	24302	A	10482	126	333	MVVGORYCVMCPVT\VLCLFLLV/VWVW FLW/CSVYIVVMYGAUVLIFFFFFFS LLCTAVCLFVHLDRF
10402	24303	A	10483	240	2	ATERNMGLTSGVRLGSGNSPYGRVRE RIGGVCLWSQILLRGC\LRWEDHLGLGG GGCSRPRSSFCPTTWVTQDPVLV
10403	24304	A	10484	136	2	NRPSYTFSPFFFTESHSVAQAGVWHDHL SSLQPLP\GSSDSAPA
10404	24305	A	10485	161	328	RKRFKPYSCRPFLYTFETESRVA\ RLCESGTTSAHCNLRLLPGSN/SPAS
10405	24306	A	10486	193	347	TLFSPLLIYTFETESCSVAQAGVQWHD HGSLSRRAFG\SYNAPALDSQOTE
10406	24307	A	10487	114	2	GAVVQSEVQWRDSGLQAPPPG\SRHSIP

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						ASASQVAGLV
10407	24308	A	10488	314	49	IKRSTEHSEPRYSMVCRQRPQGGPCL\RSQLLGRLRQEDHLSPIAGDCSEPRLH\LACTPAWATEQEPVLKRMSPGTLFCLFLWPLPCQ
10408	24309	A	10489	291	1	KSPPPPNRRGLTLRSRQQLNGVSPYYEAPVTDPIFFPQSLVLTQAGLQWNLSSLQLPLDPG\SSDSPASASRVAPVSQGHATAPQGRQTLSSC
10409	24310	A	10490	226	3	GSRCIMPRRLAHAPPAARMKRRVSVSTEWATEEPPKRSARLSAEPAPAKVETK/PEKAAGKDESSDKVKQTKLV
10410	24311	A	10491	2	153	ARGDVFVYVIVEMTLCHVAQAQVPLTISEPP\LGLPKCDYRREPPRPT
10411	24312	A	10492	123	342	THYLCILLRFPFLDRGFLLLPRLDG\NAPISPMNLRLPSSDSPASASRVTOITVWNYARLTLFLPQNTILE
10412	24313	A	10493	194	2	IRGNFFKINFSLPFLFFFFFMESCSVAHAGV/GSSDFPASASQVAGTSMRINAWLIFVFFSRH
10413	24314	A	10494	373	1156	KVQLKVVLYFPFLRLSLALLPRLECSGITLAHCNLPSPSRFBQPSCLSLPSSWNYRRPPIHARLIPVL/SVETGFHVQAGLELLTSGDPASA/FPKCDYRHE
10414	24315	A	10495	181	3	SPLNKPSLRGVGPRVRG\SA\LLGGASQLGYSGLRDPITQEAVCPSDILKLCAGRTITLTK
10415	24316	A	10496	156	2	AASTIRLIGDRDPQGHSETPSLKIKQLG\SGGGHRLRQENCLNP\GGRC
10416	24317	A	10497	157	300	TQSWFNTLKSTHVRHSNRK/EVNHIVSTDAEKAADKIQHPFLIKKQ
10417	24318	A	10498	3	289	LVKRLTGSTLGKSYRHSPPSINQGHNAIRGAAG\PLPRKAGY\LGQPSPLAYGLAWGDKLTTHQPDTRGSVLSRISKGRGPL/CSCLPQTECLSE
10418	24319	A	10499	138	1	WYGLIYLLLENSCYVAQGVQWHDPLSLQPPPP\NSSNSPASSC
10419	24320	A	10500	138	1	WGLIYLLLENSCSVAQGVQWHDPLSLQPPPP\NSSNSPASSC
10420	24321	A	10501	200	343	LEAHSPLGFPPIPIITFFPKSHSVT\RLBCSAAISAHCSLLLPSSNS
10421	24322	A	10502	84	339	PRDGRRRDKQKQETGGHYZHSQLRGLRQEDHVSPOORGCSEPSRSHCTPAWAT\ESNSVSXKS
10422	24323	A	10503	141	362	BWNCVC/CCCCCOCPC
10423	24324	A	10504	198	320	TIKKQNTGGLIFNSYLPPLFLPGL\RLFDLDNREKLVF
10424	24325	A	10505	30	356	GYPGNPILYMSTVGFTTSLDFDIPLEHPILKVCPTHTIATRLDLSDRSNDGRILSTSNSSLX/EKDPKNKAYFTK/RDSPVNDIIST
10425	24326	A	10506	16	375	KKFKKKKKKKI\FFPPPLENFFPKRVNFPGRGWPKSPKKKVPFKPDGGGFKPPLKKKKI\FFSPPVKNGPKGFKKGPDPFFPPPPPPPPPPPPPPFL/LCLIDR
10426	24327	A	10507	156	2	AASTRLDRDQPGHSTPSLLKIKQLG\SGGGHRLRQENCLNP\GGRC
10427	24328	A	10508	313	2	QSKWLEESYTGEDAVTVENTYDLE

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10428	24329	A	10509	325	1	YTRNLVTKAAGFERTIDSNPESSTVAK ILNSNCVC/V/REILHEGKSRPMQTSL SVFKELQTTQHSALITLTSPRA ECAKENNAETKRNIADATETQRIIRDC YEHYNKMNLEAMDKPLDTNLEPLRIANHE EIEINLEPIMSNETETV/I/NSLPSKKK SSGEGPTAEFYQYKIPILKLFKK
10429	24330	A	10510	126	14	DSGQVQMLKPTIPV/LKEPEAGRSPVE RSSRPACPTW
10430	24331	A	10511	435	769	PFKFPPLSHACGGSLFCRLRLCSGVI T\AHCKPQLPG/SQSDFPASTSQELGP/ TGACHYTRLICCREEVLHVACAGLELL CFKDPPTSASOAHDRYH\GHPACL
10431	24332	A	10512	147	412	RFVCSSTIKVRLDSSDRSNFGRLSTSN SSLY/EKDKRNKAYFTK/RPSVNDLIIS T
10432	24333	A	10513	251	466	QCCTPSFALLELNSATQWELVRSLL LNGIALKDEND\SAVKGLASLMSYKAA AAEDYKADCPRNPGP
10433	24334	A	10514	286	1	SPARKFCLEGVSPRVKQSA\LLGASQ LGSGVRYPLEAVCPFSHLHLAGRTT TLFKAVRQEHLSLQRLILLVGRVRGN DSRCDRVIGH
10434	24335	A	10515	28	428	RFVCSSTIKVRLDSSDRSNFGRLSTSN SSLY/EKDKRNKAYFTK/RPSVNDLIIS T
10435	24336	A	10516	263	2	IRKPADSESAGALITLFPASQTVRNSFL LLTSHSVCYFCYSSPNGLRQQLKLIIF FFLRQSCSV\SRLECSGMILAHCNLC GNN
10436	24337	A	10517	62	292	PATLFGVILPTNSINAFSGSDSKSAK K/CENLGTENFNFTCHTHIAEHSNST ETHHTHTQTHHTHTPLLFYE
10437	24338	A	10518	172	2	RKKKIFFLEKGLVNRKILALFFFFFE TDSHSV\TRLKGSGTILYHCSLCLPGSS DF
10438	24339	A	10519	42	194	ILVETP\CLRFVSLENDVGRFLKIKKK KKKKKKKKKKKKKKKKKKKKKKKK K
10439	24340	A	10520	120	1	IFAKGNFIKFFPFFPETVHS\VAQ AGVQWCDLGSP
10440	24341	A	10521	202	375	SFLNKLHLGSGVGHVQCQSAALGG\ASQ LSYSGVTDITLEAVCPFSDLKLRAGRTT TL
10441	24342	A	10522	272	402	PKFIYVTKAMWNYPTITETCYSFIR KFFIHIETKYEDNKGSN
10442	24343	A	10523	147	439	LILVNYISRKSTVYDSRHPCYYLIFE KNCKYKHCNFICT/SSSIPFPTPTSPR ASPKKKKKKKKKKKKKKKKKKKKARGG
10443	24344	A	10524	7	415	RFVCSSTIKVRLDSSDRSNFGRLSTSN SSLY/EKDKRNKAYFTK/RPSVNDLIIS T
10444	24345	A	10525	321	442	TSFSPLFFV/LETFHSVA/RLEGRTI LVHCNLCCLPGSSNS
10445	24346	A	10526	477	3	IEGKLPNKKDIHTKNSVCRHHQRKQVD KTKMKKKQSRKTDNSQCSQASPPPKER SSS\AMQSWTEKFDK\REDFRGSIV SKL/RRTPTWKEVQKTEKLDWTTT ITNAKSLKDLMEKSAQELDECTSR ASANCVAVQAPDRSHGQV



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10446	24347	A	10527	265	411	RFVCSITIKVLRLDLSSDSNPGRCLSTNS S/SPVRKDKRNKAYFTK/RPSPRN
10447	24348	A	10528	81	390	RFVCSITIKVLRLDLSSDSNPGRVLTSTN SSLY/EKDKRNKAYFTK/RPSPVNDII
10448	24349	A	10529	253	23	RIFLFYFHSFLRQGLARAGQPHNHSSSL QPPPPG/SGDPPASASRAARTTSAYHHI PLFFFRSYCAQAKIINLSLL
10449	24350	A	10530	10	398	RFVCSITIKVLRLDLSSDSNPGRFLTSTN SSLY/EKDKRNKAYFTK/RPSP
10450	24351	A	10531	289	423	RFVCSITIKVLRLDLSSDSNPGRFLTSTN SSL/QRKDKRNKAYFTK
10451	24352	A	10532	152	401	PHCSIHISQVRIQANVHSGHQRITYGVI PHLPLHLVLKKTFSLRDHFVSLSKKNL VLTCILHPL/GVPTFRDPPFVSNNLPT
10452	24353	A	10533	2	515	LDRYSLLPLFRKCSGSPVASNNLYLP/G FKRPSCLGLPSSWDVRRASPRVAKFVL VDTGFHVGQAGLKILTSDDPPSLTY/P QCWDYTRREPHLAFF
10453	24354	A	10534	469	566	PTKNTYKISREBWCVPV/INWAFARSLSE PGKQRL
10454	24355	A	10535	354	47	KPKNLPGGGGPPFYSSPSKGGKILPLPNK AKVPINQILPLPPHPPGGGKKTTPFKKKKK KKERKKKKGATVQKGN/PHKYHKGKGS YNVIQHAGVNAVNTKRTGS
10455	24356	A	10536	1	409	TPKKRFFPKPKPGFPPPPPKKKKIFSP PPKFWPPQKNFKAAPPFFFFFFF FFFFLKSNPFFFF/SIGNPILKPLPLPL FRVFPFKKKKKKDP
10456	24357	A	10537	204	435	TSGLSYKLLGHDGLGKRTTIFKQGGHQ NSSGWHPEATTG/VNWAFLGLHWDPKA LHLGLGNLAL/QEK/RGNTRACY
10457	24358	A	10538	208	382	RFVCSITIKVLRLDLSSDSNPGRFLTSTN SSLFER/DQRNKAFFPK/RPSPVNDIIS T
10458	24359	A	10539	63	409	GNRLTNFPYVKGTPSTSGQLLPIPLLN LMGRKPSISIMKREPRKQNRGKC/BF MKKKKKKKKKKKKKKKKKKKKGGGAF LKI FRGGNPFPGEKIFFFFLGGGIKSR GGGFG
10459	24360	A	10540	3	1322	RGYAWNGALFASVTFGFAACPGRFLC SVNGRQAPAGSSGFLPPVPVSLCPHTVCR ATPQCKEDSTCISLRRFTWGSETHLLCP APIPSVPGVPGTFTPQCEDRSCVKTLS ASPLILLCLPPHLLPSPDCGLQGPSSR IVGAVSSEGEWPQASLQVRGRHICGG ATLADRWVITAACHCQEDSMASTVILNTV FLGKVVONSERWPGVSVFVSKLLLHPYH ERDSIDYDVALQLLDLPPVRSAAVRPVC LPAN/SRNRQGLQ/CSWTFHGLALRSG GPISNALQKVDVQLLPQDLCSKARYQV TPRMLCAGYRKGGKDAC/QGSEFG
10460	24361	A	10541	154	3	GVGNFFFFFLKSLDTLQAQGVQMSLGS LQP/LTSGSLFRQPSCLSLSPTRP
10461	24362	A	10542	3	406	LMVLTARLPAAPGSRSTLLLAFLALL CLPMLQE\AGAVOTVPLSRFLFDHMLQA HHAHQLAIDTYQSFERTYIPKDKYSFSL HDSHTSFCFSDSITPTPSNMESTQKCNL ELLRISILLTKSRLEPVQVLTSMF

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10462	24363	A	10543	3	414	HSSAHAYGTVESSGKRRYLQRPSTABL KKALKGKNRLLQQRSSKVTSSSSSR DSSARDSSSERESTSTSSSDSDTDES SSSSSSSAYSTNSSSFSDSDSSS\SR GRSTSTDSADD\STNEESELE
10463	24364	A	10544	240	509	TFTSFTIGTPNLGEFCCKNNFGL/GKFR MKVACQIETLGLISFFFTESRSVTRLK COGATLAHCKL
10464	24365	A	10545	275	2	GCSRPPDTALPLMGYPPEKKLLPERNK /DTCTCMFLAAHPPVAJMWIQPKCPSIN EWIKNPVTILYITHHTYMCIIYIYTHICV CVIHIYI
10465	24366	A	10546	233	2	WSWPAIQSVLPQTAPELKKNKYSCTGT PLIYTFKQSLPLSPSLKCSVILAHCN /LQ/RGSTTFPASASKVERTGA
10466	24367	A	10547	2	420	KKKIPNRGGCLKEDTKAFELTPPLMQRR TPPAFPGKPGGLPDNPPLPSKGNPPI YSWERFFPRFFINIAWVPKANLLSFPF PSIFWRTGSRYYIAQAGLELLGSSYPFAS CLFESWDSRR\DHARAPTI
10467	24368	A	10548	190	1	AASTFFACVCPRLFFVFFVETSPSVAQ AGLQWHSSSLOPPNPLG\SGNPPALAS PVAGNC
10468	24369	A	10549	155	1	ARGERYFLIEGGGFFFLVFFLEQSHS IAQAGVQWCD\LNMQPLPFRVK
10469	24370	A	10550	223	392	RFVCSITIKVRLDSSDRNFCRFLSTLN /SLAVRIDERYKAYTK/RPDPVYDIIS T
10470	24371	A	10551	183	3	WQKLLFLGTESSCVARVGQVNRHLSSP KPPPP\GSSNS/PASASRVA\TGALHEA RLIFVFL
10471	24372	A	10552	297	10	TDRELCSERRKNFF\DMASIPGSDTV NTDSMTKT/DLEYYINLVDKVSAGPERT DTNP\ERSSTVSHMLNSITCYRKI/F/ RERKQQMQTSFLSP
10472	24373	A	10553	509	3	LLTDRTLCSRSVGVPCSVQCCALLEG ASQLG\SRGSGVRDPLESAVCPFDLQL ETGRTTALFKAVRGHLSLQRLLLSF\V CLCPAPRGAYRG\TQASLSOGLHPVRA SRLLCLPKQAMMVGTFPP\TSLPCSL ISDOCSQGRDS/VGVGDSKPGAGYNLV VRRP
10473	24374	A	10554	262	453	GWGILTANLLVGGGSLTSERIFFSPL ATGPCSAQVAGVQ\LIINCHSLFELG SD
10474	24375	A	10555	112	372	KKKGGGPPPPFFFIIFELIRQRKRLVVL AFNRRLGRKPD/IFYAGVGKIVKKYS GFFIELVTTGKNYLMCALAVIDPRDIN IIRS
10475	24376	A	10556	50	358	RFVCSITIKVRLDSSDRNFCRFLSTSN SSLY/EKDKRNKAYTK/RSPVNDIIS T
10476	24377	A	10557	203	350	QLHADKVSRRFATIAECRGVIMAYFN.LN PH/PIRSSCLSLWSSNDVYHAP
10477	24378	A	10558	98	387	IQDTDLIRGVYRDKGRAREKDSPEER EGEKEREIEKQKKKER/ERKKERKESST HQKE
10478	24379	A	10559	237	3	EVFPKNTIFETSCSVTQARAQGDHGL

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						QPPFTFG\SSSPPTLASGSAVITTSVNHRT QSGLTTPQSPKQKALGKICISSGG
10479	24380	A	10560	37	359	RLKCGGPIVIAKYCKLEILGSSNPTTSTSW VAGTT/TCHIAQ
10480	24381	A	10561	170	3	RPFPLEWGGKKPQGVSEFFFLVFFBI GSHSVP\RLKCSGTITAHCSLDLLGSSN
10481	24382	A	10562	1	388	LPEPLMVLRTANLAVMAPGSRITLL\LA FALLCLPWLQEDADAVQTEPLSMLYDHAM LQAHRAHQLDIDITYHELEETYIPEDQKH SLLHDSQTSFCLSDSIATPSNMRETHQK SNLEMVRISSLLLETWLS
10482	24383	A	10563	224	392	CVDPILKWPFLRTATRGCPLS\LPNTIV LEVLATAIRQEKEIKDP/QIGKKVVK
10483	24384	A	10564	185	2	RYPGPDSPQNGKTVFNPLFFFFFETRV\ HSCCPNESNISTHNCNCLPGSSNSPA SASQVA
10484	24385	A	10565	175	324	ARGYTKYRVLCKILLRLRHKNHNL PGGRGCSFPRSHC/ITPAVVT
10485	24386	A	10566	3	367	HELLMSTIKVLPYLRSDRSFGGVISTN NSSLC/EKDKKKNKAYTK/RPSPVNDMI ST
10486	24387	A	10567	128	391	GETCEGVYGPQQGKQTKVVFHSKDEG PCSRTWDVGLGSSPQIFLKK/RFFFFF FETESHVSVRLECSGTPGT/HCNLCYPG TS
10487	24388	A	10568	251	485	SFLWRFPLEGVGPHVRCQA\LLGSGAQ LGYSGVRDPLEDAVCLLSDLKAGRTT ALFKAVRQGHLSLQRPLLPLFSY
10488	24389	A	10569	176	3	FVPPILKRMGPFLLKKEGKFFFFFSSEM ESRSVT\RLBCSGA/TISAHCNCLPGS SNS
10489	24390	A	10570	212	386	RFVCSITIKVLRDLSSDRSNFGRFLFTSN SSLY/EKDKRKNKAFPTK/RPSPVNDIIS T
10490	24391	A	10571	134	489	SLFPLSPRDRWGLTQSTEMPSPKFFPG REIRSPILLAMHSLLIQPTAFICPSTTL LLSLKPDSLRGTSLFLSPFFFLYFRACS VA\RLKPSGTTISAHCNCLPSSSDSPAS AYIVSG
10491	24392	A	10572	1	470	QSGRGIPLLLTDLLEKPVSLLSVTNLY SKNSAQFSTILQTLSPFATFTTSPSIFL SSAYFFFFSDRVS/LLSPRQSCSGLNLG AHCRPQPPRFKRFSLSPSS\SWGLTRR HTTTPGLIFCIF/SVAGFPHVAQTGLGLE LLSLSNPASA/FKCDHRR
10492	24393	A	10573	242	410	VMLRMQIYPSLINPIFFFFTGTGSHFIA\ RLBCSGMIPPHCNLCFFPGSNAPASQ V
10493	24394	A	10574	236	1	ARTFFTHILKASCGDNATIGVLRDATW CPSVLLDRDSLSERVCEILCHAC/VMR THRHHTTYIYAHHTHTHTHTHT
10494	24395	A	10575	241	35	RSSYLFIFNFPFVTRSAQGLKCCSA WAGTPG\SSDPFTSSSQSAGIIGMSNL FLOWLITDQAGTN
10495	24396	A	10576	294	72	FKNFKPLFLSFFLLLTGTRFCYTAQKG LK\SWPGQDPSALASRVAGTRGVIRHTQ LQVSPNYKYKVLAMHSGSQL
10496	24397	A	10577	1200	1625	PDGWSYSSGSHWLPETASNGRKANSCH

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						VTPQLSPFPQAPPSPATHLGPPTPLA/SP PQAPPFPATHLGPAPPPLSSAP\PPPD TLGPAAPPFPSSGGDPFRYSP/VPFQ LSPPQAPP
10497	24398	A	10578	226	325	ERHTHTPHSHTRSHRLTHTHA/YTHH AHTHA/YTHHANTHPPS
10498	24399	A	10579	108	320	TINVLKVNVMKLSYLRPNTRNCSPFFL AGVQCDHGSIQTQPPG/SSCDPPSSAS RVAGITGAYQHTQLIF
10499	24400	A	10580	1	288	ARGERERERERERERERERERERERE RERERERERERERERERERERERERE CVC/RPSARPRERERHAFVSAFSLQKK KKVFGCRGTHSLFPYPCQNSLR
10500	24401	A	10581	1	476	REWGIALSFELICSVVILKLSLGLGL KRFSLRLPSMKDYRCAPCPSLNLPFV ET\GPHYVAPGWSLLQSSD/PPPLASP KCRDYRHE
10501	24402	A	10582	210	346	PHCSITHSQVRITQANVKKHQRRTYGSVI PHILPLHLVLKKT/PSLRDP
10502	24403	A	10583	316	461	LPNHLGVVLPFVSETGFCSVTHAGVQWC DEHGSLSQSTFG/SSDLTSD
10503	24404	A	10584	172	383	NLDLYLTSYIKINSKVIIDLNIKTIK LLE\ENVAGENTPDGLGKEFLD/KTQK ALS\TNKKIDKLNIFR
10504	24405	A	10585	273	374	GPQTEAHRNPSTLGGRGGAIT/R/GQE FKTSLAKM
10505	24406	A	10586	150	344	KLCKIIIKLGIKISPAVIVVVEIGPHF CYLGWQW\PIRTHPGSSDPPASQSA GITSMSHT
10506	24407	A	10587	199	3	SFSYIRVHLGHKIKITRHKASCEVYANCK AKGIIITGKKK/RFWPGTVAHACNPNTL GGRGRIWTLV
10507	24408	A	10588	216	1	PRGAPTRHRCQSA/LGQVLQGYTV/V RDPLESAVCPISLXKRCAGRTTALPRAV RGRSLQKFLPLV
10508	24409	A	10589	190	3	ISAQFWAAFERKFTPTYPADA/LKPMIF FSPFKGVDFPTTTPPFEMESRVARLE CSGVI SAH
10509	24410	A	10590	369	40	KTERNSINIKNDVHTKTPSKGRHQRP KADKREMRKQHKKAENSKQNPSSPP RDHNSPARKQNMENEFDELTEVG/FR KVGNSSELKEHILTPCKETKNRTGW
10510	24411	A	10591	114	398	RFVCSITKVLRLDLSNRSNPGRFLSTSN SSLC/EKDKRKNAYFTK/RSPVNDIIS T
10511	24412	A	10592	132	1	ILYLWCVCVCVCVCVCVYLILV/CKVL SCLGEPALSVGAPQMS
10512	24413	A	10593	3	287	IGFITNLVGLYLYLLCYIYVYFFQVNYI VFILVLAVFLKNRLLRYNTALYNEEVT REKISHYFI/NSYIHTVGKINKND
10513	24414	A	10594	2	363	RAEVGVNAPLYLLLLLSGALGTLDTWAG SHSLRYFPSTAVSRPGRGEPRYIAVEYVD PTHILFQSDTAIPRMEPRKQWVQEGP QWHA\WTCYAKANAQTRVALRNLLLR YNQSHAGE
10514	24415	A	10595	156	3	NGLELSDGCIALLFPYTFETFCPS/VA QAGVQWCDLGSLLQPLGPKPTRP
10515	24416	A	10596	80	306	MDRELLPRDEQRKNFLEMESTGEVAVNI

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						V/EMPTIKDLG/YTYRNLVDKAVPGCERVD FNFRISSTGWVWMLTPALPVL
10516	24417	A	10597	232	389	ILCWVFCVCCCCCFETZPLVIQAGVHNC DLDSLQ/SPPPGSSDSPASAS
10517	24418	A	10598	463	154	MGQGGKPRFLEFHPFYIFFLKQGGFSL PRVOGRAKKVPGTLASNGOKILLPOPPR /RVQRNCLNPGGGGSEPKLPPSPFPAN GEKGGSLIKNLIKKTTHIC
10518	24419	A	10599	208	38	LGPQGGFFKTAPPPFFFTTESLSAQV GVQWDLQSLQLPPPG/SSDSPSLSKKF LL
10519	24420	A	10600	200	3	CQPELSCHMRQVRSILGGLSPSGMEVR DVEEAVCPFLABLKRCNGRALLNVRCCS LQSQAGFTK
10520	24421	A	10601	73	427	RUVCSYTKVLRDLSSDSRNPGRFLSTN SSLY/EKDKRNKAYPTK/RPSQNDIIS T
10521	24422	A	10602	193	401	GEVSLISPLEECNGVISAHCNFR/LPGF KRFSFFFL
10522	24423	A	10603	181	395	RFVCSYTKVLRDLSSDSRNPGRFLSTN SSLY/EKDKRNKAYPTK/RPSQNDIIS T
10523	24424	A	10604	384	10	PRRPGGECVHCLADSLVDRYSGLRSS DOTLSGDPMFAVPSNLSLCSHYRLKPA SGITWGCKQAGFFSFFLFKQESHVS/T RLECSGALSVPCNLCLPGSPNSPAGGS LGPSSRRFPWTT
10524	24425	A	10605	215	379	RFVCSYTKVLRDLSSDSRNPGRFLSTN SSLC/EKDKRNKADPTK/RPSQNDIIS
10525	24426	A	10606	1	163	QTHREPAVLSPADKTNVQAD/WGNVDA HAGEYGAEALERMFLSPTTKTYFFR
10526	24427	A	10608	283	2	IQKHGLIRCPQETFPFGNSDVGKQVKG RSEKIMQLVYFFFLMS/HLSPLE/ CSGALSAYNLRISHSSDSPA/VDTIG ACHFTOLIFLIVE
10527	24428	A	10609	144	327	CSWNSFCGCVRVSTILKRRKFFMEFR S/VAQAGVQGRDPGILKPPPPG/SSDSP ASASRV
10528	24429	A	10610	137	1	HKCPTSDWDERV/WCMYKEYCSATK EEIMSFGKTMWLENIMH
10529	24430	A	10611	201	334	SFFKRFCLGVPSPVKQCA/LLGASQ LGYSGVRDPLERAVCPF
10530	24431	A	10612	146	2	KTPLKKGILKRVPPFFFTTESCSVTQAG VQMHIGSLQVPPP/GSRHSP
10531	24432	A	10613	205	259	TMFGLSFCTRTKSNKNSFLTLDGSR VDLFLYLLLPETIFQNF/CGRDKVLLCC PGMSQTPELKQLICLDLPKYNDRHREPL CLAYPFLAQNLTKI
10532	24433	A	10614	153	2	GVLMSDVGSLMLANLFPSPFLP/LPET QSHSI/SRMCSGVISAHCNCLP
10533	24434	A	10615	213	8	KPPTTTTTTTTTFLRWQSHCVVSGY/C KGTILVHCGELLLGSSCPPAPQVSGIT GLCYASITPFX
10534	24435	A	10616	146	1	ILVTRDYVKTILFFFTAPKFS/VLPR LECSGALSAHCNCLPASDS
10535	24436	A	10617	208	2	NNFWFSSSGGQYQYSSSTESRSVTWGH DLYSLQPPPP/SGSSDSPASASVAGITG SCHHAQLILVIVE

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10536	24437	A	10618	120	2	STFFFTFETESRSVAQGVQVHDLSSLPQPPG/SSDSFSL
10537	24438	A	10619	162	1	SPHWKRLRGAGQCMRCISA/LLGGVSQ LGYSGFWHPLEBAVCPFSDLTLCAG
10538	24439	A	10620	193	419	TFFFFTFESRSVAQGVQWRDLGSLH/S QPGQOSETP
10539	24440	A	10621	313	460	KPGLWRGTRSQKQVLFEPESHVA/KL ECGGTISAHCNFCIPRSSDFSA
10540	24441	A	10622	243	505	PTGCPKQEQVQMLRPVVFVFETQFN S/VPRVBCSGTISAHCNLRFPGRSDSPA LASRVAGICRR/CATTAGLIFVFLVETG FCHLVG
10541	24442	A	10623	67	430	LARKTWKQISSTIGCDLFFPPPPPPFF LKKGVPFFPBGHSGFFPLMKPLN YKRFFCFLFDVNLISVQPLAFFFFFF WRGGSYLLLRVC/LTF/LAGAPLPAPM PFLFLRGKL
10542	24443	A	10624	3	207	PGGQLSGECSGVRMDRDM/TLKSLTIG ESVGKSLLLRFTHTDTPLELAATIDP SSVVNPARNAATP
10543	24444	A	10625	151	380	KMLPGVQVQLTPITPALMEAGGSL E/LRSSRPALKRSETSSPSPQCKKKKK KFPFRAGQMLEVPFGRVAG
10544	24445	A	10627	210	3	NFCQVQGFQKSSQTKGFGKNKKKG SFFFFFTESHVTLRBCGTIIVHC SLDFPGSGDPPTSA
10545	24446	A	10628	237	2	LCFLSGASCSPYIDVTEVNGVNPPTI I LTNKNTFGPLPLII FFGETESLSIA/ RLDCSGAISTHCKCLPGSRHSP
10546	24447	A	10629	1	352	RGPLSTQDYTSKALFPLLLPLLLLF PEVRSCLTQAGVQWCNHSISSLQSP TPGVSPDPPAS
10547	24448	A	10630	48	200	ATKPKNLFSEETKSSV/QAGVQWRDL SSPQPPP/SSDSAPRN
10548	24449	A	10631	209	376	SPLNKFLKLVGGVGVQQA/LLMGASR LGVLGVRDPLYEAVCPFSDKLCAGRTT
10549	24450	A	10632	141	1	AGPFFFFLFFFTESHSEVA/RLQCSG AITAHCNLCWGSNNVHAS
10550	24451	A	10633	18	522	PLYSLTAKRHTPREA/KDHLKSTQLLSVI DAISEGPIEGVPDGLKSVLNSPTVLDT EGNINISGVTVVPAGEQEQTPPEFES SGSETVIGTEVKYDTPITRTITSANIDR LRPTFGVQALVETTSKGRNPSEVRLLV QIQRNGGWTRKDI TTGKKTSSQYLASV V
10551	24452	A	10634	127	2	NLSPLFFFFFTGSRSTQAGVQWDLGS LQTDPF/GSRHSPTK
10552	24453	A	10635	336	452	RIFFFLFETELSAVAQVQWDLGSLQ SPFF/GSSSEPA
10553	24454	A	10636	259	3	GTRIFPPFNSSPLSPFPQKKSVPFFP F/LFFFFFTESHSEVT/RLBCSGALSPH CKLHLPGSRHSTASATRNVLRLNRHA SCA
10554	24455	A	10637	96	413	QDNTQSHAILNYFIP/FTPLFF/ETG SHSVAQAVRLKYSVITAHNTRLEGSS NPPKKKKKGAVLKDPMGQSLPLGLATY YFFPYRGANKNLGDPMGSLFV
10555	24456	A	10638	180	473	CYWRKANLVLNLLFLKKKKKKKKKK

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						KKKKKKKKKK/EMPVKQKNRGRALYKK KKQGRPPPIEWPPPPFFFLGGKKHPGG FTRKKFFFGGKKKK
10556	24457	A	10639	312	480	ETVDSSTSGEDDVNTAEMATKDSSEYINL V\GKAVAEFERTDSNFE\RGKQMSKSI
10557	24458	A	10640	2	516	NKPLENLQS\TASLARGATLLRPVLRRLC GLPGLQRPA\NEMPLRARSIDGAGPLYSHH LPTSPQLKALLAAGSAAMALYNPYRH/E ERPRI\STSLDGLGKSLPBGSLGREYL RFLDVNRVSPDTRAPTRFVDDSELA\YVI QRYREVDMLHLLGMPFINLIGEIVVKV FEAYQ
10558	24459	A	10641	56	455	PICSYIQFIYHKSFNQNSISLVHTIFLS KLDPYFSQLSYSTSYLQCHF\IHLLSIFPI TYKCIYFWYVH\ISVWYICVCLCTN VCVCV/CLLN
10559	24460	A	10642	272	33	GRWFLPLGPKAKYFLTGRRFSPDFGDLK INPPF*F*F*F*FDTSSPAQAQGVHWNEL GYLO/SPPPG\SSDSAPA\SFHHTV
10560	24461	A	10643	285	1	MN\FLKRFKKNEKFF*F*F*F*F*F*F*F PGKSPFKTPREALPLGVPPKHFF*F*F*F*F FSETESRSRVARECSGMISAHCNL\NLH LPGSGYSPAL
10561	24462	A	10644	100	466	FLFKPRIREVP\SRVRCQSA\LLGPTSQL GYSGVRDTLEBAVCPFSDDLK\CAARRTNT LFKTVRQGHLSLQRFLLPVQLCPVPRG GVYRGQASLSCSGVHPVRASFPCLCLPK VPPFS
10562	24463	A	10645	260	460	LKPIAERETIDGRLPYIS*F*F*F*F*F*F*F FVAQAQGVQWHDYSLPPPP\PGSBSGSA QIGHICATVEKTHLRGIFFL*F*F*F*F*F*F*F CSVTVRLCSQFTLAHCLCL
10563	24464	A	10646	360	504	WEVEVP\PAACHLLKRDYTFILLLPLF FEMESYS*F*F*F*F*F*F*F*F*F*F*F*F*F SRDSPGIPPH
10565	24466	A	10648	76	462	FLWEYQEKAHILWLSFLSKLLGRSRTTV KEKVRQKPGILLFIYLFIFEMESCSVAQA GVONDLGSLSPQKKRDS/DQSKATTFV EGINSKRGGWGPHF/HCSLEMI\FLI
10566	24467	A	10649	3	359	QTQREPTMELTPADKTNVKAANGVGAH AGYVGAARALERMFLSPFTTKTYFPHFDL SHGSAQVKGHGKKAADSLTNAHADHYD LNALTAINDLHAHKLWVDVNFKL\LSH CLLVTLA
10567	24468	A	10650	266	3	TPKKKKKIGGLGADPPGYPRKKIWDPPNF FFKTKTKFFQFVGVWAPPKPS*F*F*F*F*F*F*F EVKSCSVAQAQGVQWRDLDSLQSPSP\GS RGSP
10568	24469	A	10651	278	461	RKTCGFF*F*F*F*F*F*F*F*F*F*F*F*F*F IGSPPG\SSDSLTSASRVGMSRHVRA VF
10569	24470	A	10652	161	456	VFFPQRIALFVBEKTTLSYHFMCTBMT ANKKVENTKQGWETIGSFNCHLESK KVQSLN\KVWQFKWLN\VKLLYGLAIP TGICPKKKKKYQGY
10570	24471	A	10653	91	486	PCFNEIGHTWYMYFFSLSLTLFF*F*F*F*F*F*F*F FVILAYKTSFSPFITIRVLQRHRQKFV LDGFNVQDNNTLIGSCVSLIKIFLTE

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						SCFVAREAGMOWCNGISLQAPFPVGSCHSPGISPPVLS
10571	24472	A	10654	267	470	NLHMCKEKNQNTFKLSFKDLFLGLGLWLF FIFCFWRRLITLSPLECRG/NIFAHC NLCLPGSGHSPASA
10572	24473	A	10655	775	1401	TFPSQLEYGLEKRPNSITLSPLECSGA ISAHMORPPPGFITPFCSLSPSSWHYRR PPPRPATCVCVCVCVCLVETGPHRVN QDGLDLTS/S/IPPASA/FPKQNDYRR E
10573	24474	A	10656	287	454	LPLIYFLYFYBTECHPLAQAVQNRDLS SLOSPPF/GSNDSSASASPVTPTSAM
10574	24475	A	10657	212	64	LFLSKYFFFEHSCSVAAQALQCDLGS VQLE/PGSDESPASAWGLD
10575	24476	A	10658	368	473	QFIDATREPERFCE/LIDETWKKWHH TTEVYSAL
10576	24477	A	10659	358	1	LIAVFCFCGSAPFEGGKLTFFPNKGR ETPLALNVTWPGKARGV/ISKKKLPE FKQPNVNMWISFFFFFETESHTIARAG VOWHNLCSLQSPFPQ/SSDSPGRWSLQR TEIAFL
10577	24478	A	10660	2	235	KRDLIRHYPKREDIYNANKYILK/CSTLT MHTETLIRITMRYHLILIKVTIFKKTDN MTAVGVHICNENTLTGHSGLA
10578	24479	A	10661	9	538	CVTIVRIPSRPTPLSDSKSNFGRFLTS NSSLY/ERDKKKNKAYTK/RPSVNDII ST
10579	24480	A	10662	374	38	SFLWKHLRLGAPGCIKCSA/LLGVSQ LGYSQVRDPLERAVCPSPDLKPRAGRTT TLFKAVRQGRSLQKFLFFVQLCPAAR GGVYRGQASLSCSGLHPVRASRPLCSR R
10580	24481	A	10663	268	47	ALLPLSLLTYSAPHALLLETVTSPPKM KCSGALTSHCSFNLPDSSPSPTASR/V IGTIGARHQAOLWPIYFC
10581	24482	A	10664	64	451	FSSERKSHMSITANKKLEMLRSEGLS KAKVGQKLVRHLQTVSCVVDAREKLLKL IKSATPVNIGMIKQHNLIADIEKPMIW TDCQTSRHTVLCORLIQSK/ALTLFNSM KARRGEADDEKLEVRKG
10582	24483	A	10665	355	474	ILFYFFIFFETKSCSVAGQVQWRDLGSL QAFFPG/SRDSP
10583	24484	A	10666	317	481	GHCTCPIWOTFFFLFRIDRVLHRPGWSAV TOSWLTAAIT/FGPKRSCCLNLLINDWD
10584	24485	A	10667	57	329	VKNTOWGKDSLNRKRV/FPKNWASYRRI KLD/LTSYAKINSKWKDLNVRLEIVKV LQVRYPSFKILGNGSVLDFVFFYSGIFA LHLMGRHP
10585	24486	A	10668	86	468	ENYKILPMGKKNFLLFSPIPPYFFFFSR LGLTLPLRLKSGDHCSLQPRPPGLKRS SCL/GFPKCDYRNEP/CVPR
10586	24487	A	10669	254	25	GSHICKVPAAIYSNTICSSRHLDGGVVG GCSGSGTHSPVADSPFVIVRTVSL/S VTOAGVWVCLSSLOQPPGI
10587	24488	A	10670	206	3	YGRPKLKNIGLKGPLEPTHWQHRVT SFFFIIMETDSREVAQGVQWNLGSLHP PPPG/SSDSPAS
10588	24489	A	10671	20	355	GFTSQSELLYSIDPIRTPDQVTTIGISA



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						QSYCRKHVHKNVYDLDVESGHPNGAPAI KGSVCSTIKVPGDVSSGRSNPGRFVST NSSLY/RKDKKNGACPTK/RPSFVNDI ST
10389	24490	A	10673	112	359	NKAQQCVHENHFKLKDANTLNKIVWRNI CHSSPNQKKYGLAILNLDKSGFRSRKDT GDDE/HFIKIKKSVIQEDPSIINIYA
10390	24491	A	10674	317	2	TGPGFFPQIKVVFPPFFPLKIFFTQKFLV SFWGFKTIKVGPPVFFFKGQERFFSPF LQVQAEKFFPFFPFFPFCRSGSHSV AVLECSGALSJHNCWGPFF
10391	24492	A	10675	240	495	DHRPKTKSSTCCAGRVLLGLVEFES STDVRFAPF/MRG/HICPTQSTNSNIN FVWKHPHRTQDQNVFNWNSPHGPKVLM HKLI
10392	24493	A	10676	271	484	NPAQTCIRIKSFFFSFFETESCSVTQIG VQMHGHSNQCSLGP/SDPPTSANSSA
10393	24494	A	10677	364	121	KQEVVRSLSHNLCDQASPLFGSRRK SKQKLKAAFCAGSSIGKHL/HKCCWIK THHTHTHTHTHTHTHTHTHTHTHTHT
10394	24495	A	10678	354	539	FFFFFIVPESHALAAQGVQWCHLSSP HLR/SPPPGFN/DSPASASSAGITLSS SVRL
10395	24496	A	10679	123	853	RWSLCHERLVCSGTISAHCK/L/RAPG FTFPSCLSLSPSSNDYSARHARLIFFV LVETGFHVSVQDGLDLIT/SG/IPPALA /FPKWDYRE
10396	24497	A	10680	251	30	ASLQVSAPLCIRVSPCPNGDLGKTWV GGGFFFEHPS/VLPRLECNGTISAQ CSLCLSSSNSPASRIPP
10397	24498	A	10681	203	1	NFFAPGKGLFPRDSLKTAFFFFFFFETG SRSA/BAAVE/H/CDLSLQPTLPS SDSPNSAGSVAGITG
10398	24499	A	10682	237	397	DSLTLSPLECNSTSAHYNL/RLGSS NSPASAS
10399	24500	A	10683	8	388	LYMCWFRPGFLAHNSHGHGSLTLCWG ASGLKQCP/CRLSBKKGKGGKKKKKKK KKKKKKKKKK
10600	24501	A	10684	201	463	IYWEDIVQGVADRLTSRKNHSKFLGEC LMFGQGLFFEMDSHSAARAGVQWRSLG SLRPLPFG/SQVILLPSSDSPALASVD ETAGV
10601	24502	A	10685	151	1	PEKNRKTQKAPPPFFFFPETGSPSAQA GLQWRSHSSIQNEPPAGSSDP
10602	24503	A	10686	165	3	CVFVRDITSNFFPFFNETESRVAQAGV QWRHGS/ASRVATTTGVHHAQLIFR
10603	24504	A	10687	292	384	NTEIGWVWLLTIVIPALWAEAG/ETTR SG
10604	24505	A	10688	161	365	RPPCWIRTSRWCWRYRFDGSTITKVLRL LSSDRSNPGRVLSSTNSLY/EKDKRKK AVFTK/RSPVNDII
10605	24506	A	10689	286	3	QPSVMSFESVICAAPAPSGHGLEPBLQ QCIVGNFASRYTMTKSAVLELLIFSLI FKLLEL/RKAPASLVSFLPQMLRIKWE SBQNLVLLCDRG
10606	24507	A	10690	169	2	SDTPAMWPRKHVFPFGPFFFFETSRSPV T/RLKCSSTISAHNCNCLPGSSDSPASG S



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						RLECSGTIMARCSLDS\SSNPPISASQAAGTTGACYH
10626	24527	A	10710	180	11	LLFFPFTSRS/HVSQTVVCGMISGHICNLRLSGSDPPLASRVAGTTGKIQNIWLSR
10627	24528	A	10711	234	408	MKLIMLKVILFPQIHLQIQNPYQNIFFETELCSVAQSGVQWHNLSLQHPPP\GSSD
10628	24529	A	10712	312	470	TGPHCVT\RLECSGATTARCSLDFAGLS TSPTSVSQVSGTTGTWAKLETI IL S
10629	24530	A	10713	64	392	PRMVI R I S S E T S L Y A S L P L Q M G Q R Q K / C P Q P Q K K K K K K K K K K K K K K K K K K R A R G
10630	24531	A	10714	169	427	NNQKTNNQNGVSPYLSITLLDPAEALNAPIQRHVAENIKKKEKKKK/DPGICQLQQTILFFYKDP/HDPLRLKIGW/RKYTPSRTQIK
10631	24532	A	10715	176	410	ARSSWGLHTAVPVAFTSLRPLLEIPLDRDTRCSPPAALFFFTSGCCVA\RLBGRGATAQCSLNLGGSSNPPTSASRVA
10632	24533	A	10716	234	389	NSGNNDRYKDVNTYTQNTICWPGTVAHACNPSTLGGRGQIL/RQEFETSLA
10633	24534	A	10717	190	2	GPFPHPGGFLRGFFVNTIIPPTTFFFFFFLRRSLSVQAQVQWCLSSQLPLPPGP\SNSPCQ
10634	24535	A	10718	201	1	WPLFLPKMFPPFKRFPFHGQSPWVGAQAKKKKIPFLTGSHSV\RIECSGTISAHCSLNLGPDSH
10635	24536	A	10719	195	419	EYHTSLVTCGNPCVYRSNNKLNQTSRRKVITKIRASLNEIETEK/LQSGGETKWFPEKINTLGLLGGSDPPVH
10636	24537	A	10720	218	407	QKMLAPKKKKRKEKKRKKSPSQSNNSAKIEARTNIKLVKHWKNCETIDA/LQKAPGDNA
10637	24538	A	10721	231	409	GTQLHLGQFFFESEKLSFCFWE/MPALFEMRACSVT\RMECSGTVLACHNLRLPOTSNSSA
10638	24539	A	10722	40	401	PLCPSESSGNTLMASDSTPAVPPNPTTHPPLCLSKSHLPLRPKQGLPSGNLQLPLTLILPLLGPVACWQLPQQCTISTFFETKSHFVAQAGVQWCCLGSLQLPSG\SRDGPDSAC
10639	24540	A	10723	210	14	HVMGLLLLFLNLKLVNNEGWLGFWCLGPFWFSPFFETRSGSVT\RLECSGMISAHYKLCIPGSSH
10640	24541	A	10724	347	462	TFFFFFETKSRCDIQAGVQWCDLCSLPSS\PDSSDCP
10641	24542	A	10725	169	386	DKQAKTIKWKNSFSNKNWNNICLATGKRMKLP/YLTPYKK/INSKWKDLSI
10642	24543	A	10726	257	54	PLFFFFKRGILTLSPRIECNGIVTAHYNLKLIGSRDLPTSASP\SAGITGLSNPARLFTVLPFHQLQ
10643	24544	A	10727	2	401	NEYDRARQIYQYMCINPTPYCLQGHLLCNDIYRLKVKGREMDIENKRWQVAI LVSNDKDFKPTTVKKLLIYIKGSIQPE DLILCTYSPIARSRFLKRIIPDLRKEI A/HTVKVQDPSISLNLRSQNT
10644	24545	A	10728	154	1	PMCSILGLSKGGILFFFFFEAFCSVAQ

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10643	24546	A	10729	34	151	AGVQWRDLSSIQPPPPG\SSDS PRPPVPSLLDRGLQLWRQRLHRAHS NGFTGGKQIMKLKYNVRFVGV/VAVA IMFDPDRYPRSWIEDDNYGGSVASAT VHIRMGSLVENDNKS
10646	24547	A	10730	2	408	VFLLTIVRTLICRSVGVWRSTPDNLVCLG ISSGGCKRTANIGLYQMLPDHSSGSGFCL RGVPGHVRQQA\LLGGPSQGLVSRVDR PLEEAVCPFSDQLQAGRTTTLFKAVRQ VHLILQRFLLRFWLCHAFRG/GVIR
10647	24548	A	10731	274	89	ERLIVTFNPVPCSLAQFQF/CYFPLK CKLCILKHKRVFY\PLFFFFETEPHVS ARI\CSG
10648	24549	A	10732	251	1	TFQWQKCFSHRKIPHNLLDKASYKITVY KEDPPSPSSISSSSVLKDNPFLRTESC SVTQAGVLWCHLSSIQPPPPG\SRDSP
10649	24550	A	10733	375	1	APFPPLWVRGSPFSPFLVPHPLKLPFL ABILGFLFKERKNGSIRKPCLFKVKGLVS VWPGLELQ\IPKFLGFPFSPFSLVGRKP NFFLGVPVFFFFFEKESRVA\RMECKGT ISAHCNHLPGP
10650	24551	A	10734	82	398	SFLMKLRNGVPSHVRQQA\LLGASQ LGLVGRDPLEEAVCPFSDQLPAGRTT TLFKAVRQGHILNQRFLFPVQLCPASR GGVYRGQASISCGGLHPVRAS
10651	24552	A	10735	2	341	TFCAISWLESGVDRGPSSRI\SYRISTFF FFFKGAPSPKEVGRKPKGLAPTSLPGA HGTIGLSGWTFPSIGGQPPPPPRENFK GSHPPAPVAGDTFQ\PKGPPPLKVPFP K
10652	24553	A	10736	171	1	RVFYLLAPALEVDTGSPFVSQAGVQWCD HSSIQSQTSG\SNDDPASAYVAVGTGV
10653	24554	A	10737	190	1	ERKTTVREKIPKMEKALSGSNMIRITTF LFLFETKSCSVT\RLNCG/SGISAHCN LHLPGSSNS
10654	24555	A	10738	252	413	GLLGIQNFPSYKVLHFKHKKCSMLDAV AHAYNPITLGRGEM/IQEFQTSLTV AGTSRCL/QELSDLEHLEQNCINPVG GRGCEPQSCCHCTPAMVTETQKK
10655	24556	A	10739	101	249	LGLPVHTMKNSSHYHLGHHLHLQHUUH HHHCHCHVHS/HHINSQHPPPPPPPPPP HHHHHHHHLP
10656	24557	A	10740	185	403	LGLPVHTMKNSSHYHLGHHLHLQHUUH HHHCHCHVHS/HHINSQHPPPPPPPPPP HHHHHHHHLP
10657	24558	A	10741	119	425	IKPHLESNERTHLPLNMCWAHQRCNCFK ADFVITDDIKQLCPQSNWTRAGKPLPG AGRGSGHMLSHHPWRPHADILYLGVLG QPGQGGTTPSL/LKNTGNSW
10658	24559	A	10742	112	2	GETFFPKTSGSSVA\RLCSGSAISAHIN LHLPGSSKSP
10659	24560	A	10743	188	3	PPPLFFFFFFFFFFKTGSGSAT\RLBCTA HCNCLPGSSHPTSAIQVARITTDVNCN AWLIFV
10660	24561	A	10744	176	3	SLYSKKNKPSHLLFLPTPKFFFFFET EPRSVAGVQWHDLSLQPPPPG\SSD SP
10661	24562	A	10745	250	1	GPRIIFFLKRFYPRFVGKNPAGGQFNS GGKKPGFPFNPRPKIKFFFFFETEFRS VAQAGVQWHDLSLQPPPPG\SSDSP
10662	24563	A	10746	155	3	PPHFFPFNDLPIKFFFFFETEFRSVAQ

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10663	24564	A	10747	157	1	AGVQMHDLSSQPPPPG\SSDSP TDRPPFPNPPPLKFFFFFTEFRSVAQ AGVQMHDLSSQPPPPG\SSDSP
10664	24565	A	10748	157	1	TDRPPFPNPPPIKFFFFFTEFRSVAQ AGAQMHDLSLQPPPPG\SSDSP
10665	24566	A	10749	153	2	FPPLSVVTFAFLKFFFFFTEFRSVAQ AGVQMHDLSSQPPPPG\SSDSP
10666	24567	A	10750	157	1	PPPPFLFFRRLKFFFFFTEFRSVAQ AGVQMHDLSSQPPPPG\SSDSP
10667	24568	A	10751	155	3	NTPPPFFPLTPKFFFFFTEFRSVAQ AGVQMHDLSSQPPPPG\SSDSP
10668	24569	A	10752	86	406	SFLMKLHLRRADPGCKRCRLA\LLGGSVQ LDYSGVRDPLEAVCPSPGPKLAGRTT TLFKAVRQGHLSLQRLPLFPVQLCPAPS TVQVQGRQASLSPGGLHVPQGRS
10669	24570	A	10753	364	469	GQFLHSLD/SHMKKSDECF/LMFPHSEN VSAHLQCH
10670	24571	A	10754	250	61	GEKKKKRVPVPPPPFTEFRSVAQ ECSGVLSAHCLRLNPENDSPASASVA ASAKLG
10671	24572	A	10755	66	446	SFLMKLKGVPVCVRQSA\LLGGSVQ LGYSGVRYPLEBTVCPSDCLKLAGRTT TLFKAVRGHLSLQRLPLFPVQLCPAPS GEAYRGRQASLSCGLHVPVARSPLCLP TQALAMVGAAPPGLSL
10672	24573	A	10756	252	482	RLPRQPVKRVAGVRGCCVMGTVYSLSQ RSTTLDMQGPQGRGPIILLFFFTLCH /TRLEGNGETSAHCDLCLPGSN
10673	24574	A	10757	205	488	FLESLSPLGLPLSRVASSVSPVICTIY IYIYIYIYTHTRY/HIHTHTHTHTHT QYIFVCVVFLKDRVLLCHPRQSAGARSW PRTSASQRQEM
10674	24575	A	10758	272	471	YSYVLFPPFLGIESCSV/AFSAGVQMHN HSSLQLQTPQLQSSHLSP/ASASVA GTYVMYHARLIF
10675	24576	A	10759	17	342	GTLSSGAGVLTGRISTVUVGLKPMWAG GCPSPRAVHLLASDWRPSLQDGAQSW KKGANGNNHR/GIAVIDSDIDFKTKTI KGD\KKSHTYVMKGTQQAIIITINI
10676	24577	A	10760	42	498	EFREKEREKEREKERTTERMEDREKRA EREREKEREKEREKEREKEREKEREK EREREKERE/RHEPGSL
10677	24578	A	10761	1	305	ASWDDPAHNNNFHTPGGVVAHFPCRL DCPPAPRPPAPR/VLL/TPAAAAA AASRPEKKRAENVGAIPPKRPPEWEE RRGRPGSAPPGRGAGRAR
10678	24579	A	10762	364	2	FPQKONGQYLPFLPKPTGLCGRGRTRIG FFLIANYGKKKKKRGRLGPPFPQIUMGT SIYRGSWYFFFFFPWRQVSLALLPMLE C/RGMIRVHCSLDLVGSPNSPSTASQIA RTTGTCNCHI
10679	24580	A	10763	152	484	RFVCSITKVLRLDSSDRSNGRFLSTSN SSLY/SKDKRNKAYPTK/RPSPVNDIIS T
10680	24581	A	10764	208	420	SFLMRPDLRGVPGHVCQSA\LLGGSVQ LGYSGVDRDPLEDAVCLLSDLKLCAGRTT ALFKAVRQGHLSLQ
10681	24582	A	10765	319	85	GKLLNNRRCFSGKPGQIMFPGETESPY

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						TTQSGVRWHDGSLQPP\PFGRSPFASAS\RGITGARKHTQPIFLVNS
10682	24583	A	10766	122	3	KFFFFFETETPRSAQGVQVHDLSSLQFPFG\SSDSPSL
10683	24584	A	10767	240	86	RAPPPFFEMESCSTAQAGVQVLSLGLLQAPPP\GCSHPASASCCLMPFSKI
10684	24585	A	10768	244	85	RAPPPFFEMESCSTAQAGVQVLSLGLLQAPPP\GCSHPASASCCLMPFKI
10685	24586	A	10769	35	296	EVKSPSARQPPRLGSEHRLFAAAPSGREVGGQPPFGQPPCPGEG/PFPFGSPDW EVRSPSARQPPRLGGEFNSLRTHGDDGGV
10686	24587	A	10770	260	484	WDELLENNQRTWELVSSPGEDAVSIIQLATRDLEYDLNIVKGRAG/LEKHSYFERSTTVIKILSHNTACY
10687	24588	A	10771	248	393	TQSGKKLNNRSTVMAKNFSTLGARGGRTTRQGELETK/LANKIKPCL
10688	24589	A	10772	239	2	SLGKGCCLRGVGRVQCSA/LLGGASQ LG/SQSGSVGRDPLEEAVCPSSDLQLRAGRTSALFKAVRGHLSLQRLLSF
10689	24590	A	10773	158	455	LEFTLCPSLLQHIAMLELGLKPKSTIQPIFWVLQGTET/HFLVTPVR/CCLPLLKFLCLLVFGMESPSVPHAGCSGVI SAHCNLCCLGSTDSSASPSRV
10690	24591	A	10774	166	403	KKTPLGEFLWGGAKKKPKGKRNPGFPFRG/IKPRVFFSRFFFGPPPKKGPPCKSFFLKS LPOGFLGGCPPIPPPPPPPPFEMESCSTNRLCESGVILAHNCNLCPLGSSSDSP
10691	24592	A	10775	208	1	RLCEFFIFRKALLGKAQIRNLAFPRKGSFFFSSTESRSVAGSL/LDCSGAISAHCKLRFPGRSQSPAS
10692	24593	A	10776	192	29	IFRKEPFCFLNPLFLPETHESRSIAQAGVQMRDLGSLKAPPPG/SRSPASRDTGV
10693	24594	A	10777	275	490	KPGFFLLQAKRVYIPIFFFEHFECS/VAQGVQVHDLGSMQHRPPG/SGDSPSCLPST/AGIPG
10694	24595	A	10778	340	3	LKVPVGKPRSTLLGVKKVPFFGNKRRKF LALFFFRPPPGEGSTFAFLAQKPTRVVPALGFPKNQSPSPFFFFFTSTSCSVTQAGVQWGLRSPQMPPG/SSDSPASC L
10695	24596	A	10779	313	1	ANPFGGSGGDPFSSRVPPPPGPNETPFFKNKTATKTKNGKWDSPHRRGPKEGPALMDKKGNLWPFFFETESHSVT/RLQCSNTILAHNCQCLFSG
10696	24597	A	10780	116	422	ILEDTNIQTETLLAREVQIQTLRLNHFILTMAL/RTDINKQWREGKIETL IOCNRSCRMQNEVGTALFVNG/LQSLNLSLSDLAWPFLFPG
10697	24598	A	10781	120	418	TQTTGAPQLHLSRWLSRSGSLTSSQSEIEKLFMSIESPLGSSKILSLQV/CLTVCSFVFMESCSVARLECSIVISA/CLTILWGGSHFHASARVA
10698	24599	A	10782	134	1	SSFFFLCQTESCFGVQVHDLSSLQPTBSRAQA/LSLPSWDHRR
10699	24600	A	10783	2	435	CSHRGSSSYSLSGTRAGDLGGGGKDYFRLLFTNTTIFAGKESYDVCVYTHRMNC

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						LC/SCLFIYNCLCNCVHV/HYIHEACVF MCLCL
10700	24601	A	10784	432	161	FSRAGFH/RVSQDGFDDLS\CLPPLQL PKCWDYKREPPRPAMKLVCRGVHRCCTW LFIQIGSTLTKINGGLSAVRAHYNPTW GGRGERIA
10701	24602	A	10785	270	442	NVRLRLGLALSPTLECRGTINAHCRDLF PGLMQSSHLSHRVAGTTG/TCHHANLIF KFL
10702	24603	A	10786	12	424	LIQLPRLECSGALJARCNTFY/SLGSGD PPTSASQ/VLKTITGVCHAGL
10703	24604	A	10787	350	3	DSSSVQTNKGI PGQVLSDLGLSCAVKASV LTIPLRLALSGLVPLWKSQWVK SQQHSSVSGLC/MHYASHTHARTISPH RHRHTTYVARAHTHHTQMLSAYLPKQ PSGSL
10704	24605	A	10788	155	3	HAFPAFCIRNRRLCNGVILAHCNLC/RL LGSSDSPVSAQVNGIAGACHAQL
10705	24606	A	10789	188	2	RRDLSLQPPRGGO/VRGCTYTHTHHT HTHTHTHTVHWGKRIEIVFKGMSANG ESGRAK
10706	24607	A	10790	19	405	IRPTISRVERGINSLVASBQRLPMDGI ACSQGLVVQQTWGLPGFPPLGLGMFHR PTFRDINSEPAQVANVSTLSTPLPGA SHGLLVFFFTESHFVAQAGVSWGDLRS LPPPPPG\SSNSPVSA
10707	24608	A	10791	157	1	KPGFPFFPYPGELKIFPPFPETSPRVA\ RLECSGTISAHCNHLHLPSSDSP
10708	24609	A	10792	157	1	QPRFPFFNPRPKFFFFFTETSPRVAQ AGVQWHDLSLQPPPPG\SSDSP
10709	24610	A	10793	83	387	SLFWLHFGGAPACMRQCLA\LLGGVSQ LQYTGFRLLSAVCPSELKHAHRTT AVFSAVRGCLSLQKTLPLFVCLCAPR GGVRG/RQALLSCHRLHFV
10710	24611	A	10794	204	419	KGVVGHSGSGSPFAPLACFRDKTLPVS LKNEFVHSPWCKCTLQPLAKTVNRYLK NFME\IPYVPEIDLLG
10711	24612	A	10795	207	2	RRGFTMLNGQSLDPSTSESAHLGLPKC WDYRCKP/PAPS/LRBGSYLLHSLHP TPAPSGHLLMAALIC
10712	24613	A	10796	2	237	FFFLRERILALSRLSCSDANMSHCSL NLPG/PSQSFTLSHP/SEWDHRMPPYP VKFGFIVGDRVLALFPKLISYI
10713	24614	A	10797	342	40	DRVFFCSRLSCSGATJARC/SRLTPGL EQSSHLSLPKCNVHRCKPPRPARCSLNE SHSAKQWPGQSTSSACBEVQPTSPFPT VPYPT/LSPSAGHGR
10714	24615	A	10798	209	2	CSVIATVINPCITVVPMLST/LANDPI P RLVCPSKFFETKFCVQAQGVQNHDLG SLQPPPPG\SSMS P
10715	24616	A	10799	142	2	IFFFFEBHSSSVARQVQNSDLGSLSP PPGVSSSSPAGATPSWQ
10716	24617	A	10800	276	2	ILFLITIRTKCCFPLKSSSICSVTQARV QWHII/LSLQPTTGI/SSNPASAFQVA TGAHHHTSLIRNTLIITINWENTHCLSG CTSMHFRFL
10717	24618	A	10801	12	364	LHHYKTVSGIYKCLCVLNGPPTFRFPDF LPPIGLPYSLRHHNIISPINNPPIASK

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						YGRERMSCISLT/INT/LA/MTKLNESLLKANSDEKLC/LR/SVQVNVNAYEKFL
10718	24619	A	10802	235	3	HRPSEDLDFPHNA/MRAQYPSWDIREGGPRSLFLFLFFEMESYSVAQL/EGTISAHCNLC/LPSSSDSPTSRALCSL
10719	24620	A	10803	349	1	NQTFFFFFPGGTETTTSTLCS/YGLLTLKYP/PA/ESASQRDPWEAAR/MRMLEPGSAQPPSAPAKGQBLDPVVGQRVPSPDDEWQMPYTNVLLIEIQRFISVVKRTLTLDTLY
10720	24621	A	10804	365	3	IDVCHVCVRKQYRGPCDQKYRANISVPYPRKQSHRVYNTPTPHCETMWNVILHAQSH/TS/LGQRETHRTHTHTHTSKLAPPASRALPGVAHVEAQAALASPSSSGYLAI/TM/VQ/CI
10721	24622	A	10805	406	96	CPPEFSERSPRLLKFRUGGYIAPQVSKCGLGVVRI/PKV/FWSPKKVQTSLFFFSKTSKTSHT/RLBEGDITLAI/CDL/CAPSGSDPPASATRVTVTVGLPFCPAR
10722	24623	A	10806	58	369	FFFFKGDAAQNS/WGRKCLLNKGWMDIWISTCKMKKSTP/LTLHTKLSKGLK/LIIRAKRIHLKKYIGINLHDLGLK/DFLNMTPKTLATKEKIDTLDPIKIK
10723	24624	A	10807	126	1	KEPPPPPPPPFTSCSVAQAGVQRNLSLQHQPTG/SSDFP
10724	24625	A	10808	204	415	HLG/PD/LTTCISLSDGLRYKATVFLVFFFERBSNC/AWABECNPGISVNCNLRPLPGSSSPASPSRGVEIT
10725	24626	A	10809	168	2	KTSKEPPPPPPFPENGSHYVA/KLECSGVITAKCSL/LPGSSNPPTASWVAGTTGT
10726	24627	A	10810	97	389	LAVSPSLSLSLSLSLSTLGLPYSLRKSNLEITP/INTPABSGVCSSEKKBGSLSPNEKIEVITLSAQD/SNTKIG/RKLDLLCH/TSQVNVAREKFLK
10727	24628	A	10811	24	416	LEYIARRYLVQVNLVFFPPFLNRQGEKRGPFKFFPRGRFFSTRNGADPPGGPMLPWGGGGPPVPGQKQKGGAP/PPKGRFPKGGP/LTQPNLPKTP/ENPKGPPTRGFFPSGPPPKGAGPP/IFRVGPG
10728	24629	A	10812	60	435	KRRKNFPQKRISPYFFPLKRFKTPPLMVKNQTPPV/CCFPAAPSLKPKPRGLKKG/WGKNFPPLVPQKKKKCDTAGVALLVSDDKDFNP/TKIKKDKGHYIMVKGSMQZGLGCPDAWVPS
10729	24630	A	10813	618	1519	FWFGVNCRSVCVP/PLP/LC/FVVCVCBERGVLQRSQMGQAQSKPTSLGTM/LKHFKKGGFRGDI/SVMTIPGKRLTCEIDWPALEVGWPSGSMDESLVSKVHWRYCTKPGCPDQFFYIDT/LQ/LW/IRPPV
10730	24631	A	10814	179	15	KVKRLKPPFFFTETETCSVACARVQWHHSSLOP/OP/POPKRS/VTSVREACT
10731	24632	A	10815	61	422	NCF/LKGPP/LFFFFFFFFFLGTTVFFIYKFAFLPQMEPRSLPRLDKCNGAISAHCNLSLPSWDYRNLPRLANFF/LFLVETROPASA/FLTCMDYR
10732	24633	A	10816	170	440	RQGLSL/PLELCSMTTACD/LK/LSSNPPISAPHIALG/LTGLCHHTQL
10733	24634	A	10817	322	443	FTFIFYPPFETRSHAVAGQVQWRD/LALL



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10734	24635	A	10818	134	3	QPPPP/GSSDSPA
10735	24636	A	10819	76	245	KKRAHLPFFFFFLRGTRSHSVA/RLECSGT ISAHONCLCPGSSVS
10736	24637	A	10820	233	440	FLLRKGTGQGGPLSS/LEENIVRDVLAR AIRL/EKKIKIDIQIGKEAELSLFADMI IF
10737	24638	A	10821	293	402	FFEPGALKKKNMTHKKVBERGKRTTLNG GGIKAAKTASLKKHLQGMGKVMIMANL LGRERAW/FPPIRIG
10738	24639	A	10822	168	1	RNPFFFLTEPHSVAQGRVQNCNLSLQ PPP/PGS
10739	24640	A	10823	97	405	PLRGLSDSSIGIMKRMATDLSLQPLPP G/SSDSPASASRVAGITDSHHAMVIF
10740	24641	A	10824	186	2	LCVNICRFPPLWGVEMLHILIGVGLTFF FMESCSVARLECSGALSAHONLL/LFP SFGSSDPASVT
10741	24642	A	10825	199	1	EPOTISLVALKLGKMPER/SDHLRLAVR DQPGQHDTPSLKNTKISWAQWQAPVI PALEPV
10742	24643	A	10826	252	381	KKTQIGGARGGALFFPPFFFTGPPFVA/ RLQCSGTNOQACSINLSSSNPSPPALQ VGTGPSACP
10743	24644	A	10827	77	427	GQGEFFFCPSVQAGGQWNCNLSLQAPP PG/SHHSPASASRVAG
10744	24645	A	10829	20	518	IFQVHCPSFPFVMDACIPRVSSFTSVWF HNLLFPSECPGLPLVPASSHPFCVCCR PCTSNV/CPLMFRPPCSNSPV/TCVPLC PCLCSIKIPSCVPPW/WTYSSLCMNSHV PDSPCPLP
10745	24646	A	10830	351	3	SFAPSLQHLTETSFAINCSKATLLFL SVFL/RAQTLTAPCQTRGPRRGKDRSG SSSPSOPKATKESVERRKSFDSGHRFA AA/GRIMNGAERSEBAQVGLQRDEDDA PLCSDVLQKQCLDSPEKILFLBEPPLK EDLKNIDKLALADDIDKTHKKKPTAV
10746	24647	A	10831	8	376	LHFSPLCHQRNTKVMKASQGRHSRT HGAPFLHQDEICTRPLRLSAASSGPSLL SDHLLSTLFAFTCANLSRPSGSSPSCC SCLRA/CCTCHFDLSLTHHMTTRTHHT HHTMY
10747	24648	A	10832	336	38	GMLPAHLADVLHNSVGRPEHRVMAGA LEGDLFGPKAE/SHRG
10748	24649	A	10833	206	1	GVATRGVGRAGGGEPRQPEQ/PPQPPY PPPQQQHKEEMAEARQA/AGAPMDDG FLSLDSPSYVLVS DRAEWADIDLVLQNV GPNPVVQLIYSKYTLWK
10749	24650	A	10834	226	376	TYFPFFPLGLEFFIAGIFFFFFLTEGSH/ SSLRLCSGLITASCINLDEPNPPAS ASQVARTTCATMY
10750	24651	A	10835	213	1	RISQALISFYFFFLFETESRSVAQAQ WSDLSSLQPPSPGV/SDSPALPS
10751	24652	A	10836	351	447	DRVLLSPRLGCSGMITAHNLHLFWFK RPSCLCPPE/SSWDYRCPLP/PPRLTSV FLVSTGPHHVGAGLR
10752	24653	A	10837	71	472	REBLWTEVTPALREKAGI/LEPRSSR PAWAT
						SASTAPMAFVKGLVVKQ/K/KKKQVLK FTLDCIRPIREDGIMDA/NS'NTYBQFLQ

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						ERIKVNRKAVNLGGVVITERSKRLTVTPEVFPFSRRYLKYLTKGKLNNNLCDNLICIVANSKESYELRYFQITQDKSEEEK
10753	24654	A	10838	37	382	SRCINAPYLGYCIRSPFLWKSPLYLGVPGHYSVSLFVAGRCGVRNQRLCSVKMTSPQNTKATNVIAKARYLKRDGSGNKQVYSVPHFLIAGAGKERSQMNQSSEDHK/LA/PVRNAV
10754	24655	A	10839	313	617	APFLIVFQYVARERERSRS/VNCGLYQHCYFRTL
10755	24656	A	10840	309	511	WEQGSWEHVLQAPCSLIAPRITHAYTHTHTHTRYTHTHLYPH/APTSIL
10756	24657	A	10841	269	450	TFWPLKKEFPFFLKNLSLAVAGASVQNRDLGSSDSP/LQPSRFKQFSCISLSPSSNDYR/PC
10757	24658	A	10842	420	1	LERGNGTRDRRDKGLSQCQPMDSVLPPLCHPPPLIATVMEETWLPIDIGSSMYKAGPAG/DDASRAMFPSIVRCPNHGVVMGMSQKDSYGVDEAQTKEISILLTKYPIKHDIITNES/NDNMEKIWHTFYKNLHVAPCI
10758	24659	A	10843	431	1	GEHSWASDLAEDVTKVIRGPIGLPLFWGLCSGNLSFGSGCVPLPAGAVPMPVFPFGGA/SWVWKGSPSPWTLHLJLRTWGLGGVGRSLGRWRAMPNGNPGSQGGAPPAHOGATGTPRSRTGSTGGIETVTILEGSHVSGNGIR
10759	24660	A	10844	55	297	QRNPGTLLGVQPG/APPDSTASGSGGAROGFPVPTLEGGNTGSRKWDPCMGSSQNSPSSDGSKPPPGPLTSKVCDDSLSE
10760	24661	A	10845	109	427	QTGPSAAGLLEFARGPLQTLFARVPAAVAAEQDFVRECCCLVPLFCILRGVPCCYRCOSALVGGASQLGSRGSGVRDPLGGSGCPSFDLQHAARTALFTA
10761	24662	A	10846	17	416	SPIMKPCLEVRVQPARCTSLA/LLGASQSLGYSGVRDPLESAVCPFSDQLRAGRTTTLFKAVRQGHLSLQRIILFPVWQCPAPIGGVYRDQASLSCSGLHFIRA/SRNAPVTOASAMAGAPPDSLPSCSLSN
10762	24663	A	10847	265	429	LSGASOCLFSLPTVLTALLLSVLSFSFCWCVPSNLSPTPLFLTPVLFHL*RPISCF*VNSNPKNLTFMVNPGQKMKIGIALERICIOGCSLYVFPFAILETSQNLFCCTYACAGVLSVYDYLLALLAVSLFL*FFSLFFFFLYLFLFALGASLGLYLILYPLLCCISYSTF
10763	24664	A	10848	12	462	QTIGTKMNEGLFATPIAPTILGLPDALLILLPFLLIPTS*YLINNELITQH*LVKLSKQWTHTHVGRKT*SLILSLIIITVNLGLLPLPSFTFTTQSLNLNAAIPL*AGRVIGFRSKINLALHFLPQGTFTPLPILVLI
10764	24665	A	10849	2	462	TTLHAPFRNKKEAPITLLCLPSTANSRGVYARDAHKSAAHRIKDLAEKFLALVLIAYAYLQCCPFEDHVKL*NEVTEFAKTCVADESARTCDKSLHTLPGDSLCTVATLRETYGEMVDOCAKHEPVRYECLFHGDDCPNLP*VVRPEVD

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10765	24666	A	10850	164	1	RGFQVRGE*NSGRSTER*REBS*KLARE RAIGQREBEREKSRRAGRERERERKKE
10766	24667	A	10851	417	100	NMLVVGNELETRLWSQAQTTPCTQRSSS FFPVLNAAIFRSKSKVLNCLLEYFLGWL FSWDLIPRIEFLPSHYHYHHSHHHNQY *KS*QWSASNTRPQGLIDINSY
10767	24668	A	10852	339	3	ETTHSRARRGRSAASCRGSAIRRRGFP ESRRGREAAPVCPRHVLL*GAQSKQAAV AGKRSQTRHASKWPKSLFIPRRRRISLK RALHPVQSQSADSPSPSRIPPHGVGSS
10768	24669	A	10853	1	373	LQQGGRKRRAGQSSAPAGVSLRATILC LAWAGLAARDRIYLFPHVLTINBS* EQLIKANAGPKPDPTIPAPIQANESV DREALQDQLVLAAKLDVTKLAAANVT MLAIFLGRIVYG
10769	24670	A	10854	1	423	VSCSFLKLNKMHGILLALLCGPLKSGQ VNYTESGFFRARGHRPLDKKREBAGSLR PADPPITGGGYRARPAAATQKQVER* APDAGGCLHADPDLNV*SPTCQLQBAL LQLERPITNIVDELNNNVEADQSSTSS L
10770	24671	A	10855	343	3	RGCEAHPLPRSRGPAQSALQPVMYCTI FAGILTALSSH*FFT*VGLEINMLAFI PVLTKINPRSTEAALKYFLTQATASII LVIALLFNNILSGQ*TLTNFTNQ*SSSI I
10771	24672	A	10856	147	1	TRTPQGCQVSPKSMPLGAVAHSCNPITL GQ*GRRTI*QPEFDPSLANMV
10772	24673	A	10859	189	422	NHMDQFERRELLKREBERLEARRI AYQNDDESEAAAR*RRRRARQRLQK QREESLGQVDQVEVNAHNSVP
10773	24674	A	10860	90	273	SHREIBQNSAPFRKRGGISPMFYCL RNNQRYMT*RL*SGIGWMLSSGRMGY ALPG
10774	24675	A	10861	25	411	APCAKPCGDGRSRGSLVAMSGCNARKG DCCSRRCGSHL*N*IPIDWFLN*FFLT AKVKRCFKKRESIYQTVY*SPG*KN*T *DKEHPRYLIP*LCIQFYHLCWVTGTG GIILKHGDEIYIAPSGV
10775	24676	A	10862	33	302	SRRTATLYVDMNCEBPGTRVVAQGLKL GGSPSMLALNGRSQVSAFRPGRTFNAPP SLPATATRALGTVNRAKEFKVKTNGFLR Q*QPRS
10776	24677	A	10863	1075	1521	YCHTGKGEQLGERFCBGVSRRGPAERGS DSQTPWPWPLCAAGTISAGTSHSGSSG AFSSWPCWTAASPAARKRGAPAGSSWSP ATGAPGRCHRIILSRGAGGAGFPVCSGL ABSGL*RSSSPGRSGS*EQQRHEQNG LBAPPSTGV
10777	24678	A	10864	245	418	TSKLAPPISIPVIYANKVCB*PSKKKKK KKKKKKKKKKKKKKKKKKKKKKKKV FPEGGPGFFF
10778	24679	A	10865	132	398	LNMGKGDPPKPRGKMSAYAFVQT*RRR HKKKHDDASVNSSEFSKCS*RWKTM KREKGFREMAKADKARYEREMKTYIPPK GETF
10779	24680	A	10866	115	455	LLTRNMDRLILLAGGMPQLGQGPPTDAP AVDTAEHVYISYLALLKMLKHGRGVPVM

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						EVNGLMLGREFDDYTVRVLDVIAMPQS* TGVSAVADPVIIQAKMSDMLKQTGKPFMD
10780	24681	A	10867	64	483	QGERPAAAMKT*SLTLLSFLLLAAHVL VBGKKVKVKGlyIKVDS*KDTLGNTHI KQKSRPGNKGKFTVKDHTNCTMAVTRQE EGI SLKVECTQLDHEFSWAYAGNPTLCL KLIDEIVYWKPVARNRLQNDIMLYSPQ
10781	24682	A	10869	229	1	DTTLLKGLRLTLQNLLESGKSHMSPTL NOK*EII KLSKSCMSKASLSQKLQCFQ VGSQVMHAKRMLLKEIKSAT
10782	24683	A	10870	934	515	KRVLLCLGLIGCGGVTLAHGSLALPGSS SLHSLQSSWGLIGM*YDARLIPVYFFR EHLGSCHIQAGLGNSTNSIIPPTLVYSQNV QTTQVSHRAQLAPVPCPFVLLVLDKAL HFGQKSNRIFFFTLLIPQGSREDDEVA
10783	24684	A	10871	373	424	EFKINLANWG*CLKSQHLGRPCANHVR LGVNQNLQGHGRTPLFLK
10784	24685	A	10872	1	469	RSRQSDSLVACDRPSGASLALATCETIFS AISCNDPLPAPSLRLTPSCQPTMSSQIR QNYSTDTSAVNSLDNMYLQASVYTLCL GFYFDRDDVALEGVSQFFRELAZENREG YDRFLKMNQNRQGRALFQDIMPEDD* GKTHNMTAAMGLETK
10785	24686	A	10873	244	2	NIYSCKETFSVPLLAITHVYHFLVGRGGS QGTEMLWHRVDLRYRQAGHSQSL*SQ HFGSPRQVDQLRYGVSDQRQGHG
10786	24687	A	10874	83	427	ISLANNIRIAALNASSFTDDDE*SPTRH NTQYKSAQBAKAPALYH*ALDLQKHDR EESAKAYHELLEASLLREAVSSGDENEG LKHPLGLIKYSTYKNAQLASQREDLETA MB
10787	24688	A	10875	94	1	KSQKACNPSTLGG*GGNIT*AQEFETSL AMT
10788	24689	A	10876	2	413	GVTRGPMIRIEKCYFCSGTYVFGHGMF VRNDCKVPRFCKSKCHNFIMKRNPCVK RWTKAPRQNGKELTVDNSSPEPEKRRNE PIKYQLELNNKITDAMNRVEELKQKQQA KFIMNRL*KT*ELPKVDIQEVQLN
10789	24690	A	10877	65	417	RFAGAGAPEARAWPTDVAHAAEESKEMD LPDLASRVFCGRILSMVNTDDVNAIILV QKNMLDRFEKTEMLMLNENNLASARLEQ MSRRLRLHRTIL*DMKPDLSLFRPIRT LEWKL
10790	24691	A	10878	4	442	APTDDAMGHFEEDKVTITSLAGKRVNVE NAGRETLGRLLVDYPTATRRFDSFGNLT SGSVIMGNPKVKAGKGNVLTSLGDAIKH LDDLKGTFA*LTELHCDKLDVDPENFKL LGNKLEDTMAHFGQDFTPEVYAYLQNM VTVVAN
10791	24692	A	10880	1	419	GKHTRGYHEKCTGQRLNTHBYLLGNHL AKNLLFKRRABEKESVETPTDITQ QMTYYPVGMGNTPCS*KQNRPRSSTV MYICHPEKHEILLSVAEVTCEYEAIVL TPLLCSPHKPKYRPHASAVNDIFQQLSPG
10792	24693	A	10881	54	335	REIFPMSGALDVLQNNRSDVLKRLAVIT HLCKTKTDSPMQIIYGS*TEYIYSIKL NRT*QNLMLAVP*NYDI*NHDEVTVMTF

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10793	24694	A	10882	216	3	NNTLQMFP MSIKSMSICLRKKGKGFQIRGK*NSG RTERERERERERERARGQERERQKT SEGGHKKKKKKKK
10794	24695	A	10883	3	390	GELKCSKEKQCSMSAKSRITWIGAPFL KGQPRGVGEGPTVLKAGLLEKLEKHE CDVNDYGDLPFADIPNDSAFRIVIKNPRS VGHSQTLAGKVAEVKRSQ*ISLVLCVN LGGGLCELCGKAKVYSR
10795	24696	A	10884	3	375	STMRWIFPFLCRAGALAVPQQSSLPD ETEVVSEIVAEITDVSQANPQCEVGE FDGCA*ET*DVAVARPCQHCKGKGV CELDENNTLMCVQDPTSCALIGEVSK VCSYDILTFYSS
10796	24697	A	10885	95	2	KCTQGPSAVAHACNPNTVGGREGKIT*G QEF
10797	24698	A	10886	1	114	NGPHIVSDGLDVLTL*GACPSLPKQND YRREPTILAH
10798	24699	A	10887	1	368	EPTMELTAEKTNKGAARKVGAHAGEY GAELERMPFLTFFPT*TYPFHFDLSHGS AHVKGHCCKVADALTNAHVVDNPNAL SALNYLHAHKLRLPUNFKLLSH*LLWT LSAHLHVEFT
10799	24700	A	10888	336	9	FRGQVIPAIFPPFQTTLSYFOTQGN* TPFFQKILKLTGGGKLLDPOTPRRLRQ KREDPLFPGV*NON*P*SHPMWTKQNP VSKKKKKLKLSTSSIFVHRVSMSP
10800	24701	A	10889	3	362	GFLAPLENGELPTPMIRILQITTAEQE TFLTPAILLPHPQTYSIASAVPLAKPD T*PKDVGLLALGVFPAQYEDQTDLENY NNVKALKYTEDLQQLMGFCVQEDINS LCLTVBQP
10801	24702	A	10890	66	333	TLPGNIGTISFVERVNEIRPOLIRIDGR NYRKNPVQEQTYQHEED*DFYQGSMEC ADEPCDAY*VEHTPQGFRTILRAP*LY TPIVG
10802	24703	A	10891	405	49	IPMWTERTASRAQDVAGPARNPACPL PBQCFPGPAEWGPTLTPPGSC*LRPGR ERHGPWCWGPRLSSGGTTPPSQGCA NTPCPHHQCELLAGGAVFYKLFYRYG NSPKWDL
10803	24704	A	10892	2	197	POPLRVLMTHALAMARSRTSLLLAFA LILCLPWLQKAGVQTVPLCTLFYHMLQ THRAQLVLDTYQLEETYPKDKHYSF LHDSQTL*FSDSIPPTSNMEETQQTNS L*LPDIPAPGFCPLDPAASKGWRPNR SAMHATLRYAFAASRAPTGH
10804	24705	A	10893	3	334	DQLPEPLKWLATLALAGRSRSLPL FVALL*LPWQAGAGVQLPVSRLFHA MLQAHRAHQLADTYHEDETYP*DHK *SFLHDSQTSFCLPDSIPTPSNMEET
10805	24706	A	10894	3	341	LLTPGVSDAICYLDSGVIINSDFITAY VIG*RFYVNG*HATVRFPAVPPVALPW LGV*WDRNPRGTYDGTHTVYFKCRHS TGGFFIRSNKVNGLDFVTADKNLYLVD Y
10806	24707	A	10895	25	351	AMIQTRDLQGGRAFGLLKQAD*RLDEI CTQLLDDIKYSNEDILPSRLEGFFREYK

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10807	24708	A	10896	364	38	EFDLIGNGHIDIMYLKIMLYKLAVPQTD LQLPRISIGEVYSGSGSTISYPDFLM FSQFKIAQFLKKIPFGSPFPFONGNF LKFSKFFPNKRGFPPHFF*KRGPFFCP KWGPQGHIGAHGPPAPQGGKI PPFPVVK KMGIKGTTPPGGFFFPFFFPFSW
10808	24709	A	10897	136	3	STLKKR*RFGMVAHACNPSTLGGSGRI T*GQQFKTSLTNVVKP
10809	24710	A	10898	193	269	GNKYCLTILLLLLSLFSKQSLTLPL RCSG*TRTPGPKSGSLNPS*VAGHGGV CL*SQLIRLELWEDHLSPGV*GHSDPL HHCTLTWATE*DSVS*KTTTTTTK
10810	24711	A	10899	316	374	CCCCCCCCCCCCCCCCCCCCCTKTNFS QQ
10811	24712	A	10900	38	206	VYGVLPFTICLLNCSLGLPHPEPFF FTESCCVAQAGLQNHHC*SLRLLLPHAIL
10812	24713	A	10901	364	2	DYQHSPEKHKRFGSGWVLMCRKKK RKKKSTKILNQPSTIL*KPRNSARK S*QKEITKIGADSLIERNRKIKIYIN ETMSWFIILNKIDQPLARLTMIERKDS TKFRNERG
10813	24714	A	10902	132	3	ATSSPWSAYSRAVAILLFLFENLAF VLXGV*NYFLQEI
10814	24715	A	10903	234	352	NFCFFETGSCSVT*AGVIMHCSLDLPG SSNSLTSVSEE
10815	24716	A	10904	250	356	TMENMLDKKQI*ATIFLF*FRNGDAET TLINNAL
10816	24717	A	10905	280	322	QT*SLILVSLICIAITNLGLLPSYFT PTQLSINLMAIPL*AGAVVIGFRSKI KNALVLCTSTPLPTSTMLPVDMDTSSD IHPKI*SIR*QTCIQHRLMLKC
10817	24718	A	10906	271	365	KHRPGVVAHTYFNSLIGSGGGWIT*QGE FCT
10818	24719	A	10907	135	358	LYKLATNPKLTLTCSGLPLKGNVIG QCNQVM*YQHGRRPQDCISPGIQQQH GQHKSLSL*KSLKISWS
10819	24720	A	10908	107	212	YKNEGQGVRLNVPVLPALNEA*VGGTP EVSHNL
10820	24721	A	10909	165	383	PKNRPTPLKSSSTNPQDQKSLRPL TPMGPHFKRGNYSYDENLCLCPVGNK GGSH*GLLTCTCRGF
10821	24722	A	10910	119	291	GGYRFPYVEDTF*K*GWPLFLIILKPL AGHGAGLWSWIRMLRK*EDHLSLGGRG CSLWLCTLA*ATE*DPVS*KVRLALAN FVYNTKTSRAWCMFPVLATHEAEVGG SLESGRSLQ
10822	24723	A	10911	283	2	SDNTDTLFLPIFYIYIPPIWEQGETWK KNPRNSRLKTLRSETIAQIPLKCNLWP GMVAHACNPYTLGD*GGWVT*QGEFETS LANMARFSC
10823	24724	A	10912	1	360	PHAFGIMKGVTFMSLLPLFWSWNRGGF RQNPAPKSEVAHRLKDWGKKKFKANG*MA LQNLKQGPFWNHGKLGKEVEFAKGV ADDAENSGKWLNTLGHYLAFAVAVRE TYGERAC
10824	24725	A	10913	270	361	SKTWPTVATCNPRTLGSGGWIT*GQ EF
10825	24726	A	10914	157	1	VFFQLSRLANKGFSRFF*VPE*ESHIVA

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10826	24727	A	10915	1	357	*AAVQWRDLGSLQAPPPGPTTFSS LEEMGPREFAESEKSKNTKKKIKNS TPPKPKPARKGEEKPGPKRAITTFVAR IPLFLCLGFLWPS* IIGKSSPTPGSKG HTGAPNCPCCPLAAPPKDVNPNPNKIVE AVKNPIL
10827	24728	A	10916	102	471	PSTPILITSSYPHYKSSVSTSTFIISLF PTTFMCLVQEFILSN*NLPTTQTTHLS LSFKLDYFLIIFILLTFLVWSTIEFSL *YINSNPNINQFFKYLILFLITLLILT ANWLPQLEIG
10828	24729	A	10917	2	138	REPTWLSFADKTNKAVNWKGVKAGAG* YGAIVLPTWMLNVLNSD
10829	24730	A	10918	178	393	LVLCTVLNKKRFPFSDLSLITKAQDVTE NLSNPTVLRGRTGPSAVAHNTSPSTLGG *GKMTQGOEFETSLA
10830	24731	A	10919	278	124	TAWADGKSNSTPFLKLPKRLT*GGGVC LEFQVLGRVPRPNPNLNQGFN*PKFR PWTSTGAKQNFV*KKKKCNKNPK*NS RHTPPP
10831	24732	A	10920	221	243	IIIGSLPIDIKSKFLKIVAPQQAQMP VIPALWKAERASPEVGSPPRA*PGSLK VHVDNNWESIN
10832	24733	A	10921	33	292	GTNMLIRHAEVQCVINSELNPTSGD KPEQC*DHLYLT*YLILGKGI**ISGA LEKKKKKKKKKKKKKKKKKKKKIKITGG FI
10833	24734	A	10922	108	3	KLAVTGSVCL*SQLLGRLR*EDHLNLGH GGCSEP
10834	24735	A	10923	106	2	KLAVTGSVCL*SQLLGRLR*EDHLNLGH GGCSEP
10835	24736	A	10924	195	2	ASLPKSQLNRAPIYLPITYVIFETGSL* PMLVCSGVIHACHNLVLVGGSDPTTSAS QVAETMYL
10836	24737	A	10925	127	2	YVCIKRLKRGPRGAWAYACNPFSLGGQG GMIT*GQEFKTSL
10837	24738	A	10926	639	282	FFLSIKGVVQWPMPIPTPWGLKQEDHL RPLRLDQPVQNSKTPSILKI*KLARGG ACL*SQLFRKPR*ENCLSTGELEKGGGI FIRLVQNKIPTTRGERKKQSHGTGSYQCP KIKKKK
10838	24739	A	10927	1	363	ALLTQALTCRQAGARAHAGATPSPIMFP SLPQGFRCDCSPSDAAYTMKMTIDKKQNO VILIFKFRMGHKAQITRININAFGPEI ANKGTVMNRFINFCRDESEDDE*YAO PSKVATDQL
10839	24740	A	10928	53	379	TEARLLTLYLLPNALLNFTSPPLMFAD RRLFCPTNHLIDIGLYLLFGA*AVVLGTA LSLLIRBELCQGNLLCNHIIYNNIVTA HNFVILFIFGLLEIILGGPN*LFPL
10840	24741	A	10929	180	350	EPMAKSKTESPGPRCGI*IVYISQSG TLRPRGAGLPMGPEPLRGLNLEIPRG A
10841	24742	A	10930	361	379	RRYMWLG*VQWMLNPVLPALWEAKGRSP KARNL
10842	24743	A	10931	121	543	HRNTGTHSAHAYHIVTNP*PLTGAL SALLMTSLAMGIFHFSITLLILGLLTN TLTYH*WRDVTRESTYQGHHPVQKGG

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						LQYGIILYIT*VFPPAGFF*APVHSIL SPTPQLGSHWSPGTGTPINPLKDPLNLT S
10843	24744	A	10932	227	339	VGGVKSQVLLNCHFSR*MKKKKKKKKK KKKKKKKKKKKK
10844	24745	A	10933	64	409	DQRNKSARLRAHLRKRKRKKKKKKKKKK KKKKKKKKKKKKKKKKKKRGGEL*KKIN WAPFLPLKKRFVGENFLKKNFFWOGNT GQIISKKYRGSGK
10845	24746	A	10934	2	362	NKLSGPYPKVGVTPLPVMNPLAQVLVY STIPAGTLITLSSH*FTT*VGLIEDML AFIPVLKKKINPRSTENAIKYLFGATA SLILLALLNNILSQ*TTTSTTSQYS SLILIRAW
10846	24747	A	10935	154	3	GCPLSPILLNIVKVLVWANNQRKSKYS IQIGLEVK*SLITDNNMLVLSN
10847	24748	A	10936	250	363	TAMPGLYLSFSSFLY*ETTKIALGAVAH CDPSTLGGRG
10848	24749	A	10937	199	339	NVLGILLVFRIVIVELVYRCRMLGVAN TCNPSTLGGCGQGT*GRE
10849	24750	A	10938	130	240	KNEQDPRDL*DNKDKWNNHIVGVPEEDK DNGTERVED
10850	24751	A	10939	35	235	FILVENTKMCICPLNNMIYATILVFP SVFL*BEKKQ*GITTEKKKKKKKKKKKK KKKKKKKKIKPGGL
10851	24752	A	10940	179	12	DQPGQHNRTLSLQENNNKSSNVQCC*P QLLGRLRWEDCLSPGGRCEEPCHSG
10852	24753	A	10941	297	278	INQDNELTLINGSSKQIKHNNINQTLRT KMNENLFA*IIAATILGLSATVQILF PILIPITSKYLINRLITTTQ*LIKIKTSK QMTTHNTKRT*SLGGD
10853	24754	A	10942	3	318	FGSGGVNTPDAFVLSVLLPSRLLP LPHLFLPPLPACAPKPL*VY*E* *LYYSQSLIPFTYREKCKLLVFWAINL FFLYYYNNMNNMLTLCYKXN
10854	24755	A	10943	190	3	KLSHKGSVYKFTFT*KNHLPK*KNLN VYPNDKEFFFFPESLALSRLQNGTIL AHCNLR
10855	24756	A	10944	281	1	KKWLFSSYSSLYGNGLFLYPPFLRVSGF GKGFWKKFFFLRARGALEWGSPLKGF GFFWVFFFF*DGVSLLPLRLCNGIISA HCNLRFPGS
10856	24757	A	10945	169	319	NGVEDAFNNMVLGAQWNTSVIPALNEV KVGSPSEVRSFRPTRPI*KYGRFLGTG YICNPSTLGGQRRIT*QGEFQTNPANN VRPC
10857	24758	A	10946	312	1	FARPGLLKSSDQDP*PLDPVWGFFKRF PINWLEFRIFPLIIMAKKKLSKSLFP FPFLG*FRD*GQKTPFFFFFTVSLLLPK LECNGLSAHCNLCIPGSSD
10858	24759	A	10947	208	329	IFTGDRSRNRIG*ARMLTPVIPSLWEA ENGSLEPKSL
10859	24760	A	10948	116	374	FFYGLYLLFSCFDEAPCSRG*SWBARG QSPCNLIFPGSSDLYVSAPVARITGAR DHACIIIVFVVDGGCVDTITSLAGWLR RG
10860	24761	A	10949	264	434	QLAFCTDILTSVREQCEQL*KCVKARKR IELCDEQ*SCRSHD*DTDELFDFLHA



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						T
10861	24762	A	10950	226	429	NFOFRLDKTVFFSKIRINAWAQWPMVPM PELNKAKAGGIT*AELETSLENIVRPM LYKKPKN*VWNC
10862	24763	A	10951	188	433	YSABWRIDLGIEVFWGRMTYKQ*PFWP VFKFLFF*RGRTLSKKLEWMSVITGHC MLDLGSRRETFASAPQVMTWIGSCHS
10863	24764	A	10952	298	445	LFSKSSSKSKEGPGVVAHACKPGITG GRGGNIT*GSEFESSLANVVK
10864	24765	A	10953	244	1	KTPQGILVVFCLFKKSPLGKKGVMGVL ICFPLKSRINLNPRLGQRKN*FFFFFP ETDYSVAQGTGVQ*HNLGSLQPPSC
10865	24766	A	10954	199	3	QETKKBNKKNKQIK*RTSRKHKRQGTN KTKSRQERQGT*PVGNRQTPTLGIIHARPR RRTATSPRA
10866	24767	A	10955	157	3	YSYTFSEIITTSILTIQLTSGHGKACL* SQLGLRLQRDNHNLNHEGGCTRA
10867	24768	A	10956	263	357	GLSLKVLTKQLGAVAHACNFTLGGRGG *IT
10868	24769	A	10957	333	2	ENKADMPLPLVKSFFPLGTFPKMPTNSK RYIFLQLLQAHSPPSFIRCMEL*WY PILCYGQSNQPSV*LAYCRDLFNELIF FFFFFETEFHSCCPGGISAYCNCLSC
10869	24770	A	10958	130	228	GSSFLGGSPVAQGHVLPDHGSLQ*DK SPSVQMSKNIGCSGACL*SQLLRRLRC QGRLLSP*QACACSEP*SGRCTPAMATRGD PPKRLPYTTDS
10870	24771	A	10959	250	3	VQACSITGALYQRNADEPQTARPISG PTTSIAMRLMLLTCSGHINPVDALAFSG IMP*GLFPFSPRQNLSPRLSCSARA
10871	24772	A	10960	199	326	VJGRWNSNQNTYLLARN*KIK*NNTR CWGGGQATRELIHC*QECRI*KCQPSQL WRTV*QPLANTLIR
10872	24773	A	10961	323	3	LLFPHLEDNQW*YVFCGYNLSFLQFYI N*IIQLVVFVWLLSMSIILKSHPCPS K*LSVTTFPQSRSSRWLENSGALSAH CNCLCPDSSDS*CASAS*VAGSC
10873	24774	A	10963	120	3	PPPPPP*EMESCFVQAQVQ*CDQSSL *PSTPLGKQSSC
10874	24775	A	10964	168	441	LTPIPALNWEARAGESPEVRSRR*SP PLK
10875	24776	A	10965	19	207	APLKLNVAMELSLQNDVRSNLEIPL KKGDTRGVQMLTPIPALNWEAVDRTP VTSVTRC*PLKLNVALESLGQNDVRS NLWEIPLKKGDTRGVQMLTPIPALNWE EVDRTPVTSVTRC
10876	24777	A	10966	209	1	TKSALSNMVTTHIGLCRNFICVL*DRV SVTIQGVOMIDLSLOSLSPLKOPPTS ASRVAGITGMHLV
10877	24778	A	10967	109	1	DYLRSGV*DDPQHGKTSLLRIQKLAR LVGPIISC
10878	24779	A	10968	141	2	GLAMLPLENIIPRPGTVAHACNPTLG GRGGIT*GQEPKTSLSC
10879	24780	A	10969	175	348	LVYCKHLLCVENISLFPFH*TCYK*RG VLMLEGAHACSPGTGGRGNTMAGSD RD
10880	24781	A	10970	108	2	RTKKLMRSQVVAHTCNPS*TLGG*GGWI T*GDSC
10881	24782	A	10971	184	2	SPLNKLHLRGVPRVRCQSPATRGASQL

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						GVLGVRDPLEEAV*LFSDLLKLCAGKTTT LFLV
10882	24783	A	10972	245	339	SQISGPGIVAHACNPSILQGNGWIT*G QEF
10883	24784	A	10973	295	340	KRVFF*ARKKNPFLSP/LGLTLENPLGF RLFLNPLFLGLKISQFFFPQI*PLAFFF WGTLPRLN/LKPGVPPPPPPPPPP*DG VSPCCPGWSQARRYIEINISLSTCPRA
10884	24785	A	10974	186	340	RPYLTRIRFKGHPNEPIQ*SFVFLPYC FDTESRSVTRLCSCGNSAHCNL
10885	24786	A	10975	253	491	FLECTSLLKQRVRFPQHSKAPFKELQ TTGRGALLQSHLLRLRQBHC/LGPGVG S/SSEP*LEHCTPAWVIEGSSSK
10886	24787	A	10976	141	1	S/SFFFKSP/MDLQVFF*HFFFLRSH SVACAGVQWCHLSL/KPFA
10887	24788	A	10977	3	138	HEETGPHLVSDQGLNLLTS*STHLGLPE CNDYREPPPPGREGDF
10888	24789	A	10978	186	323	YESPSATQAGVQWCHLGLS*PSTSRFQ* FFCINLSSTWDSYGLAPS
10889	24790	A	10979	183	3	IKILFPFFFLRLSLALLPRLCSGTSPA HCNLC/LGSSSDSAS*VAGITGTTTSPM QLV
10890	24791	A	10980	309	55	KNFGPNNVK/LOOKGEMAF/LGXFFFFF FFFFEKESWVFVQ*MQWGDPRSLQGP PPGVTQISRLKGKGGPLFKKKKREGRN M
10891	24792	A	10981	637	838	SQHLGRPMRVDQLRPGV*DPQGHQEM PSLRLIQR*AGHGGTHL*SQVLRVRQDN CLNNGGGCGSE
10892	24793	A	10982	275	2	ENRTLRNEFLSWPFGFWNLLNMIRPKN VKDTSKSMENITDSPHFLFKELGKINA FOTPDSSLVRGKPSDSIHNTFDM*RTK EYNESA
10893	24794	A	10983	98	346	GHGHATLRLGLCVLTFSPHYTALSVSOTN DAEDCCCLCEQKPGICQVIRNLLYLLK DVCVRPAVV*VVERVYSLSRYSLWRD
10894	24795	A	10984	30	410	LPFTGRPRTRTRGFSINHTDITGLYL LFGA*AGVVGVIAVSLLR/LAGLQPGNLL GNDHMVNAIVTAHAFSIIFFI/VLP/IIIG GFGN*LVPLIIGAPDMAFRINNICE*L LPPSLLLLSAIAIR
10895	24796	A	10985	141	360	QTLRTMGNENLPAFSLIAPTLGLPAAVL IILFPPLLIPTSKYLNNRLITTOQ*LI KLTSEQMITIHNKTGRT
10896	24797	A	10986	3	347	HELRTKVNEHLTASPMGPTSLGLFAALL IIL*PPLLIPTSKYLISNRLITTOQ*LI KLTNSQMITIHNKTGRT*SLILESLLII IATNLLGLLPYSFTPTQISINLMAI PL
10897	24798	A	10987	46	317	KMTPIRKINPLIKLINHSLIDLPTPSN ISA*WFGSLGACLLQITTLGLFLAMH YSPRA*TAFSIAHTRDVNG*IRYL IANCAE
10898	24799	A	10988	245	1	VSCILLEGKLNREDTITKN*SVHIEHOR PKVDKTKTMGKKQKNRTGN*SKQTASP? PKK*SSSPATQSNMNDPDELEE
10899	24800	A	10989	255	1	SCLFWANNISVQNGHKKFLVIRITFFPI GSFHVT*LLGPPLLISPPRIFFFEITG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SPTVARAGVHSIGATSAKCNRLRLGSSNSA
10900	24801	A	10990	166	307	GEKFWGPIIAGGLVGRSSWASCVLELL*EMVFRHVAQAGLKLSSSNPPASASQSAGITGVSH
10901	24802	A	10991	109	330	TNQFKTKKERRRAGKKRVKLERRERRRKKRKBQRKNEKERR*P*ND*RRIRSRNHSFDVYVFLICGLLNLLHV
10902	24803	A	10992	244	326	GRYLEGNWLDGPA*AVVLGTALSLLLRPELCHPAILLGDLSSVIVTAWMSLLV RVPLIILAGRN*LVLTIIGAPNAFRINSISF*LLIPSLILLPPPI*QMGAGVGEREVRVR
10903	24804	A	10993	101	2	KTFMARFVGTCI*SQLLRPQEDLRLGGRGC
10904	24805	A	10994	177	1	TPSILLFPVNIICPCINPGGGYSECKLCLCTPAWVTE*NSISRNPSQNSRQSRQVNLHF
10905	24806	A	10995	214	326	KEERKNPRAIRVV*PWGFFPFLPKRISLFLVFRFWHGYPFGAFTSQKMLV*TMVLVFFFFS*VSLERLECSGVISAKCNTFLPGSSDC
10906	24807	A	10996	184	379	LGWVYHFFPSILLYL*CKLFFSPKLEFSSCCPLECNGTVLNRSLRLPASGDSPT SASRVAGIGTCI
10907	24808	A	10997	136	3	GRVDGQIMTHQSHAYHIVKPS*PLTGALSALLMTSGLAM*FH
10908	24809	A	10998	274	363	PRAYAEPLTHDRTYSCT*SLIRASFTLFA*TRILRLP*STPTTQLCWNLAMA IFL*AVAPDGYSSMITALSHLPQCTPTPLSILGIIETVSLIQPIITGVKRTANIT*CHLLMHLIGSATLSITI
10909	24810	A	10999	305	1	NLHTPSQIPIT*PLPNININHLTTQ*IKYLLILPSNLFPENKPNLKTAYSVPSPNHLHPSSSNSPASQVAGNAGRHYNWLIFFVLVETGYSLLV
10910	24811	A	11000	154	2	IVVGITQSRRCGRSL*SQHGRPRQADCFTGVPDQCYFTLLPEVFFLV
10911	24812	A	11001	142	367	GVCLYQRISYIKTKKLSGGLFYFLLLLLF*EGGSHSVTKLRCGGVSAHNCILASSHPPTSSSQVAGTTG
10912	24813	A	11002	60	385	GNTLLSHTLRAHLIENLEAFIDRTILGLPAA*LIILPPLPIPT*YLINIRLMA NRH*LIKLTSEMITTNSIGRT*SIILVSLIITATANLLGLLPYSITRT
10913	24814	A	11003	214	83	SKKSASPLTNTVFQVLNVSRRRETRYTMRKKRIKLS*FVD
10914	24815	A	11004	241	368	SYLL*PSP*PLTGALSALLMTSGLPMRFHFSITLLILGLLNLTLTIQ*WRDVTRSTYQGHITPPVQKRLKHLITLESVFFPARF*AFYHSLAPTPQL*GEWPLGINPLANA
10915	24816	A	11005	3	396	HEPHALGMPLTADLPMSASCSTSLILLLHLHLPLWI*EARYAQAGCSKLFDSAM LQAHRAHQLITDTYQVRETYIPEDHKYSFIHDPQTSFCFSDSIPTSPNTETTYQKSNLELLRISILLIESWLEP
10916	24817	A	11006	156	335	FGCCCCFLFF*LVYCCYVRLYYIVLYI

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 5,168,351	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						SPGPFYF*YWIN*YFRLVYNLYLVLYL LYMS
10917	24818	A	11007	107	2	KCSSSKHPTKEDSQITNKHIRKCSS*LL VREMOII
10918	24819	A	11008	129	412	KTRSGFKKTPGGKGTPLKKTKPKITGP GGGALKPPFSGGFRPENPLNRDKSSG PKTPTFFSPMGKK*NFFQKKGNNLLYPG KIFFFWAKNI
10919	24820	A	11009	63	268	CTFFPFNMHSTIQSTT*LDRESEKKKKK KKKKKKKKKKKKQPL*2NPSLKGSG
10920	24821	A	11010	154	422	NFFSFFFFPKKPPFPPKPGQGTQNGG *LKPRPPLNMFSGFASGRAGITGCVPH PG*LIIVF*VKAGPHENLVWNSSTGNQP ACASO
10921	24822	A	11011	23	375	TRYLTRIKKKKKKKKKKKKKRGAFLK TPWAGAPFPFGSAIFIPFFFGQFP*PLDG FFWETLFFWGGKILGHLSPKILFPWGGK NFFWVKGGKNNLNSPLKIFFLGVFFKK FFFPG
10922	24823	A	11012	151	361	ACTTTPSSSFNSNIDTVSLCCPG*VGRN NSSLINFPFSLRSWYRHPHPHAPFPF ILIRSRVQAAGLEFLALRDTPLSDPCP TVHYPPSLAN*SVFF*FFLTQSPVSLPRL KKK
10923	24824	A	11013	146	378	NFVVFSIEFLHICY*YISFICLIRKVL* *KKKKKKKKKKKKKKKKKKKKGNLKGAG GKKKFLGGGRNNSFFRNGGCF
10924	24825	A	11014	82	264	TELETTTLCNWSAILYILC*BNKVPLSF INTEKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKIERKI
10925	24826	A	11015	381	2	GRALPFLLLGPTTHRQVPTPLRVPFG SYTGISIRQSGFFPIKRVIFPRL**KAL FLLPFLPFPFSFFLKIGTYSVAQEQNGM IIDN*NPELLGRRNPSTSAQIAGNTSA Y*HTQLVFLCEDGI
10926	24827	A	11016	1	251	PNCIVHSLRTGTINFLILLLLCFPF*F LKNLNFESQKKKKKKKKKKKKKKKKR GAPLKKTPGGPKFYASKKKILSPQGG
10927	24828	A	11017	234	1	DINIKGSMVRGIPKPSVLQLFNSKI FPN*KLIKKNPNRPGVMVHVCNPSVSG GRNGQMA*GQEPKASLANMAKP
10928	24829	A	11018	107	342	FQLCIGALVHCLPMKQHSSEYKSTDEHA SSECHTVQSSQLSTSAFQKQ*THKKKK KKKKKKKKKKKKK*KKGGAS*
10929	24830	A	11019	264	1	CFKPLLFYKPGLIKAVNLPSVISAATHF KF*YVTFSPS*KKFLCVGGKIGSHSITQ AKISGTIKAKCSLSLPGGDTPTPTSRV ARA
10930	24831	A	11020	1	288	KTRGTSRSSRAATLFFPPFPKGGCFPNC NLPTTTTGKLGKNGKFFNLFLVGGPPLPHG GLKKGPGAPQVPPLFLKKPQTSP*GLR EGPPPLKKFYLF
10931	24832	A	11021	115	287	STCEISFGCSRKCKWDYLMVRFSSHFP *FLETECCSVA*AGVQMNLSLSQLHP E
10932	24833	A	11022	186	1	RPKVDKTAQRGRDSRKA*NFKNQKASS PPKRYNSLAREQNWNEFELTEVGR KSVITN

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10933	24834	A	11023	180	353	IFCFICISRDGVSC*PG\SQSPELMIH *NTKIS*AWQRPVKIPATQAEAGESLE PG
10934	24835	A	11024	155	1	PQARRGGTCLQS*LLRRLRLRQEDRLSP GV*GYSEL*SCPCTPAWETERLV
10935	24836	A	11025	22	325	KLILLYDQLTFIFINTRAVVAHCAFC WP\HFVPGNYGVFSCSLFTFIVVSGKA DLFFPKPKKKKKKKKKKKKKKK*KGK RGLKNWGGGPIFWGPFK
10936	24837	A	11027	127	259	GGVQWLTVPVPTLWEANVGSGTKLRSSR PFSTP*PCIVMLTG
10937	24838	A	11028	37	408	IASSLGFFFFRVVKRGDFCTEGAYGRQ FTIPWKKRAREKTRNENLAKGNVKNHS RGLKTPRGLGGPYLKKGP\RGKGPFO GGTLGGGG*KKIKQTL*IRRNYPYIR RYNRFKKQKNM
10938	24839	A	11029	146	3	LLVLKDLPRINRVSAPTLYIYITVLYIY IYIYTHTHTHFIT*VLFC
10939	24840	A	11030	268	435	LMCLNENIN*F*EVE*WLGAGAHCPK TLGG*GGRIA*QGEFTRLRNIVRP
10940	24841	A	11031	322	2	KLPHLQQQGVKVCYCFPLKNKGIGGG VCL*SQPLRLRLQENHSNPGQCTSAWVT QRDSVSKNKKGRMEKYPSSVRQNKPVK HTRKMSPTKADTKSTHGGGVR
10941	24842	A	11032	251	380	HKRLHTIYYFVPLKKMGPGLVGHTVNP STLGGGGQGIT*GRE
10942	24843	A	11033	64	324	FWFFFFFFFFFFINPPGGGKKKKPPPL GKKKRGKKGGGKFFPPPPRGGGGGPKK ISLKRVLKFF*NP\PGGTCKGGPFLIPP GSP
10943	24844	A	11034	420	534	CPGVVAHYNPSTLGS*GRQITIDREIE TILANMAKPH
10944	24845	A	11035	196	1	KNHSLFPGQKGTFFPKKKKTPKINHS ELGSKAYSNPQTVVAHNPSTLGS*GG WIN*QGEFE
10945	24846	A	11036	10	248	PSDR*LFSTNKKDGTFLLLFGA*AGVL GTALSLLIRAE\GQGNLLGNPHIYNVI VTAHAFVIF
10946	24847	A	11037	32	405	DVSKRKKKKRKKRNIVLETSISSHLVE WMLCSRYHPLIKRSSVRILIALLCQK VRDMS*GIGGKKQCDWSLWIKMSD PFLIPYPKINA*RLKDLCEBRLKIIIX REYLDYRVKKV
10947	24848	A	11038	337	448	KNRPFGGKNDFFNGGPGGPPPKKMG FGKKKP*FKRSGKKKKKKKKKKKKKK KKKTG
10948	24849	A	11039	307	415	RFVCSITIKVRLDSSDSNPGRVLSTSN SSLK*KKK
10949	24850	A	11040	213	403	VHRGIKYFLNKLDPFRQTFKK*G*RL GAVAHACDPSTLGG*GGNITLGQTFETS LRRWKS
10950	24851	A	11041	104	2	SAFFFT*RTSSCSVAQAGQNCDLSSLQL PPPGFK
10951	24852	A	11042	177	3	AYTAYICVCHITLYLY*HYICINWYCK ITYLYIYKYLKYNAILLHGIFSP\HTI S
10952	24853	A	11043	314	395	TVYILNLSINSQSVLSVPHRLRHP GRVQWLTVPVLPALWEAQAGGS*VRISO

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10953	24854	A	11044	310	403	IKTPA RGKGGKKPRNPGGGKS*ALTCKKKKKKK KKKKKKKKPGGALKKKPRGGQKKTGGGK KKFLPKRGAKKKPGDFGKNQIGGGGK RGKTPPKKKK*GKKKNLKGKGKKT SGGGKKFPprrvv*KKCLPPGG
10954	24855	A	11046	181	3	EGPISTSLFFFFF*ROISSLLEIKYSY TIIAHCSFKFPSSRNPPTSASQAAS VHI
10955	24856	A	11047	392	41	KESRSLSQGGREKPKFLAPPAPKFKR IRPHPLKKLPGKPPSPS*ILSLKKK GGPILLARMFWNSCPQSGPPPPPKRIG FKGQPPPLP*KKKKPFLAGGNQKVN FFFFF
10956	24857	A	11048	147	307	TVIFVFILRKGLTLAPRESGTMMAHK S*PDGLKQSCSCLLSSVYRRRRG HGKIPSPILQ*HK*DAYGSACIQSOLLR RLRWESRSISI
10957	24858	A	11049	118	1	RKIRREGGLHMLNLLGRLEWDLGLRLR WEDRLSPRRGGCEPLRCHCPPAWATE* DPVSKKKKKSLFVKKPQGGG
10959	24860	A	11051	130	340	HNMFHAALGSRINDFDDDDDDFFGFF FCPPVGRAGTHGLLSPFPRV*QYYN LGTVAHVCPNPTLGGHVGES*QGQFKIS LANIVK
10960	24861	A	11052	140	337	NIIMFFFFFETVSPILLGLEGGKTIW N*NLCLPG*GDSPIGCS
10961	24862	A	11053	197	428	IRSNINPTVASQSYSNKSHIPLILNQ LDMIKFSBGMKAKIGLLQTVGVVN AKEKFLKKNQSATPLSI*IRK
10962	24863	A	11055	180	1	ATTALYSRLGDIAREPFLERKKEQNG WTVTVNPTSLGGQGRTA*TOBFKSSL GHIA
10963	24864	A	11056	158	426	FFFLPLPLPTVLSFPRSPDAEPGLDCT AAISAHONLPA*FSCISLPGACNCRAP PRLTASASRGAGLADGVSTQCSMVPR ECSGV
10964	24865	A	11057	220	421	YALHLMNNNSYF*MKKKKKKKKKKK KKKKKKKKKNKDPGGAIVYKKIP
10965	24866	A	11058	162	464	SCSVGLKLFMSKTLALSYYCLLLLLTL HYYYYYYYYY*SLVFM
10966	24867	A	11059	1	134	APENRVDPRVKTLVPLILPITTLANP CKKD*YPTVKISIAIC
10967	24868	A	11060	382	273	SSCL*POLLRLRQEDYS*GA*GNEL **CHCSPAWTEQDPVSKNIHTYIHSQS INYGSMIGYIHEQGLIADHKPIIAEPR DSTYPRDHT
10968	24869	A	11061	298	378	SCSASPCSSSRHGSPCG*QTCILLATA LRCLPWLEAGALHTGPGCLFDMAMQ AHKAHQIVIDITYQIGENHYTPDQKNSF LLESHSPCSPSDITTFNNMETQQKSM LLILRISLLISTWLPFLPRIVANI
10969	24870	A	11062	39	486	RPTRPDAIVKPSF*PLTGRISALLW SGLQMFVHHSITLLGLLWTLTLYO *WRDVTRESTYQGHFTPGQGLQYRIM LFTTSEVFFPAGFF*AFYHSLAPTPOL GGHNDPTGITPNPLFVPLINTFGILAY GGGIT*ARR

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10970	24871	A	11063	269	429	ATWQKPLQIQKNYFGLGLVAHNCNPST LGGQGGRLT*GQFLAQPANMVNTH
10971	24872	A	11064	248	65	ITEGQAQNLMPVI PALWKAAGGSEFVG SSKPA*PCDPPASASQSAGITGVSHRTQ LILNS
10972	24873	A	11065	176	1	LFPFPPKKVPPWQNTQFKSICLAYTINFFF FETESRSVARLECRGTLSPHCKP*LPGS RE
10973	24874	A	11066	2	397	MVLWTAHLRAMAFGSRRTGGLTFALLCL PWLQEGAGVQTVFISRLCDIAMLQAHR HGLAIDTQEFKETIYPKDHKYSLLNDS QTSFCDSLPTFYMESTQKTLNLDV RMSLLIEDS*LRPAQSWR
10974	24875	A	11067	172	399	QILYL*RYAYVTWQHLSHPL*KKKKK KKKKKKKKKKKKKKKKKKKTGG
10975	24876	A	11068	192	3	EKLTPMLKLIVHITILLPLT*LSKKHII *INTTTHSIIISILPLLFNQITSNLFS CSPTFC
10976	24877	A	11069	204	345	DKSGEHSSTSSIQKNRLGAVTHCNPR TLGGQGRWTT*SQEFQTSF
10977	24878	A	11070	3	416	HELPOPLRLVLTADHGAATAGSRTSLLL DFALLCLFWQEDGAGQTVF*SRLFDHA MLQMRSHRILGIDTYQEVVETIYPEDRK LSFPDDCHTYFCF*HSITPFSHLGETLL TSNLELLRICLVLDSWLEPARILTS
10978	24879	A	11071	108	2	PSPPFFETESCSVT*AGVLNRDLCSLQA PLPGSSC
10979	24880	A	11072	400	278	KVK*LRQENQWNSRGRDCSEPRSRHGT L PWTEQDSI FINKTKPYKIS
10980	24881	A	11073	139	3	KLACGGRHLSFQLLRRLREDHLSFGG *GYSEPWRYCTASA
10981	24882	A	11074	17	421	DRVIGQPRWLPVLLALNBAEFGGLEP KVQDQPGNCKSLSLTKKKRRNFFG RGOTQLCSQLLRRLRVGCCIDPKLHCL PAWMTERDPTFKRE*KKNDVLEAKNFFT ILTNNNTTKEKNVAQRIGSLFEG
10982	24883	A	11075	412	1	QFFFLVGCCTPIFGVGGKGEKKKKRQ FPPRVFFFNQIFSPFFFGPFFFLGK FPPFGRRLFLFSKSKFFFGVFKRGFP FPPKNFFFP*RF*KFWSPPKPFPPFF FFF*DRASLCIHPNSTVAQS*LTSC
10983	24884	A	11076	279	410	VPCCVAGRDRGAFGVIAFFAOKPFDGG FPGP*SAGVGPPPIPR
10984	24885	A	11077	12	386	IAHLLLSFYHKDTGTYLLFLGAGAGVL STALSLLIRAEKGQPGIIVGNDHYNVI VTAHAFGIIFFIIPILIGCYGN*LATL IIGAPDMAFPRINNISFGLLPTSLILLLL AYALVDAGARTGW
10985	24886	A	11078	412	3	IAILSLSLSIGFPYSIRYKNIKIRPINN PMAKSKSSKRTETPFLKNIEMLEKL ISKSTANAKILKVLFLVFSQVTAHKK FLKEIKSAIPLAHQMR*QTSLIADMEK VSVL*IKDPTSYNIPISQS*THSK
10986	24887	A	11079	78	443	RHLPSDTCLTAAVFP*PKGSKKKKKKK KKKKKKKKKKKKKKKKKKGGGFKQNS GGQGNFAGGKKKIFFFFGVFIKPLMIF WKKTFWGGKISGQLSQKLSLWGEKKI FWGCGETSF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
						LQAHRAHHLAIDTYQEFETTYIPKQDKY SLIHDSQTSF*PSDYIPTPCSMEETQK SNVELLRICLLV
11007	24908	A	11100	1	359	LQLPFLTLVLGTAHLPAHCLAYATALIL GCALLCLA*VE*ARAAQTVPQSNF*DHA MLQAHRAHQLAIDTYHEFETTYIPQDQK YSFLHDYQTSFCLSYIATPSNMEETQK KSNLELL
11008	24909	A	11101	1	370	LPELPLTLMTAHLVMAHPSRTSLLLAF ALLCLPWLQAGADQTV*SWLFDRAVL QAHRAHQLAIRTQYQEFETTYIPKQDKS FLHDSQTSF*CF*DSIATPSNMEETQKS NLELLPISLLL
11009	24910	A	11102	2	361	AHLAVAPGYRTYLLLAFLCLPWLQ AGAVQTV*SRFLDHAHLQAHRAHQLA IDTYQEFETTYIPKQDKYSFLHDSQTSF FSDSITTPCNMEETQKSNL*LIRICLL LINESWMEP
11010	24911	A	11103	8	366	PLRALMTAHLAARAPGSRSTILLALLL CLPWLQAGA*QTVPSRLLDHAMLQAH RAHQLPIDTYHEFETTYIPKQDKSFLH DSQTSF*CF*DSIATPSNMEETQKSNLE LLRIFLL
11011	24912	A	11104	3	341	EPLDLMTAHLVMAHPSRTSLLLAF LCLPWL*EAGAAQTALFLPLDHAHLQAH HRAHQLYIDTYQEFETTYIPKQDKYSFL HDSQTSF*CFSDSITTPCNMEETHQRSLN E
11012	24913	A	11105	240	329	ENMPGAEAHYTYDSTLGRGRQIT*GRG FE
11013	24914	A	11106	2	316	HEERERERERERESALVQIHTQGBGLT ELVFPYRRAPAPSGLKFTFVYVQEHILGV GGNGLSPILQIGVILRDGRGLAHLRCGTR NKILRLKSGRAPDLS*DLV
11014	24915	A	11107	169	1	EDGHHGSLHSGKQQRPAWPSMVTHTCN NTLGGRGGWIT*GQEFETSLTNMEKCL PMTLGGQGGRT*QGEFFENLAYRGK
11015	24916	A	11108	192	355	GMSLGHNSYILNLNLFWPCVVAHTCN PMTLGGQGGRT*QGEFFENLAYRGK
11016	24917	A	11109	145	383	EVNRDGRKYHVSQGISFVYVYVYFRR LIYTMITVNSALLYTELVIQGRRLV FDGFP*FWFETESCSVQAGEQ*CDLG
11017	24918	A	11110	199	400	TIKGFPPFPFLRLGRGPGGAPFPLNPL GGRGQGF*IPKKKIYPLLLPLFLVKQNT PSKPPFFFFFLRQVLLCCPGWSAMAR SRLTA
11018	24919	A	11111	373	177	QFETSLGMSGSPSYLKI*XSARGCHTC MRFLQLQRQSRSDHLSGVRHCNP*LH RCITTNVTK
11019	24920	A	11112	204	399	NHFDVVVTHFSPPFF*FEFFENLCSVPR ARDQGMNLS*INPLDPLQLQFFA*PSQE AGIIGPHH
11020	24921	A	11113	192	16	EKTENNKR*RGYGSTETPAHCGRACILG *PLNKPV*QFLKKLKKMLPZDPTIPLPA IFS
11021	24922	A	11114	113	369	AGGQGNLFLQKFGPPGT.KGPPPT.PLP GGNYGGGPPSGRIGF*FEKKGFGGVPKV GPNLRG*RLDLPAPSKAHLPLNGGFSR N

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to last amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						FFFFFFFFFFFFFFFF*TOPHLS PRLECSGTISAHYNLHLPGSDC
11041	24942	A	11134	361	2	ASQSAGITGVSETRTPHGFQDT*RKPA EPEVTIH*I*ITLMSCNIESPEKVCADL IRGAKENLKVKKPAGTPIKASRTITRK TPCEGSNTRDRFQMRHKLWLDLHSPFD GRVGGRV
11042	24943	A	11135	1	370	IRQTFPKREIVGILICYVNVGYYSQIH *SSRLMWIFHYRVIVSVKIVLVLVPH EKKKKKKKKKKKKKKKKK
11043	24944	A	11136	273	2	GGRAGQQLFCRGINLGFPRSCQCTFRS PFGAL*FWECFSLPALKIRFPSPFLPF FFGKPSRLSPLELCNGVTVAICNLRLP GSSNFP
11044	24945	A	11137	130	354	GQLNKISGYPYPRNVGTYLPLVNLPLQF VIVSTIFAGTLITALGSH*FFT*VGLEI NMLAFIPVLTKKKKKGGPL
11045	24946	A	11138	366	2	LVEMGFLEVRQNLGLLTS*SAKGLSK CNDYREPPCPASDWVFLTSPLHLALD GKEHTHTHTHTHTGLGICQSSLGKQS GGWGLSANRGQSPFAVCLVSLPLPEV PVVTSALFT
11046	24947	A	11139	228	1	CRAGRLPAAVLITLFPPLLIPTSKYLI NNRLITTOQ*LIKLTSKQMLPNTKGR T*SLILVSLIIFKATNLLG
11047	24948	A	11140	157	337	HIPTPHHTCPEPSSIRHNSIYYLKRYC LLRILISLLPLQTS*PLTGALSLLMT SGLSM*SHLSITLLALRLTYTLTIYQ *WRDVSRETYQRHHTPPVQGLRYGII VFSTSKDIVSGSLF*AFYHSRLAPPTQL *CHNPSPGILTLN
11048	24949	A	11141	188	3	IPTPGGPFPLFPKVLKFGNPRAPPGV FFFFFFFFTDSRSVRLCSCGVI*AH*NLH FRGR
11049	24950	A	11142	224	3	SVSFFCIYNHVRVDSALLQESTSSR EVMTHGFHYLIYET*LRSLAQSLALC SGTISAHCNLRLPGSSN
11050	24951	A	11143	262	371	SYCGPGVVAHAYNFTSLGGRGRIT*GQ EFETSLTN
11051	24952	A	11144	244	379	TIGKORCHAGIEEVSQAPALKPVP AL*EARAGGLEPRSLR
11052	24953	A	11145	1397	1565	DRLESILLEHIPPVYNQWNTNFYLFY FEASHSVAQTGLQ*KHLGSLQLPFPQV
11053	24954	A	11146	284	1	GRGRGGDSSGGEGGNRAVDITGSLVGK GGAGRAFVAVVWKEIRGFVVEGDMQ KERVVD*GL*GGRRERERERERERE RRERKRESLV
11054	24955	A	11147	64	286	THALATNRQRTGSGHGAMCLYSHLRK LRQNDHLTPGV*KCLEL*LEH*TPTWTT KPTAKAIFPNLKQDSWD
11055	24956	A	11148	230	358	VSVSLITELATNLLGLLPSPFTPTQL SINLSMAIPL*AGNV
11056	24957	A	11149	81	367	QTLTRKAKGVASHLDPTPLGLEPHEL IILFPPHLYPSCKVDVNNRLNTTQQ*LI ELTWEMQMITHTKGR*CLILECLIMV IATTELGLGLP
11057	24958	A	11150	257	2	SVCAVITKYLELGCADAAADTORLPPA TVKLTMFNLATHGELGICP*LFVDEK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
						PKTARNFHALSTGRK*PSYRGSCFHRILP
11058	24959	A	11151	257	1	WRGGEKETLRWCWECKLVQSLGRTVVR FVRELKRLPFPNPAIPLLGHPKREK*L DPCPCMFIVALVTIARWVNPQKPCPSMDL V
11059	24960	A	11152	17	367	NHKGKKTEKKQSTSPQKQDCSSPAM ESGWTEWDFDELREBGRFRSNYELQEEL QTKGEVKHFEK*DKCITRITWENCL KEAMELKAKARELCEBCRSLSRCDQLE ERUSA
11060	24961	A	11153	213	2	TFCHFFFFFTESGSAQPGVWRCDLGS LQAPLPGPTPSMRQRLQ*AEIVPLHSR LKLHFKKKAGVFSC
11061	24962	A	11154	1	347	GTSHFFPLTYQVHNSIDYPRNRCIN PSLRFTSSKPLPARPHIMTHQSHAYHI VKPSP*PLTGALLALLMTSGLAN*FHFH STITJILCJLNTLSYQ*WRDVREST YQG
11062	24963	A	11155	223	3	YSTNLRLRNHPLFF*DRVLCLCPGWS AVASSRLTANSASCLSLPSSWDYRRAEP HPANFCTDRFHVGVQV
11063	24964	A	11156	143	1	ROFLNQCSQNFPPFFFTESCSVTQAG MKWYDLS*MQPPPPR*KLIV
11064	24965	A	11157	149	355	LQPLPGGFERFSCRLRLISWDYKDVDS ALLSNVPT*KYISKTLGRHQSPETVREF LTAMKSHLTKVG
11065	24966	A	11158	156	370	RSDGQKIPRNLGGWSVLMHTVDEQ*G PNRYIKKCSASLIREHINTVRRCLT PATMATVRRKITSVG
11066	24967	A	11159	298	4	HPQVIMRRQLVGRQAQKNAALPTDSH THLCYLKCVYFCVCMCI CVFVCV*SR AL*SLYLFCLCAVAGHSVSGLESQH YGRLRQADHLRSGV
11067	24968	A	11160	364	285	NSWGIKILKGR*PPPKIKIFPPKYPQS FPLSP*KKKTNPFRKXLYLSPGIFLK ADPPLIFFFFFFFFFPPPPPPFPG
11068	24969	A	11161	198	406	KSVMTLKRRGSPHERGDVPAICNFF *IHYIMCVYIHCYIYIYTHIYIYTHI QIYIYIYIYIY
11069	24970	A	11162	95	376	KITTRHARTNPYTCINM*LEITLQG EPKLRPPKPKDKKKKKKKKKKKKKKK KKKKKKKKKKKKKKGGGGPKKKGGGP KIRGEEKIPFFPLGDD
11070	24971	A	11163	343	391	WR*LSSTRHNDILLTLLFRARAGVLR AVSLLILABGGQPGMLGDHLYSALDP ABAFAMFTVIVPLILCOFN*LLAVRN GAPMAIPIHNNISC*RLPPSILLLLAS AIVRAGAGTG*TAYPDLF
11071	24972	A	11164	1	158	QMTNRRGLSP*PLTGALSALLTKSGL AM*FHFHSITLLILGLLNTLYQ*WR DVITRES
11072	24973	A	11165	265	466	KILTSLSFNNLRRTVGLRLSQAKY KKTPLRGTVAHVCPNSTLGGQGGNIT*A QEFETSLANVA
11073	24974	A	11166	204	458	KRCLLPLPDSNTQSSQCRREIGRAIR KILTFETQNIKRLKTEQLLKLLE*SGK LTAHCNLDLPSSSPPTSASQAGITAG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
11074	24975	A	11167	256	3	S KILFFKRGVLSPPWGGVNFQQLMPPFQGG PPKKRGPLSPPKGPPFFFFFFFFFF*ESR SLLPKLSCSGAISTHNCNCRLGSSRTG
11075	24976	A	11168	1	457	HRTPSVPTNCRGDPKRVSTNKKDITGL YLLFGA*AGVLTALTLIRALGQGN LGNNDHINWICTAHAPVLIIFVILPII IGGPGN*LVPLIIGAPDVAFPRINNISC *LLPPSLLLLRASAIVEAGAGTG*TVYP PLAGNYSHPGAS
11076	24977	A	11169	343	428	GR*LFSTNNDIGLLYLLFGA*AGVLT ALSLLIRALGQGNLGNNDHINWICT GHAFVIIFFIEPIIIGGPGN*LVPLIIG APDMAFPRINNISF*LLPSTLLLLLAS GIGEGAGAGTG*TVYPLAGNYSHPGAY DLT
11077	24978	A	11170	91	2	PRODPSF*FFFF*TESGSAQAGVQWCD L
11078	24979	A	11171	219	1	IFGSKILCLPPPEPNFFFFFFFFFFF FMRHGGACCSPLYGG*GERMT*ASRV AGTGVCHYAWLIFVFL
11079	24980	A	11172	292	365	RI*SLGQAQWLTPTVPTLWEAKVG
11080	24981	A	11173	251	1	ICDLQILTHGTTCTVKGHLLTLFVSGIT FLIIHSLAIKPGV*KNPS*LGTVVHCN LS*GGGRLA*AREFTCLGNIVRP
11081	24982	A	11174	200	407	KLFETDVTCKSNLLCNASLSFSRYTG GPFYALN**FLSYPSFLETSSHIVAPLE CSGMILAHNCL
11082	24983	A	11175	11	155	STNFFLPSETGSGSVLQAGVQNPGLDLL ASSHSIPAS*VSGTTVDA
11083	24984	A	11176	140	1	PSTFPDVMARVSVCLSGDKGV*WLT PVIPAIWEAKGGSPESI
11084	24985	A	11177	210	1	TDEELLLEDRK*FIEMESTPDEDAVN IVRPMKDLLEYINVD*VWAGLKRDC SPERSSTVGKMLSN
11085	24986	A	11178	133	148	STSTR*LFSTRKDIGAHLFGA*AGV LGTAVSLLIRAWLAQLGNSKEA
11086	24987	A	11179	236	1	KFWKKPLTKGKCPDKRGGGIFSRKK KNVFFPKKKPKGGKKNFFFFKKKKKK KKKKKKKE*LFISFAHIAVHL
11087	24988	A	11180	210	1	QSLGQRNLQVFFPLFGP*PNYLDKGEKN IRVGKIWHGLFFFETESRSVAQSPRLC CSGAIAAHNCLP
11088	24989	A	11181	292	348	KKGALFFSPGG*KNFPPGGKKKGPLFS KKKNNP*KKGRKKTRPPPLGLGLG GFLAKCGKPPNNVLADPNPPGGKKKK KTPSPGKKKKKKP
11089	24990	A	11182	168	3	KPEASMLNDYFF*EAGSHVAHABVQ WYCCSLQPPPTPLSDPLAPSKVGLIT
11090	24991	A	11183	87	351	KGIKWSLIIQBGVQPLHSYNSFFSFF S*DWILRLRSCSTTTAHSLNLPSSD PIPTSASQAAGTGMHCHTRLIF*ETGFH HAVQ
11091	24992	A	11184	55	344	TSINLCFFFFWKGKSPFLPPGGDEGPL FGQLDTRPWGIEKIFAPP*KGKRGVP PGGEFKNPAPKGPPLS*KK*NQPGQ GAPPTPPFLGGAKKIFSPQGRVSN* PKRGSPSPGGKGDSPQKKKKQGR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, />=possible nucleotide deletion, />possible nucleotide insertion)
11092	24993	A	11185	344	190	EV*+PNSPGAP LVTRTRHVSQDGLNHLLTL*STRGLSP KCWDYRCBPFRPANTANSINFP
11093	24994	A	11186	135	3	IFPKVFGGPPPPPPFF*ETESRVAQVG VQWNLGSLQAPPGPPT
11094	24995	A	11187	305	14	IMLITSIRSRSLSSIAEKGLSLRLAIG RVAKYILNNRLITTR*LIKLTSSQMIT ILNTKGR*SLILVSLSVVGYHLP* FD*SILLY
11095	24996	A	11188	198	1	LEQTFRMFPFNKSLIGTSPSGFLKSL FPFLIAFF*DEVFLILSR*ECNGTILAH CNCLPGSSD
11096	24997	A	11189	352	3	QLCNTPLPKTNHMLTSGNANTLIYRS AIAAASDPIILPASKILLNSRLITPHO *LILKASKOMIALPNTKGR*SLILVSL IICFEVSLISHCWVVISRLMRYLEVG NRGG
11097	24998	A	11190	270	137	CIINRLVVCVYIIYIIYIIYI*YIFMYV YNILCILGHRRESGVI
11098	24999	A	11191	18	342	ACRRKRMSKFAIRATGNCYYSCTFCSI SFPHPK*MPCYQKKKKKKKKKKKKKK KITV*K*SKTKNIKIKGLGAR*ELSLA*L LGEPPIFAKGHPMLMKWVEICKRP
11099	25000	A	11192	169	3	ERSGIIRVYQ*NQCLAWSLA*KIIRPW LAAVARTCNPSGGRHWIT*GQEFK
11100	25001	A	11193	407	1	KRACFRMLTLLSTLWEAKQENCLNAGV HQPGQRBETSPQRIKSAWHGGHRL* EVRWED*LSQGG*GYSEPCSHCTPANA TERDPV*KOKRSIPNKLASERKDSGR RNLVREMMPSQQAQSVIQVRI*ST
11101	25002	A	11194	110	412	VCGFRLLHSPAILMLPMSYPRRHSNT EIKPISNPTVASKRASKKSTSLTNLQ KLEMIKLSEAT*KAEVQKGLGLHQRV SQVNAKEEFLKEIESA
11102	25003	A	11195	34	155	ANHEGMRHVSDGLNLTL*DACGLPK SNDYRRKPPCPA
11103	25004	A	11196	289	453	NQPGKSPMISTTFPMRQETFLVHGV*W LDLGLQPPPPRFRKPSCLHLPSGMDR
11104	25005	A	11197	177	432	KWERQATLGGGNPPGPKTRVGNRPER LRGNPFFLC*KRGRKGDTPWPKKAPS GERGIPGKGGKTPGPGFGPMKIKRG K
11105	25006	A	11198	139	3	AMVSLSPRLCSCSMIARCSLGSGSSD PPTSAP*VARITGMHDP
11106	25007	A	11199	150	492	GDPLRGHPHV*EVRRFFARQLPRLRSEE PLRPVATPSGK*GASLSGSHPIQGGGG GQPLPGHLPHPGWRSGVKPPGQEARPG QSKHLLPATPTVK*GGPGSQDHLSSGR RE
11107	25008	A	11200	239	64	VQRYYYIYFF*TFESRVARVSSGLSL AHCHILPGSRQLCLPPTSAVFGQESH IT
11108	25009	A	11201	31	396	ILIMRRIVHQAGQCRNIGAKFREVIT DEHGMDPTGTTHGSDLDLDRISVYVNE ATGGKYVPRAILVDL*PGTMDSVSGPFF GQIFRPDNPVFGQSGAGNNAKCIYTKG ARIGDSVLVD
11109	25010	A	11202	85	407	VLLPHSEALRGADTMPSYFALSQRK



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						KKKKKKKKKKKKKRGGGGGANTKPTV GENRKPLPLFFFF
11131	25032	A	11226	271	3	NFLSVFNFTRICLGMCFSLIFLLIFGGS LKYQLFLAOGFFFFFLAYFFTSSIHSSLL Y*MLDFLDLFFLYLFFCFNFVSVLFCIL LSKFF
11132	25033	A	11227	3	413	SPASPFRSYTWANVKVGVNGFGRTERLV TRAAPNSGKVDIVAINDPFIDLINMYVM FCYDSTHGKFLGTVAARAKLVINGNPI TTFHURDSCKIKRGDAGARYV*STGVF TMDNAGAHLLG*ATRGILSAPSD
11133	25034	A	11228	48	413	VTVLVSGFFFFFWKKKICFPWFGCKK RGKIGTGTGTFPGPKGNTRGPPPNKCKK GGPPPPNNNGFLKCKKFPQGGGG*KT RNFCKPPAPNPPKGGDLGGGPPQTGGNG FLKCKKCKK
11134	25035	A	11229	172	404	EFENSCSQWQRRGVMIQGVTVDMNQO EFTRALVALKKSRKLVPEWVDTKLIA KRKSLTL*DEKMFYT*AASTT
11135	25036	A	11230	247	2	QPKKGVSKKKKSLPCDPAIPLPGIYP KEKSVYKIDNHLRLVYCRVFTIAKIN NQPKC*SGDK*IKKI*YITVLDLR
11136	25037	A	11231	1	372	TETTVVAVCEQLDRKLTKSQRKFKEE AEKLGKGLQPNIVRFYDSWESTVKGKKC ILVLTVELMTSGTLKT*VQYYS*PRSM RSFDFLAFRSTFSLTVQPKNGTVLPTV TVLAYFLAHKVL
11137	25038	A	11232	311	464	KKATPRNLQWPGTVVAHCKNPSTLEGRD GWIT*QGEFTSLTNWVPP
11138	25039	A	11233	64	418	VFVASRRERECGRVGGGAMADLAKNLI DSIIQRLL*GA*GAKPGKVLQVHENEITG LCLEPREIFLRQPIIL*LVAPLKTQGD HGPPYDLRLLFYRGLPPEKSNYLFLEDY VDRRQH
11139	25040	A	11234	233	421	PTTSNRSLRLRGASS*KKTAGPOORN EPALPRRWGRSADNPFGSLRSGKNM OKTGTGA
11140	25041	A	11235	343	1	NNTHGLSHSVGRNPGAVGGSGCSGTX LSEGLRSLLEAVCSRAAVIKCHSWVAS NNRHFFSPSSGG*KSEAKWAGPCSL*R RVPSLPLPASGGSRHCLVGCVTFFSAF TW
11141	25042	A	11236	122	419	RTPRGPKNPGLOKRTFFLTGGRIKTYL GLKGLLFFKGRWDTLLPKI*RSREN KNF*REKVALDPTGCLKNGARQGHFA HLLILRDTKTYMLAF
11142	25043	A	11237	1	379	AFNHLAAGHGLGAAKSEVLLLCILQL WGHSSPHGPMWLYYQPKDDP*TEKAS LKAIDYINQNLPGYKHTLAHIDEVYKV PQ*PSGELFDIEIDTLETTCHVLDPTV A*CNVROLNEHAVO
11143	25044	A	11238	1	397	OTMTNPRGLPCSDLRSEHVISLPLHS ATHTRPTNQHNTNIPMARSTRKILIR APHTTCPKRPSIRDNPITYLRNFLRRI FLSLLPLQPSYPPIRKALAPNRHHPAK SPRRPTP*PLTGALSALLKTSGLAM*FH FHSIALLLGLLINTLTITYO*WRDVALE STYEGEHTPPVQGLRYGILLITPSRIF



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						FFAGFF*AFYIISLAPTPOLQGHMPPTG ITPLNPLEDFLLNTSVLLASGVST
11144	25045	A	11239	267	3	PVSVRITFTYASAAATWLSYVWVWASSFN VCPDGRVALSPRVECSOTTSAVRNRLRL PGSGDYPA*PADGWAPPQYRCPFPRL ANF
11145	25046	A	11240	391	31	VFFFFFFFFFFFFFFFFFFFFFFFFF LKNPFRPPNNFFFCPK*ILPLN*TF *IKT*I*KI PGFFLNPPFFPPFFPP IKLFFFF*EGVLPDSGWSAMSHLLS EKRLKTPRMSYN
11146	25047	A	11241	371	491	KTFCKARHDAHACNPSIFRGGGHIT* GQFKTSLANV
11147	25048	A	11242	1	221	HKIDPLCRSAAAFPLSVCHCRVSDQ LDLLTS*SAHLGLPKWCYRCKPPRAL NCFPKTISQILNLCIKD
11148	25049	A	11243	382	333	TVYKIDFKTF*RWPHNSVRVSAKLEL SRGQRQFLARSESSPGGFTLSVR
11149	25050	A	11244	169	477	TQKDEKSTTTTKGANSKQSAVSSPS DCNTSLARAQ*ERAFMDDELTEVGFRRR VIMNFVKLGKHLTQCREAENHDKTLQK LLTSITSLAWNINDLMELK
11150	25051	A	11245	200	462	SLIYNELCTHILYQYVA*QRS*CFQ LMSFY*RTLKNLSESLCKVALLYPSFLK WKRGLWTGADT*KPSTGGQGRIA*A QEF
11151	25052	A	11246	484	301	ITCEKGL*FOLLRRVRKSPFNPNQGS CS*LLSSPCPPGWITR*DPVSQKKKERK RMQVNLVSAQENKPKPSVOLQACARS MLAFSTTPR
11152	25053	A	11247	226	458	NTVAVGAPKCFPSLLSHAENCDMFT KRLFTPHMLLLKQDLMLR*QGAHAC NPSTLGGGGWIT*GQFFTS
11153	25054	A	11248	304	436	SPSRCK*KTG*QWLT*PVISTLWEAKV GRSLDPNRSANTWY
11154	25055	A	11249	216	451	THKYLFFYLGYNPMYIERTGSCSLA* AGVQWYSHOHLHP*PSGLKSSQVAGVI CLANFFFFFLKWSLUVLPRLG
11155	25056	A	11250	260	474	DKYFLLYPLKALNVVLGAHINI*RVSKI MC*K*DKNMYNFFFS*GVSLLLPRIG CNGTILAHCNCLPC
11156	25057	A	11252	193	496	MTSCSYFL*IKDASVVKKKKKKKKK KKKKKKKKKKKKKKSSQQAQDYS KASDYK
11157	25058	A	11253	348	478	DLGNLKGITVAITYNSTSGGGRIT* GQFKTSLANVVKPC
11158	25059	A	11254	174	475	MHWVLILQDIDDT*NONLHFTSLCSQ LSIQEKKKKKKKKKKKKKKKKKST
11159	25060	A	11255	292	48	LPLTCHRPVSRHTLAFSNPTAGITIF* TRSSSWNAGTFTII PKIVTFPLFFF*ER VSLKLTLEERSGAIPAHCNHLPEF
11160	25061	A	11256	347	16	TQSANWCYNP*PAHKSSSPSPHPQ*PS WLHAWDAPGPNVLTSPASACTPQP LGSKWDPQSKQCGPSGRLPQGSFPQ VGLGAGNRQALPVQIATSLIESHW
11161	25062	A	11257	238	590	ANGAYIFPGGHPTDSQVFTSLASILL ICPLCISVLPHNGMINDENNNNAIHA RACAHARTHTHTHTHTLVMNVRTLL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end-nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
11162	25063	A	11258	310	461	MLLKTRGRATGSHARCIFPS*SLIQACP LSFGDVLQLSDRPGAVARTCGFSLGG *GGWIT*GKEFFETSLANNLKPR
11163	25064	A	11259	461	174	MGPFRVSSQGLDLIT*SSAHLGLPKKCD Y*CEPLRLAPVGLFKCVQYGLVLCHGS GYMSMWIKIRMPGLTWSLGGGSAVVER YWSIWEISFGC
11164	25065	A	11260	343	472	LLRRRLQRKDCLSGGQGCSEPRDYCTP ARVTK*DPVSHKOR
11165	25066	A	11261	229	3	VKRLQ*VPVRVKI*KYTTLGLIYLKEL KGFGRNTCTLANFIALEFTIANRWMQPR LP*IGBCVNNM*YTHWGS
11166	25067	A	11263	163	399	KLLPFRNLHAHEHPTFWLNLPHNTAQ Q*HPLSSSLARWRAHLWCYLCITSS SSCIITAGYPN*EGMPASQHKHVV
11167	25068	A	11264	316	427	TNKKHIT*ITNTTTHLSITISITPLLPNQ INNNLFS
11168	25069	A	11265	184	418	KTPPGFFEKNPFFWGGKQGP*PPPKNLP LGKKKKFLKNGGKTKTFFFF*KGSS SPPP*PPGEGQAP*PPPKSPPR
11169	25070	A	11266	219	13	KFFFSLEHNTGGGOVH,PPPKRGFLP KKPKQGFITPPLKQKIKP*PPPGYSGPP RVL*KGPPHIFX
11170	25071	A	11267	3	173	SHARPETGFRHVSQDGLDLT*SACL GLPKCDWYRREP*PQARKLYCLGRNTE
11171	25072	A	11268	157	2	PUNIT*HVKITVGLGWVAHCNPSITLGR GGRIT*ARGSRFLLPHTWSEL
11172	25073	A	11269	291	468	ISEGKRSILFVILHFLFFETGSCSVAQA GVQWCDLDSL*PHIPGPK*SSHGLLHTG ACH
11173	25074	A	11270	29	478	GNNFYNQQDIGHTLYL*SGRAGVLOTAL CLLIRAEGLQPDLLGNHLYNVITAH AFAT*FFVTPLLIQGGN*LVPLTGA PDMAVPRINNIS*LLPTSLLLLASAI APAGA*TG*TVYPPLAGYSHPGACVLT TIFSLILAGV
11174	25075	A	11271	61	474	PYNQGNDAHAWPHLTKWRSQGTTEIC REPBGAWQRPQPRLHKGRSPGQRLALS QNI.PSYSGSHLLSAYVVDITISIGHFIN TIGWLGTVAHACNPSTL*GEDRWIT*AQ EFKTS LANVL
11175	25076	A	11272	277	478	KIYQPVKITHGPRGVAETCNPSITLGR DGWIT*GQEFETSLANNSPSL
11176	25077	A	11273	350	11	KEKTAQQRWLTVPVIALWEARAQSPSE VRSSRPA*PPP
11177	25078	A	11274	138	3	NYINLYAWLGAVAHACNPSTLGGRGWI A*AQEFKTS LGNMAKP
11178	25079	A	11275	359	219	FVIKMGFPQVGRDGRNPLAS*SAPIGLP KMWYRHH*PEERLALFFFF
11179	25080	A	11276	262	3	FCMSLVHLFSSHQDNYTFS*SL*IFNIP SGPFLFAQDITLQ*P*DFIYFYFETES SVTRLSCSGAISAHCNRLLVSSNSPAS AS
11180	25081	A	11277	285	1	VKKQDSVSKITFRKKKKRDKILHPIYIT TVNNLIGIIGNLNMKKIYKNPTANIIL NGERLKA*PSL*SGTRMSPLTPTF*ILV DTQQVYIFMSH
11181	25082	A	11278	160	3	TDKEVPLINAQRKNFLBMSIPGEDAMN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US95/09515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
11182	25083	A	11279	334	488	IV*MTTKELQYVILNLVKEVLARPE PLNTCY*NIN*NFQPSGVAPACNPST LGGQDRWIT*QGFETSLANNVK
11183	25084	A	11280	527	356	FFVFLVETAFHHVAQDSGLLELTS*SSKL NL*PCWDYRHPQRQAQVGVGFSETRSI Q
11184	25085	A	11281	486	248	VRQLFSLLLPRELCRGVISAHCNLRLEP SCDSSASAS*VARITGASGQAVLVQVQ CLQFVQVQGLLRVDLQFLVQLQR
11185	25086	A	11282	38	157	STGLHHVSDQGVDLTS*STLPKWDYR HDPLRPASQRL
11186	25087	A	11283	474	339	FFVFLVQSGFHHVQVQGLLELTS*SAICG LPKWD*RIEPTPAK
11187	25088	A	11284	2	462	LETTTARNHSEVIALRHHS CPYKMANL IDKVCVSDYSDWPP*IFLPLRPFPYCL RHNNMETRS INNPWPS KCSSEKTNVEG MLKVIQ*KLCLLCQTS KDMNAKFFL KEIKSATPMNTSMIRKQRLIHDMEKVL VIRIKYQASHNIL
11188	25089	A	11285	65	280	SRAVEPNLIT*SAICGLPKWDYRCEP PHPAS*FSKLSSNLEKTLSSSL*DSHS GFYSFVCSLGLILLI
11189	25090	A	11286	244	488	MRIGRVPSVLFCYVRMQREGITLAEKNK PSPDIESVGAILIDFTASRTIRNKLILF IIFPG*GILDSPNPV
11190	25091	A	11287	345	445	KRPGTVAHACNPHTLGG*GRWIT*QGF WTILA
11191	25092	A	11288	223	500	SPGTRPKVLEQSTLQRAILLGSGWL WQSHRLGVQSQCLCLCVLWDLTCSLSCS FQILKLR*RPGVVHTCNPTSLGGCGGR LQGOEFK
11192	25093	A	11289	157	22	LSQGVKSGIGEAEIKQAQWLPPIIPAL WGAKVG*SPEVRSKPA
11193	25094	A	11290	305	497	KLVNCTYPKGVSTYRRELYCNKIV*HLG TVAHYNPSALQACCNIT*QGFETSL TNNAKPL
11194	25095	A	11291	478	1145	QHVQACPERPQMQLERSRAVASIKHS SYSLDSQPARAVGKPPWQCACTRVTELT EATGKLIRTSHTGKPHQSPQPAAPATQK LRPASQQGVQMTQGGASNPALQIGSHF MCKSGQPKSDQSNPSTVKHSQPKPFIHV PSQPKSSQTKSCQSPSQTKPCKGTQ PKPKSQPWPPQSKPSQPRPPQKSSSTNP SQAKAHHSKAGQKRGKH*RANSRDL
11195	25096	A	11292	352	468	TFPQGHGKIPSLILKIQKLACHGDACL*S RLSPR
11196	25097	A	11293	295	24	ENTQCSKKNRQHMNGVITWNSNPGFV STWVYRNCLACIDISFSFKWVKSHRDT SGMPTAALFTIAKT*NSGTCSMVVDYN STRTS
11197	25098	A	11294	274	429	BCEHVOTLWKIRKPLKKLKTETLPSDFAI PLKGINLKEKGV*SDYTFPWC
11198	25099	A	11295	168	469	PSLGNKSETPSKPKKRLFLGFFVFRK LVGILLKTVLQKAGGVFFGPKNPPEKN PDPLDPSPKTFRRLGAFVKTFPKGLKA AUVFPAIV*PQGMGG
11199	25100	A	11296	37	348	KTYFNKTKLYFKKKTKTKKKKKGGQPL KRPRGGPRITYPGGARNKPHIGTAKKH

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						GGYWEKNPHGGGNTGPTTPQKTRPLGG KNNLKRVPQGEKPRPRLAGGKTRSQLFSC HA*P*VQGEKPRPRLAGGK
11200	25101	A	11297	93	388	DEVASDNCYPPGSSHDSQVKGQIGSQPT TQIQAHNLAKPRRAL*NIIS*PMEMRSK CLLLAYKKKKKKKKKKKKKKKKKKKK PKYLSRGRDHF
11201	25102	A	11298	61	243	YYIHRITVPMONN*GLKENVDK*TIDLC LCKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKPQGGGA
11202	25103	A	11299	250	341	IYMSLTGLQNL*EIHLDKSHKLVQK QWNI PHANVNRQTQVALISDNIDIK ATTYKKKKKREXPTLANTYVNPNGAPK MKHLLNLKNERDQTVLQ
11203	25104	A	11300	3	285	DAWERKKRSQWQKTKTKAGVSPYLSI MAWNVNELNPLKKRHVA*CIKKTKSMI CVLQETNFIKDTRLKKIRGWKKIHPNR N*IKLAGVVY
11204	25105	A	11301	175	407	ASNPDVLQLKA*TSRGTTPN*ILLRVK RGSNSRNRNCWQWRTGMLLHC*QECK LVQPLWKTIVRILPDLESEL
11205	25106	A	11302	75	280	YHNLVLVYPHPPKRVK*KKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK FFPGGKKKQFFF
11206	25107	A	11303	299	3	IHASFLPRGCTIAPTVRCSHRSITSS TSDLTHYYYYYYYYP*LASQSVALAGV WDQLGSHNPPTAS*VASTAGASHARL IFNFFVEMEVSLYC
11207	25108	A	11304	137	323	PFTVNRGRHREKKNKQNLGLHDFLD NPILLF* KYLGRKKKKKKKKKKKKKK KQKKKK
11208	25109	A	11305	64	481	RPTREHVHVIVKPIP*ELTKLSALLMT QGLSM*FHHPSITLLILGLTNTLTLYQ *WRDETRESTYQGHHTPPVQKGLRYGI ILFITSEDLEFAGFP*AFVIGSLTPTPOL GGHNPPTGITPLNPLEVPLNLTSVLLA
11209	25110	A	11306	142	330	PFTVNRGRHREKKNKQNLGLHDFLD NPILLF* KYLGRKKKKKKKKKKKKKK KKKKKK
11210	25111	A	11307	239	440	RPWIRDNPYYLKSCFIPTPLSLPLQ PRPYPTRRALSPNRHHPAKSPSP*PL TGALSALLMTSDLTMGLHPHYITLLILG LLTNTLTLYQ*WRDETRESTYQGHHTPP VHKGGLGYGI ILFITSKVVPFARFF*AFY HSSLDPTPOLGGHNPPTGITPLNPLEV LINTVRL
11211	25112	A	11308	433	3	FPFPPDTRHSRSIIPFSPGRAGFINFA SKGQEPALPGGYTPSPKKKILAFCSPP LPTWKGNSKPSLGVGPLEFP*SPKSF CQFLNKGPTEKSPFKFPFPAAGCVPF FSBGGPPCLFLFPFDPWICHPGWISV ARS
11212	25113	A	11309	2	423	GRVGR*LPYTRHMDIGHLLYLLFA*SG VLGTALSLTRHGLGQKNNLNDHTYN GIVTDHAFDIIFFLAIPIIIGGPN*LV PLIIGAPDMANINNISV*LLPSSL LLAYAIVBAGAGTG*TVYPALAGNYSHP
11213	25114	A	11310	234	1	TPFGKFPCLKKPKPAQRGENTPGPPPP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Yrosine, X=Unknown, *Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
						LVFFFEHEGRSVAGTGVQVWRDLLGSSN SPTSAS*VAGTTGACHHARLIF
11214	25115	A	11311	406	211	LSLPIHSLISTEGARPTDPVGLVPTQDG LDLLTS*SAHIGLPKWDYRRAPFCPAC GFDIHLND
11215	25116	A	11312	379	398	KT*NPTVRGSIPLNINPMASMTFSRKK KKKKKKKROGPIKKNPGGAKFNGGRKK IFSLKGGKKKPGGILEKKPPFGGKKG ENPFKKNGKLRKKK*RGKGKKPKQG GGKNGSSSAKTPWG
11216	25117	A	11313	390	489	RYLGVVAHACNPSTLGSGRWIT*QGE FETS
11217	25118	A	11314	286	434	ILWYNYISIKLLKIIYKGLVAHTCN PSTLGRGG*LGWRETS
11218	25119	A	11315	322	3	FFPYGCRQVVF*IVTKNDRLFSSYTK NLAKIYLG*YVYVPLLRKSLKKKGS FESNLSFK*VFLWSGTVAHTCN*PSILG RGMIA*GOELETSLTNERER
11219	25120	A	11316	251	389	TPFFFEFEHFHVQVGVGQSGSLQAP PQSHSLA*ASPCWDGG
11220	25121	A	11317	313	80	EYICPRCLSPFRD*FGHJHETFLKQL QKSAGCGAHLRSQLLRRLGDRVRCLK KRIYLSLNSLNSNNRQII
11221	25122	A	11318	145	410	APKTLKVALTSAAAARESTCQLGVDEL VIFLEINRSTQDRPGAVAHICNPRTLGG HGGWIT*AOEFKTNLANVKTIC
11222	25123	A	11319	393	3	NPFRIIPTSLPPLPLIFTPFFFFFKKI PPKPLFFGVHQTCQPSIFFFKNTYFPL FWFSNPFFLFLSPSRKGPFFSRFFFFK VGNPLFFLFFFFFPPFG*EGVSLLLPR LECKNTISAHYLRV
11223	25124	A	11320	135	1	HRDVKLEYAIRKNVPRGVAAHACNPST LGSRGWIT*GOEFETS
11224	25125	A	11321	282	2	NSESVLYREKDEERKVLGFLFPSKRV LESKITPFLHSGCKRSYFLKITTSTFL *PRVECSGVIIHNCCKLLGSGDPPTSA FPVARTGM
11225	25126	A	11322	149	30	WSGGGQVRLTPIPALMKAEAGSGPEV RSS*PVMPCILY
11226	25127	A	11323	316	399	STLGRGQIT*GREFETSLANMPNIS
11227	25128	A	11324	223	397	IIKAYQ*DVNRQIKIITIFQNKIKAKI KKMIWPAVVHVNPSTLG*GGWIT*G QE
11228	25129	A	11325	3	396	NYSTAALPLRGHIWGRWGITLYGSSPI YCRGINSTLGLYPLNASSNPHPRXLCKP KIYTHIAKCPIGHKIITYPANTPI*HH THHTHTHTL*DSLWPGSVARTCNHNT LGSWGRQIT*VQEFKTSIA
11229	25130	A	11326	113	442	KRYTQIRAHSEVLCGRHGWGITLNPVQT IQTWPPFPLPLCSRVTSKSHHFPVPL LPH*NRNNHHHHHHHHHHHNCPC* ECCANISDIAWSDKSCQEPVAAH
11230	25131	A	11327	145	3	ELDTCPNPFPCHRGVQCDIGSPQLLP PGPK*PCLSPSSNDYRCA
11231	25132	A	11328	189	1	KTNLLTSLKRLGLSSSVQC*SKSEK SMVCT*CAPSCIPLFLGKVAICNPS TLGGRGG
11232	25133	A	11329	193	405	ID*QTLTKKKKKKKKKKKKKKKKKKK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, N=Methionine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AYTSKKKT
11233	25134	A	11330	209	11	GGKRGTPPTINNIPNFFP*EKGSCCSS RAC*CNGEI*AMICPLRLPGSSNSPAJAS RVQETATTFS
11234	25135	A	11331	38	390	VDGSTVCKMGQSAGCGWSDRGIKAGCL K*QRQKKKKKKKKKKKKKKKKKKGGG LKKKLLFLPGQGEKPPFFFWGPPFFPGR FLKRGGKIKPGYKNNKLSGHPPPFI.GGG KKKKR
11235	25136	A	11332	38	326	VDGSTVCKMGQSAGCGWSDRGIKAGCL K*QRPKKKKKKKKKKKKKKKKKRGGG FLKKLFFPGQGEKIPFFFWGPPFFPGRG FKKKQGEKLNLF
11236	25137	A	11333	1	234	RTRGKNWMAPIKGGWVPTGRNGGEPYKH SPLSKNTWLGKKKKKKKKKKKKKKKKK PHDKIKDLFDVP*NNKQNLISIP
11237	25138	A	11334	244	398	INILYSGNNDLIFLIVFLFFPFP*RRPG EPFLIKGWLPLFGVNLRLKDL
11238	25139	A	11335	174	1	HQVYPTVROBHYKQSCQCYIKWNNWP DAVAHGCPGTGLGAQGGNI*GQKFERT RG
11239	25140	A	11336	148	411	LFFPHCYLLNADSIYLNEPKVYNLH LCVSAVCLLVPHSPHRTCLY*KKKKKK KKKKKKKKKKKKKKKKKKKKGGAPFK KLLF
11240	25141	A	11337	237	453	GORPLLSPREKGSFFFLLETFECPAQA EQGHNILG*LQLPLWG*SNLSVSSQEV GITGAGHRPLFFVF
11241	25142	A	11338	65	347	VCRVDDFVPEARTFPFKSI*EANNKNKI KPLLSFPQVPGSSEKCKTLDAFIGI LEELINUSSCNVLAILSLATGVTG KYGSVLPCLK
11242	25143	A	11339	158	393	VPCTHEGRIKGRCLPRTREAREERD KKIPPLGL*AGKLPQHSSTWPGKVVH ANNPSTLEGRGWIT*GLEFKTT
11243	25144	A	11340	117	3	GIRPGAVAHVCPNPSPLGG*GRWISRDWE L*TSLANIR
11244	25145	A	11341	292	60	SGOGLRLGAPRGKVGAKENWPIPKLGC LVKMKIKSLEEIYFSPPIK*FEIIDF FLGASFKDEVFLFVCLFVCF
11245	25146	A	11342	149	30	TQIFPPPPPPGKKKKKFFPKKKKKKKKK ERKIDRKNKQ*KGPGVGVSPLPFPPLG GOGGGFPOGLGFKTLPAPKGPWFP*KT QKFPRRGGGPKIPLPOGGGKKPSPG GQGSNKPFPPPPPPRGKKNFPSPKKK KKKKKKKERTKTNKK
11246	25147	A	11343	120	504	GVHRCCLNDWTRRPAAATAACPAKRP PPRRREHSQILLISFQGRWD*QDVN TPNLDHARDEKAKYLPPLVMTSPS HPTATGKHSNHTRCSPNPQRSPFPV IRSKSVSSREVEVA
11247	25148	A	11344	213	399	ALVHICLTTIIVQSLSSSKYLDRCQNV AHGCHENTLAGRGWIT*SQRETSLAN TVKPCCL
11248	25149	A	11345	308	3	NPTPRSGDLWVERGSPGAGNWGLSQT LRALIKATTSYSFYCFYFETGSHSVARA RVONYNPGSICGSSHLPTAS*GAGTI GMHHIAWLIPLFFVENE

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
11249	25150	A	11346	189	433	GHCAGTSLTLTHLGLSGAMELTIHLGLC LGRMKFIHTTCTILFLFLSATQAGGQG GDLS* LQPPPIGPKQFSCFSLPRSWD
11250	25151	A	11347	257	3	KWGLCFLTYKERMG*PLAKKKRIKGV F* FGLFFFFFETESHVPAQAHCNLSLDS SYSPASAS*VAGITGACHHQLIFIFYE
11251	25152	A	11348	159	434	LSPSCRDVGTYSARAHPPHTHTVRAHT HACTHVRATHHTHTAHGSHLYTKBPGL CTLPGSSK* PGLGGRAIATAQAHVACAG ITRAAPP
11252	25153	A	11349	240	406	IKTKLAKNSISGVNALSRSKPVVAHANW PSLQGRGROIT*GQHSISLANWVKP
11253	25154	A	11350	163	360	PQLQLWKYFLQN*LEELRKPQGNLLEG LACSRSRSPCAPVVRTERDVSVPQPR PGAGGRSPFF
11254	25155	A	11351	145	406	PLNSGAKPTLFPWSPRRPELNAPPPPPG EKEFFFFLGRGFLFAPQEBAGBNIV*G KFPFPG*REFFAPPPGQGNKGAPFFPP LFL
11255	25156	A	11352	122	337	ILWVLLLVRESLKFFFFLLFFLFFFT DVA*AAVQ*SDHSSRP*PPLGRSSTS AFRIAGAIGICHLY
11256	25157	A	11353	325	416	KCVYINGNA*WLPVPIPALWEGAGRS EV
11257	25158	A	11354	260	415	LEELONTACQLEPFLSRTETKQGLLS PRLFNIVLEVL*AVRQEKIKGI
11258	25159	A	11355	150	2	ISEISTKRNYPFLKNLGVVAHCNPS *RG*GGQTTTGGQDFQTSLANWVKP
11259	25160	A	11356	160	3	ENLKLINGSFFLKI IWLGVVVTCPNPS LGGQGRTP*AGRFKTSLGNVRRP
11260	25161	A	11357	235	408	GQPLAALFFPQWELHFFELLAHPWGKT VWRFL*PLKKGPHDPAIFLID IYPNK KW
11261	25162	A	11358	11	393	OTERTPTPKPHLYVSFFPNQDPOLOQ KLNTNRQNTHTKTPSVCHHQRPKVDKTT KIGKQSRKTKGNSKNQSASPPKECSS PATBQSWTENDFDELREBGR*SNYTL KEEVRTGKEVKNLE
11262	25163	A	11359	283	475	FMVSVSIVYFFPIPIFLFFENESSCVTQ AGVQWHDCLSFCL*VLASSPGNSSPVR
11263	25164	A	11360	266	407	LETHHSKTL*FWLGVARACNPSLTGG* GRWIT*GQBAIILANIVK
11264	25165	A	11361	93	1	DVLSTLLPRLCNGATSAH*NFRLPGSS NSS
11265	25166	A	11362	131	377	MEEMI KGRGLSKPPALSSYTLKSS*LK RVRRARRFLKGRFSLDLQVAGFFVCLP VFWDRVSLCHPGWSVVVSRLLTAALT
11266	25167	A	11363	212	392	QABRCAPLFIGVRKPKNLTHNLGTVAH TSNPSTLGG*GGQITWQGFETSLANNA KPCV
11267	25168	A	11364	141	3	NELMAHQNVLEWLGTVATYCPNPSVGR WIT*V*EFETSLANIVK
11268	25169	A	11365	215	384	ANFNTRPSTSLASKCPSEKRSRTLLPLN QKLEMI*LOEBATSKARTG*KLGLLHAI
11269	25170	A	11366	48	373	EFWRKBEVLEKISSSLKTHCYSLTCLL MPTLECTAAMAYSNLELPGTSCDPTCA S*VAGTTGACHRAPTVLKIPLDRIRIFF FFTIVTYPWCHTPADPAIFKANAR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
11270	25171	A	11367	310	2	GLICLNRENAYFFVIRIQISMSCLEKEKP ARYSSPYAKSVTRGEKKRQRFSLGRAPP IPFLFFI*IV*AESRSVAQAGQWLMHFS SLQTPP*RTSDSPASAS
11271	25172	A	11368	303	50	MFALNTRGVQSPVIFLGVFLLSIQIGFT CFKGFGRFKVLVFFLVGVFPSPFFFLRAR VLCCPGNSPTLGIK*SSCLGLPQCVMIT
11272	25173	A	11369	109	419	QSNASLSHFTSPPLSVADR*LFSTOHKD IGALYLLFGA*AAVICTAISLFLDMIG QPCNLRLNDHIYYIVITRAHAFARIFFIG IPIIIIGGFGN*LVPLLIIGA
11273	25174	A	11370	112	258	QGRFKGSNFTSAGMQRNITFFMGPPK*NS RAGV*QRGEKKNPGVTKNRL
11274	25175	A	11371	823	1078	SGHFGSPRWADLRSQVQDQPSQHGTEL SLIKQKLAGRGKCL*SQLLRLRLQBN CISLGGRCSEPRSHHCTPANATQ*DSV S
11275	25176	A	11372	184	420	IKQKQLFLALVKELVQLMKTWQFLK KINIELCDPAILLIGIYPRELKMVYHT KTCT*MFIVELFIKSKK*KQPTC
11276	25177	A	11373	234	44	LATITDRLLALSDSATPLPLGIYAKEKKS VYQKDNCTYIFVALFTVAQI*NQPKCP STRTRGS
11277	25178	A	11374	73	456	PPIQSPLVPIYPSPALSSPAPRMGSH CLIPASASCHPPLETDFLSLPPTHCLAV FTKERSPPPPSPYPRF*KFLRS*KFSF FLPPFLFPGGTVLCLSGWSAVAQSMIT AASTSLGSSDPPTSTS
11278	25179	A	11375	43	456	EFFHHVGGDGLDLTIS*SAHLGLLKCD YRREPPRPASDGHY*TDATGSLPSSGTT *IRTKSPQAPASWGLNLAHPPRPSHS CPWANLICTLSGFGSGPTOPGWCPC LGLGSPARAVFKTSCLHPLATIG
11279	25180	A	11376	288	484	ENFSAVGGGGYVCLFPHCTFFETE SRSAQDGVQ*CDLGSGLPLPG
11280	25181	A	11377	129	1	NFNALNLRAGAVAHAYNPSHLLGGEDGR IA*QGEFETLSNTA
11281	25182	A	11378	307	1	DSEIPSLGLAKFWNRHREPPCLALFLTL NQLEMIKLSEBGISAKTR*KAQFLCQ RVSQDVNAKEKFLKEIKRATLVKTQMR HQNSFIADARKVWMAWKK
11282	25183	A	11379	200	397	CISLFSHYXKDLPTSGFIKKRGLGSH WLGAVAHACNPSILGGQRRIT*QGEFE TSLASMWKPC
11283	25184	A	11380	167	1	SNGLYSREARNQVTHIRPGVVAHTCNF STLGGHGRIT*AQELKTSIGNIVRCP
11284	25185	A	11382	12	395	AHSFTSLDLSVFAETCPHFAETQTHR FSTLLPLSALYPK*DYFKKKKKKKKKK KKKKKKKKKKKKGGGA
11285	25186	A	11383	160	2	TMENMDIK*TI*EIFLFEFKNGLAAET TQNNNTPGPGTANEGTAQWRNKK
11286	25187	A	11384	274	389	GQAQWLTPIVPAIWRKAGGSLE*GQAQ WLTPIVPAIWRKAGGSLELKNRPSLSL NWKDP
11287	25188	A	11385	389	37	WYESSWGFIFKISFLFSFNISAYDWYA SQILFTPKLYRTHPYFLVLFILSLIV LLETGSRFVSKLEGGGISAYGSFK*LG SGNPPAASISRRTPVVIQSCNSDLAFN





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						FISQFLLTCVSEPLLF*YCHQIIRVGRLEHEVRQMRTGKKQRIKMPFYMNNDKNVCPGVPAHACNPPTTVGG*GGWIT*GQSFNT
11309	25210	A	11407	257	389	GGSLIQKYLRLPLVALRSLFFFFSFETES*SVVRLSCNGMISAHC
11310	25211	A	11408	364	420	SQPPGRPRQADCLSSG*AQWLTPVPALWRAKAGRLRLRLSLR
11311	25212	A	11409	312	413	TSGMGPVVVAHACNPITIGGQGGWIT*GRFFETS
11312	25213	A	11410	283	425	HGHRDYYVHMLGAVARACGPSILGGRGMWIS*GQRFETSLANMVKPCL
11313	25214	A	11411	389	3	CRIDGLFFHLVFLRLVVKF*VIFPLSYFSLVLIILQFLTYMLNCTFF*QHLNLPPLIMVLLTKLNTLLSTFNCHPSLLYCLIFWFFHPIIKHMYALFL*FILIFILRQS LARSPLRYSGTISIH
11314	25215	A	11412	267	3	QRFQQRDTSRLDLRTSLCKRKGQLKQGDYKDNLSKRUVVVRTDKGAAMPQAVTHACNPSTLGGQGWNIT*GQRFETTLNRCPRV
11315	25216	A	11413	3	281	GAWSCRIPGBGSLASQAIQTPSFLYPVNPQ*ISLSARKKKKKKKKKKKKKKKKKKKKKKKGGVLLKKIYFFPRGRKKFFFWGP P KKTGGGGF
11316	25217	A	11414	275	2	KTAFHQLFNSDFKPPGSRNPGQSNSPRAKQSFCTQALLKYLK*MTNRMKLNKRSRGAVARTCNPSLGGQGWNIT*GQRFETSLANMAKPR
11317	25218	A	11415	319	1	RNLGVQVYRYVVLVRYKYSVSSNNKMKIKRDLLEVI*VPGIVTHLYRLIKRNPRLYISLFIYSNRLKKLTYRKAHAHACNPNTLGGRGWITVCSQRFETSLGNM
11318	25219	A	11416	121	428	ISCDKWEKNDWTKMLSKRLKKKKKKKKKKKKKKKKKKKKKKLGDREDRK*QSSWGGGALYINILFPSRAASGFLSLLLKYK KLGAAYVYIILGKRTILWL
11319	25220	A	11417	79	253	KIFNFQFSNNLRNNSHTTRINNYFPQRE RNLTPVILPPLWRAKAGSLSEVS*RFSCP
11320	25221	A	11418	180	4	EVGFNKPGLOGVFLRAGSHSVALTIVQWCDLGS PQHPPLGS RDPPP*ALQIVGNTR RVP
11321	25222	A	11419	154	3	STLRDRKNRLSIQPDTHAVCNFSTLGGRGWIT*VQRFETSLNNVVKP
11322	25223	A	11420	436	478	AIPLPH*RRKILHAALFFFLKGSFVLSPLRLCSTKIWAHCSLPPPIISNP PASSRGGGTT
11323	25224	A	11421	143	398	AAGFWFVLIIRFLQRRLALSPLRDLCSFAKSAQCQPRPP*FKRVCSLSPKSWDYRFDLLCAAGLVWVYLSVSRILHNKNQPPP P
11324	25225	A	11422	1	138	WYFIRVGGQDLGLLTS*SAHGLFKCWDYRHEPRPAMISYFLHK
11325	25226	A	11423	2	390	LELPILLNNTLFLFLYLYLYLYFSPNAPRILFITYLVLSFSLVPSKWKYS LILSNAPVLCMLSSPPFPLSLSTRI NKKLDWFLGAVAHAYNPSTLGGQGGWII*GQRFETSLNMAKPHL

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11326	25227	A	11424	267	414	VPOITTCIKINFWPGVVAECSPSTLGG* GGRIT*AQRFETSLGNMVKPC
11327	25228	A	11425	189	73	HQDGLDLTTS*STRGLPKCWDYRIHKFP RSARPNAWAP
11328	25229	A	11426	318	33	KRTTSSHARGKRLGSPKTAIAFFFFFF* TGSCLAQAGVVKMCHSSMQPRPGLA*F SASGSAGIIGMSHHTRPDAGFLLAKLKK KSNSTGYGGAHV
11329	25230	A	11427	291	393	DRVSTCLPGMSAVIPST*ITAAQISNAQV IFLPQP
11330	25231	A	11428	51	399	KRVARQNPFGQGFQWMCSPILYQGS AQGRNIYKLLGSGEWPCOLIIDVERBQL EDWRQDLGRGMWNTKARVKPGPLVAG *CNSTLGGGRWIT*AQRFENSLANW KPCF
11331	25232	A	11429	242	420	VKKKKRGGRPKGKPTSLACLQISFPKG APKLNRRAGE*QRWEGKNLGVQPNRFG AHP
11332	25233	A	11430	77	405	TKRGDSFFCLYRTYITDSVKNKNSKAA AAAAFFFFLRLGTLFLFLRLKGVQASVI *NFCLRGNGGSPASPSKEVGMBCAGNS GLFVFLKRRFPVNGQEFKTRAN
11333	25234	A	11431	121	439	LPLPTSGPEDPLALSFKFTTFFSTLGM IYTGHPSPERTSHLMAPPVNNKACRF FRT*KKKKKKKKKKKKKKKKKKGGPL KKKKIIPAPPGGELFFFFGPKK
11334	25235	A	11432	109	283	LTPNNLDSRECIKNGKQBNHLNLGGG GCSRPKSHHCTPAREKRNVSVKK*INK IK
11335	25236	A	11433	296	1	FLKKPSKPSKLPPLPQNLNLIFFFFPK*K CPAAKIDTPPPSP*KISSLGGG*GFTG SRPPSLMLRNPPLIFFFFFFLDRVSHC RPGNSAMASSCPV
11336	25237	A	11434	385	418	QSELTGOKRTK*E*SWLGAVAHACNPS TSGGGRGNIT*GWFFNSLIDNVKPLCL
11337	25238	A	11435	3	405	LLHQRLMLGQNGRTTLLMBENVRK FPAEPSCSALGVMLQALACYPLVVRQ* ANHWEKKKKKKKKKKKKKKKKKSGG G
11338	25239	A	11436	221	3	KHEPOTIQMESMK*NTSIKICIIYAS*IQ DCLRYQWQPAVAQAITEHPQRPRQAD HLRSQVSDQPGQHGT
11339	25240	A	11437	288	366	KMFPSWA*WIMPITPILWEAKAGGSL LWYHYTFVRDGLTILVYQLKATIRKLIT LRSRSGAVAHTCNLNLGGRGGWIT*GR EFETSLANMKPHL
11340	25241	A	11438	160	370	MQHQGVGIYSQGGGNRPDKNSQLGT AHTCNLITLGGRGWIT*GQEFKSLTN MV
11342	25243	A	11440	302	54	LSGVWFLTPPPRGGGFPPT*NGGAPGFF PPPPFNPPPRKLGPKKCGIFPPPGG RLVFLKADPPFFFFFFFFFFFPL KRLSTELQKCCCLISSTISPK*KKK KKKKKKKKKKKKKKKNDPSLP
11343	25244	A	11441	271	416	SVTGWITITSSCCYKIQCKTIQLARH QCYCL*SQLRLRLRQNS
11344	25245	A	11442	254	392	LLKNQKTLGGPAINPPFLGPRNGVPEA GNWGPDPDGGTPTFFFKNQKITPGGOGG
11345	25246	A	11443	390	150	

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11346	25247	A	11444	122	1	P*FPPLRGGGPGNPLYPGGGGCH
11347	25248	A	11445	272	403	PAPLFFFFFPTQSCSVA*AGVQWRNLGSLQPPDDDTL
11348	25249	A	11446	70	397	RPKVDRTTRGRNRGRKQVENSINQSASSPPKDRNSSPAME*SWM
11349	25250	A	11447	3	401	LCHCAFAWATERDPLVLGKKRRTNMSYCHPMMNRVEKKIVGDIKC*GYGETGFLTHC*WECRMVOLL*NIV*QCLRNINLHSPYSLAIVLLGIYPREMKTYIFKKTGM
11350	25251	A	11448	333	1	HASADASADASAYRCLAYPKSSFLYPSLPLVVSNPFLNIDLTIGPATETPLIKIVMVDLSMQLSKSEFNPFLLSLNVFFYVLSCCKRRKESQLGWSHICNPSTLGGGRNIT*QGEFETSLANHA
11351	25252	A	11449	104	402	KSGCIFFKGGVVLFFQTKTAKIGSPFVSPPRKGQGFPPQGLRGFY*PLPPPGVP EIFFFFF*DSHSVTLSPREYSQMTAHCSSLPGSSNPASDSHLAGSTQCH
11352	25253	A	11450	198	2	VVCRPLLGVSQGLYGMNDPFKEAVCLFSELKICAGRTALFRAVRQGLSLKNFLLPFFQLCPNHRGGVL*RO*ALLSCGGLHPVRAIRPLCLPTCA
11353	25254	A	11451	171	3	KYKFNAGLGGSCL*SHHFARPRQDGLSPGV*NQPGQHGETPSLQKQVSNWMLASVEARAGEQP
11354	25255	A	11452	177	461	TPFPFATSLFFFF*TSHSVSQBCNCTI SAHCNLCPLGSSDSPASASRVAGITGA
11355	25256	A	11453	247	3	PMTGKYSNSTCKPNSLSPHLPLRTQTKNMBHPRLTRGDCLSPGV*DPQGRGKTLLLQJSGALMDVTAAHVVPGLPTRERRRSLSPTQ
11356	25257	A	11454	328	57	BGECOSTESR*ILHLKRICWHINLRI TKIIN*VILKMYKQLRPGAVAHANP SALGG*GGR IARAQELERLANIVR
11357	25258	A	11455	70	435	EVHSNICALSTHOMKILTKGTTHQHS*GFF*EGEVLTLS*TKLECSGVINAHCNLNLGSSSDPLALVSQVAETRGASVLLLAICPKVNK
11358	25259	A	11456	112	401	ATRAKTLHLKKKGRKKRFFPHWQOGPTPALVPQPRTHFIPKVSIFSLKIORBOLPYTVQTQSLPLNSHMQVA*AGVQWRNLRFSCLSPSSWDY
11359	25260	A	11457	198	3	KCWDYRRRRCPCANPIC*LTFFFLGK KLNQSGFFFFFLKGSILVPLPKGGGAF LFN*NLTLQGGNSPSPS*RAETLGLG PHAKLMPVFLKK
11360	25261	A	11458	179	1	EKTSVKQSGDSNKKAWLENKTKKSLKR*GVVAHANPSLAGRGWIS*GREFETSWTRMKE
11361	25262	A	11459	210	5	PFHYNHIVCEPTITLSVNSIQSGPGR AHATNPSSTDNRNP*AGSFKISLANV KPH
11362	25263	A	11460	139	2	RLIHYFFKNLPSGGGSTA*GQFEIRL DNTVRPHFLKK*KLSQVWQWVVSATQ EREVGNGLSPGV
11363	25264	A	11461	388	272	RTIALSKLFFFFFKQESIFLPMLECSG VISAHCNL*LLGSSDLS
						S*KKKKRGGRGPRKGMFLSPAGQGNPFPM

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11382	25283	A	11480	244	407	SPQKKIGFLGPKPKKFGGSGYGNYYKINR RFFFPILGEGFSPHVF*NLBTRTTGG LLETITKTTNLLGRKLGSFLGPRSLTAA PTGTTIKLTGGFFQFWGKVFPRMYI FW KDEWKKGF
11383	25284	A	11482	308	30	SPQRNPPTYSGFKNLSASPGQKAKPRF FLKNQFLPGIMGGGRQFPLLRRVRPPNC FNGGKRKN*QKLOPCPPGGPKETVS KK KKKREKQ
11384	25285	A	11483	226	407	MEWKK*FWPKVAMTYNLSALGQQGGRIT T*GQBFKTSPSWRPRAS
11385	25286	A	11484	10	411	QPFYFLSLSLFWFVNGIITQVVAL CVMLVSCNFRFPCVACQDQFVFWL LRNPLCGVNLCHSICPNRTGTFEP LIAIILIKL*TFVKKKKKKKKKKKKKK KR
11386	25287	A	11485	184	1	TDELLPMDEQRKWFLEKKTPTSGEDAVN IFEMTRKDIECVH*VDKAAAYERIDS NFLSN
11387	25288	A	11486	435	222	AKNLNRHFSKKVI*WASRHKKCSISLT IRET*IKSIIR*HVIPGQMTFIQKTGDM FGSVSLPKSHHLKL
11388	25289	A	11487	317	408	FRPGTVAHACNPSTLGGQGNIT*GKRF KT
11389	25290	A	11488	340	469	GKGDTKCHLWLTGVHACDPNTLGGQQR RIA*GQBFKTSLSNM
11390	25291	A	11489	38	389	KRPTSLKKSINPCLSGQFFPGLSQKPK SNRSPQKKKNPFFSOGKAP*KGPFKIFL SPGLQSPQKPHLLGLGKKNYLTLEK GCRDPK*CPCFPPWAGEGNPFSKKKKKQK FFFPQ
11391	25292	A	11490	235	2	FVLNHLMPKHLIPVTEPRRLFAPPEFL* FLFCFVLVSFVLLTQSHYVTYACSGA LSVHCSNLNPGSSDDPTSLV
11392	25293	A	11491	25	417	GTLCLRGFININSHNMLKNSLFPFF WETKIFYAPQADGRGNLQ*WNPSPG* RGSPGPTSRKNGGGGGPPGPVIFGLR ENGVPFGLGKPKSLAPGIGPPGPKDR GLRGPPAPGLLKKPKVW
11393	25294	A	11492	234	438	NOVITAQCCDCTECHY*LEKARINPML FIFVTHTHTHTHTHTHTHTRERGPSYI YOKVSFKLTHL
11394	25295	A	11493	344	477	CFTHNFS*IKT*KFNISQDLVATCNFSI LGGQGRIT*GQRFKT
11395	25296	A	11494	35	482	GIPGFHHVQNGLDLTL*SIHLGLPKC WHYRPGPPRAISITPST*AYLLGNQKI GVTHHAILALFFSGTKAMISPKVYCI FVLLVSEHLGCFYFLAINATCVCVYKL FTTHMQVESHATHEFISYFFKLLCSL STRLYAVLL
11396	25297	A	11495	307	484	LSFSEHLEKCVLWPCVAHAYNQTSG GRQRTI*GQKPF
11397	25298	A	11496	487	349	FLIKTEFHPITGQGFQFLTL*FARLQPL KQWDYKGEPLRLAPNHP
11398	25299	A	11497	224	417	ASGASALVKELCSFRTYIPRIKRYA RTDGKVF*FLSAKCEGTFVFLSFFFFFL EVLFCSPG
11399	25300	A	11498	17	411	KRLVFGGRGRTDRFISQTV*AEYVSINL

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						LIFLTKKKKKKKKKKKKKGGALKKKP WGGQNKTEGKKNNFFLRGGKKKPWGD KKNNFFWGGGNWKKPPKKKTPWGGKKI FRGGGKTTPPYFCFLKGG
11400	25301	A	11499	117	370	VSESADLAWSLGICFFTEPSSDADVAGL ETAFPLFGWGTS CSVVQGV*WQHSSLL QPRPSGPRQSSCLSLPSSNDYKXMPCL
11401	25302	A	11500	244	1	EELFECYSCTPTSSDPLTLLILLTT* LLPLTIMASQRLHSSPISRKILYLSIL LSLQSLIIITPTATELIIPIYIFFET
11402	25303	A	11501	130	55	RFVCSITKVLRLSSDRNPGRFLLSTSN SSLKKKKKKRP*RDNSAILL
11403	25304	A	11502	186	421	SRKLKAGIIGVHACIWEVLILNLVLL K*ITTFALKINMPSKYSIDGQACQLMFI PALNEADAGGSLQPRSLSLGNK
11404	25305	A	11503	1	213	GEALFLVIFYA*WLPFLPEFLKFVILCLC ELQFNERFIMVLCIIILGVGGFFLFCF LL*FCDFDFFFWRG
11405	25306	A	11504	82	6	AGVQNPNSWLRLE*LFPTQVLMIFPPF YHQNFPP*KGFFFLGGLSHFFPPPNKG FFFNYPQGFFPSPLKKKFFFSPIFL APPGIFL*GPFRFFFTTTTT*EGVSL CHLGWSAVAAILAPAGTTPSSCLSLPS S
11406	25307	A	11505	245	440	WAPCIG*QLLKDPQVLFAGYKVPHPLEH KIIIRVQTTPDYSPQEAPTNAITDLISE LSLLEERFR
11407	25308	A	11506	256	370	GKLM*GHHVQAGLKLKLLTSSDPPALASR SAGITGVNRHAPPRLNVLTYTGQTIIL YHQYKQ
11408	25309	A	11507	1	149	GCNMPRTVLEAFQHKFNFLKTLGDPQ VQNLNRVIPALNEAEAGKLPEARRNRP *PRTVLEAFQHKFNFLKTLGDPQVQV LMRVIPALNEAEAGKLPE
11409	25310	A	11508	316	420	YTYIYEPG*VQNLTPVIPALNEAKAGS LEVRSLR
11410	25311	A	11509	136	2	LDNRLNPGAVAHANSTRIGDQSGWTT* GQEFETSLANNMKPHL
11411	25312	A	11510	167	420	PTPRSGNTALQPPHHTHTHTHTHTHR HTHTHTHTHTRACI*KVRVRLFSPPKK PLFCLSVSGIYVGRCLLKRLLFIPLYRH
11412	25313	A	11511	124	415	TVISVANTIIILFTIAHVLATSFPFFPK EVLFLPPRRGGGAP*VN*NLCFWG*GN FPA*PSLKKGITGALYTPGLFVFLKKT GFRHVQAWLDFL
11413	25314	A	11512	121	1	FPVKFNAPFFFFFF*IGSPSVAQAGVQNN NLSSLQSPSCL
11414	25315	A	11513	245	13	VLFILSGFFGPNYPTSPPPQLPFPFASG NHPTLYLHGFNCFFYFFLFIYFF*DRV SLCRPGNSAVARSQILVPSGS
11415	25316	A	11514	434	2	EPFFPVGSGSPFFFGSGGFWGQER KGAGS*PVVSGIILRGCGPGAGGPT PLKDDPLFFELAPPLCVTFRTFSPTV FFLPFFVCPKKGREALGVKGRPRPFFFR SFLFFFSGD*VSLCRPGNSAVARSQILTE SLAS
11416	25317	A	11515	247	390	QGLRIYSQDFFFFLETKSRFVAQAGSQS GNLG*LEPPPPS*SDPMASP

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11417	25318	A	11516	269	368	FFFRERSCSVTRAGVQMRLSSL*FLPPAFRRP
11418	25319	A	11517	256	404	NILKIFYLRI*KKKQQLGVVAHACNLR LGGRRGGWITRGQ*FKTSKKRMVK
11419	25320	A	11518	211	404	YLCFTRCSVISHLR*VFLDKCVI*MYRPH T* TGL*CMQVHTHTHTHTAHTHTHTP LSGGGDCI
11420	25321	A	11519	41	232	ESVPRRRRRVPRAQITPTTHCSIGDRARP CL*GQLLKRRLHNLNPGGAGCREPRS HHCIAAMATBQDPV*KKKSLNFKTVRA INLRMLGALISPHFLWQIWF
11421	25322	A	11520	146	2	LIDQQVNLQPRHRCSGATAHACCLLP GSSDPLTAS*VAGRPFFRP
11422	25323	A	11521	297	437	TSHFNRLLSCCTCFKTLWGVVPHAY NPSTLGGRRRIT*AGPFE
11423	25324	A	11522	244	460	NKATITTNRSIFLQQLQKHCTKWLSLI SNQSLISF*ICFVLFFETNLAVSLRLE CSGATLAHNCILLS
11424	25325	A	11523	222	1	ESKDLITFCQLAPRNSCFVLCFVFP LEIGSCSVAGAGQACNNGSLQPPPIA SAS*VAGTTNVRHYVQLP
11425	25326	A	11524	308	424	ITFLTMFKIYVQCPAIPLLQIYPRDY* SCYKDTCTRM
11426	25327	A	11525	98	2	NIGGRPGAVAHAYNPSTLGGRRGGQIT*G QEFS
11427	25328	A	11526	113	399	LDRFLTLPRLRREDCLSPGGQCSEF* SHRCVPANATE*DLLSKKKKGVLKPF LPPPSVGKPPFSPPERLFFFLRPLLG VFPFPPSKKIS
11428	25329	A	11527	280	3	PKYQCI*VLQCIQLFKLSIYNTYVTH THLSLSLSLPPPKVKNKALMSSEFTLTF KMYTFQPRVTHCTNPSILGG*GGWIT* GQEFETNL
11429	25330	A	11528	284	2	FNGQKQKQNFSPFPPOLKIOSFKRAPFFF FFFETKSCSVTAQGVNCDLGLQLPLA WATERD*LNK*IKQMSKKLHT*VCMFRT RGRTRGTRG
11430	25331	A	11529	134	2	DTLLPRLECNQITTAHCSLKLPGSGDPP ASAS* IAGTGMCSHA
11431	25332	A	11530	104	1	GRGFFFFFFFFFFEVESCSVAQGVQNL NLGSIQ
11432	25333	A	11531	157	373	CVPTTYSQLRCYIFIGNTRSVFRCH E IYT*KNRFWASTVAHTCNFTLGSRGKW II*G*EMTSLANVR
11433	25334	A	11532	237	389	ICKSKTGF*DFQFETSLGNIVRPCF YRKIKASQV*WIAPIVLATWEAB
11434	25335	A	11533	259	122	HTSPSVORHFFFLYF*TKPHVAQGVQ WCNLSLQSPPPGFKRF
11435	25336	A	11534	164	1	SSVVSQALITLLPLKTCFPGWVAHACN FCTLGGGRERIT*GQKFETSLASINL
11436	25337	A	11535	106	310	GGDKGTVMOTLHFFDQQLRLDHNKDHWI THAEPLPHLSA*CYAFKGCISIGSI *AEKRYKQPDG
11437	25338	A	11536	167	378	ASPGTITTKYILVTVVPMFKFTIYIK MYTE*RGVLGSLKSCSNVLIIGHCNLKH LGSSNLPTSASRVA
11438	25339	A	11537	101	396	VNHLKQRLGLSKRGEKKLLVLISQFGG FPCAGN IKKGKPPGPPQGLSP*KRGP



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						GKKGNFNKMGFNPKTLVFNKNQFPGGGA KPGTPGVRGPLGDL
11439	25340	A	11538	18	361	QIGPRLY*DNGETPSLLKI QKKRTIPGF GGGPLRSQLLGGGWNH*NPGGGGCRD PK*PQGLPPWGTNQFNPKKRGRRKKG EGRKBGGGRRKRTLPKRGIGALNLGGLLT SP
11440	25341	A	11539	134	365	PGFQNRKKTGGGPFPRPKIKTNFVFP*KY LKICPGFVPRKPPPPGFFILETRSLFFI FLQGFPP*ETKSRSPPTTECSGVLLAHG NRLVGGSHYP
11441	25342	A	11540	2	318	TTRFTYIRITFGPKRTVNDLPQAPSEF VAALRLARSFLLKL*SPSLVFDFFLP F*KTGSCLSPRLECRGHIITVHCSREL S*SHDPTSAOSSSGSGPHLG
11442	25343	A	11541	294	409	GTISFRTCTRLGNVANTWNPSTLGGQGG *II*QGEFOT
11443	25344	A	11542	1	123	GKQRQEPALSYDIAVTLTS*SAHLGLP KCWDYRSDPECLA
11444	25345	A	11543	69	350	VGAKGHIHMDTKIETADPONTYSOGRKR RPRAEKLPCVYALYLGNGIICNPKPPC CWKGHDFIYIYVCGHIYIHIYICTHIYI YFF*DGGLLC
11445	25346	A	11544	103	340	LFCAPFLSPSKLDPYHLSFV*TLFLKD LISLAFPLFWAAGSCSVTQAGVQGNPS THCNLCPLGSSNPS*ASQAAGT
11446	25347	A	11545	256	354	PYFPGKPRGDHWGLV*HQPGQQGRTF SLKKI
11447	25348	A	11546	196	335	ETVARLERSPVGRAGMLMPVIALMRAK ESGSPVRSS*VKKICTCPGTVAIAQNP STLEGGQKIT*GGEKTSLANVVK
11448	25349	A	11547	202	377	TIHTGVMVGNHTLVVFVNFETTF* D KILGNARMPMLPIAP*WESMGGLLEPK SL
11449	25350	A	11548	396	26	PPRIKKEKRPNGAPYPPFCWNP*KKGN LSLAKRPPRDSVFFVSA*GSYLPTTFL QLLRWVYLTSHIAVSFKHLCBPHNFTL QHSIPVLYIIEIEVYSYFINRTIYKIN MDFSIVGFVL
11450	25351	A	11549	232	371	REVFPENIKIGOVQMLTIIPALREVKA GGSLARSL*KYQNWPGAVAHAYNPSTL GGQGRIA*GQKEISPNNAKPD
11451	25352	A	11550	174	381	NRDGPFRADRAEVRQLLTCTILEHGG QREGL*RSSCTFLPGWDYR*SPSHVA GTTGISHHRTLKQAFPSQTGVSSC
11452	25353	A	11551	262	359	DYSNLGLVWMLTTVIALMRAKAGRSSE VRSS*PALWEAKAGRSSEVRSS
11453	25354	A	11552	70	380	LHKCSFIYINHCNPPYGLISLYPKQLF STERNKDFCNKI* KIL*WAMARHSGRL*SQHFGRRPRAD HMLSGVPGQPGQGESPT
11454	25355	A	11553	319	56	TFPLGGPFF*YTFVSQPLIFFLPKK FIOEQKIMARGNFFPGZLSLFFFL TLSSALECSGAWSAHNLCLPGSSNSPA SAF
11455	25356	A	11554	230	399	MXEITINQANISVCGTIRRLRHSHLI PGRGYSLEIRSYHCTSTWTE*DSCLTK
11456	25357	A	11555	376	396	F*YFWRDGVSPCCPGNSQTLRLQOSTCL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						GLPFCMDYRPPHDAASCPYFYHYLL KIMRYSFDLSCLMNLVVGIAFG
11457	25358	A	11556	176	384	KAMPNVRNNYR* NFFQFOCLNFRKRLK CFROGADKFGKIGFSCILQYALKFPIWGR EOWLTVPNPIPGK
11458	25359	A	11557	295	391	PYKLLITHTHTHTHHSRTHTI* HTLS LYTF
11459	25360	A	11558	1210	1753	NIWCNERLAIVAGSPFNNSPLRQWALNL TPILALMEAEAGQPLEQEFTCLGNM VHKCLTYNLENWGSV*DLPGQGETLSL OKFKKCVNRKGTCL*SQSLRLSHWEDCL SQGQGGCSLP*SHQCVPAWVTLDEDSK KTKTKKFFGLPSPLFVCFTHIYVKNKE YAPVLAEEASGKTTSKLTWVTSRNGLGK TKKFFGL
11460	25361	A	11559	172	3	KQKFFPPPPSHQIKIPQGAPEMPFFPF FFEKESRFA*AGVQWNLSSLHPPHHP
11461	25362	A	11560	143	1	QQAQWMPVITPVLNEAKG*SLERSSR PVCATATPQLIPK*YEGSL
11462	25363	A	11561	84	2	KPLDTLGGQGGCIT*QGEFTSLANMV
11463	25364	A	11562	12	387	QGILLPCFSMSSEERGRYSNTTSFFFF FGKGGQINPQSGGQATPRLRPEPSGL TLGGPGNGGPPPPPGNQPFKKGKGYPG GAGGVNLPGPKGNTPPGPKKARKKGGP PGPGKFL*NPFG
11464	25365	A	11563	230	375	RAKGLLSESLLSIQSPKPKSVHTCNPS TLGG*GRWIT*GLEFTSLA
11465	25366	A	11564	287	55	PPDGRVQMLTPVVPGLNEAKGGSLKSR SS*SQINPVSQVPYSLRVLK
11466	25367	A	11565	115	411	FFFFFPLGNSISFYFYKQPPRGCHIFW NFPFPG*GVFPFPPPPGQGNKGGAPPPG FFFPFP*KTGFPPPLGPGPPPLPGPPPP FPPPKGVNERFDDPP
11467	25368	A	11566	139	356	CLLIGWYNTGCIQTGSTRKIGITPFLRQ SSSVAQAGVKGCSGMILCYNLRPLSGSN LPDSAS*VAGTIDATPY
11468	25369	A	11567	101	410	FLFFFFFLLKRIFFPPPRGGGGGG* K KQTPPLAGKKNTPPPPKRGGGGTFFFF PLLFLV*KGSGFPGGAGGKTKPKNP PPPPPKGEMGRGPPPPROG
11469	25370	A	11568	417	56	EDCLRLGRVRLDLENPHMLQTAGRDGAR L*SQLQEHLLSHGPRGYSEL*SCHCSPA WATE*AYRKQNTKQNYRSSALLHLTYT MATAWIKIAFLRAGDIFLSVLFLPNSY FLFSLPSQ
11470	25371	A	11569	301	443	EDTTPVCFEVRKSCSVAQATDSPASAS* I AGLIGVCHHARLIFFVLVE
11471	25372	A	11570	44	408	RORGHGPHSPWRKRLKLVVSGRKATES KRRAYKIFLEALLCHQWKEWELDSQI KIPFL* LK*SPSIFILYFLPKQGLS LAPMLSCGAVLAH*HLRPSRSLSEAS ASQAVATTG
11472	25373	A	11571	201	1	AERPVTPGPPVVAEPGLQGRG*KKNPKN MCHPMDHLRSGVQDQGGYGETPVST KNTKITQAQCI
11473	25374	A	11572	343	1	FGLLFAPTLLEYKLYESTNHFAHCCVCRP SSGTLHVVCNRRHFNKLEWNSGGGGRQ DLTITPRILGCSGVIMAHNLVLGLSNP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						VSAS*VAGTIGASHAWIDKLFVKTGPLY
11474	25375	A	11573	209	3	VGPFPKSLFGPFPFFCFKCPPELKKKKKKKPLVAYTCNLNTSGVRGKKIT*AGEFKKSPSNIVKWPY
11475	25376	A	11574	312	430	QRYARPGPVVHCYNSSTVGRSRGIV*AQEFATSLCNMT
11476	25377	A	11575	125	3	NSLGPVVHACNPRSLG*GGRITSAQEFETSLGKIRRPPLY
11477	25378	A	11576	190	362	CVNNYID*ERIKKKKKKKRERKKKKKKKKKKKKKK*GGGAPKKKKKFTGGGKNFFFL
11478	25379	A	11577	231	340	KRITRVNQDGLDLTS*SAPISLPECDWYIMKPCLY
11479	25380	A	11578	60	3	RMQVUS*ITFPMSLQAYLYSSSSVAGAAQSGIECKYQFAMDRNMCGERALQ
11480	25381	A	11579	285	406	KKGNWPGMAHETCNPTLRGGWIA*GQEFSTNVGDMAK
11481	25382	A	11580	121	1	NLNCFCGPVVAHNSNLTIG*CRPIV*GQEFYTRIANTVKP
11482	25383	A	11581	199	384	KRTPTGGIIFCFKACGAPPL*TFPC*TPLEFFSPAPFPKPKRALKFLPKPKRGFFQIPFFFF*DGVSILCHPGMSIVARSCPRV
11483	25384	A	11582	677	934	YGSRHCIPTGLATSEILPLKNPARHGSQVQDQPOQSKTLTLRKKK*ARHNGSC LSSQNFGRLRQSGHLSFGG*GCSL*PRHC
11484	25385	A	11583	104	2	KKIGGGPFLFFFPFETSCSVARLE*SGAISAHCN
11485	25386	A	11584	349	9	GGRSILGPRKTRVQGIPEFFPLHLGGCKAKPCFPKKEKKKVRGLNKHYSKEDIQMVNRTMKECSTSLPRERKTKTMRTHFPSSIRKATIRKIKDKPKQ*GCISGGSVVRMYL
11486	25387	A	11585	163	1	TAVRIKHSYTLTFCILHSRYLTNTCNPGPVAHACNPTSLGGRWIT*GQEF
11487	25388	A	11586	192	41	SKSKYHIYDGSALCKSTYKWTFRKKG*IDVVKDAKSTRLSMSICREKE
11488	25389	A	11587	30	374	GNSPEDLPFGSLPALKFGSGGG*PFLPQKKRGGGGSSPPFVLKRVRPENRLYPGGGGFR*PQGGPCPSAMGATPDSLKKKKGPGQKKKKKKVLEKT
11489	25390	A	11588	66	245	SLCFPVFPVFF*TESCSVTQGV*WYNLGSLOPPPKKKKNKKKKKINWGRGFKRRL
11490	25391	A	11589	243	402	FLHLKKKKKKKKKKKKKKKKK*KGAG
11491	25392	A	11590	205	3	IRLLGLIKNPTPAICQ*K*KTGEPLN*VVM*FFRRLHTELSYDAIPALLCINSTEVLAPGIPPRFR
11492	25393	A	11591	404	152	MGFHVHSQDGLDLTS*STLLSLPKCDW*CWDTREPLCGHFAISFNKVVLTNTTYVYFYLILHICIYCPYKLLFLFFFYIY
11493	25394	A	11592	311	386	TVYFPIAGNLASGGA*AGIVGALSLLIRMLQPGALLDDQIVYVTAAPVLIFFPIAPVLIIGGPN*HPLIIGAPDIPRNNISF*LLPSPILLIASIVZAGACTG*TVYPIAGNLASGASVDTITPFLH



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
11512	25413	A	11612	20	362	NFVRVGVARSGRGATRCENVGLRPVGMAYGRSPSWLL*VKPSAASHRPPLPRAADT PGTAPAPTPTAPAPAAALTPSGFGSA ALTLEELQLRAIRAQRWGLTMLPRLAS NS
11513	25414	A	11613	158	2	LMLSRTPLOOL*YTLLELELPRLLAPDL LSNGSSLLKDLKWTHTSNYRASKETK
11514	25415	A	11614	3	410	RSEVYGLVLTWYQVNRVPWTHKARFT RYSRMARPSKISRSCYMLPOAHRTKS* PLVVRTLSGLCSLLGPHPLLSLLJATDLV PLPSFALLLLLELFFLPCHPKLAP*SEPT KRSFSFYFFFRDVLCCQWWSQTP
11515	25416	A	11615	189	397	YKVLFLVEKNGFFFLFFETKPCCVAPIG VQGNPHG*LGAPPCLPLPSALAAPEVG ITNGTPPPPPFF
11516	25417	A	11616	158	1	KGKPTPKTFFCKQKIFPLPVFF*TESHS VARAGVOMRDLDSLQAPPGFTTR
11517	25418	A	11617	319	425	KWLYSQAV*KWLYSQAVLTYNNTL GGGWRIA*AYEFKTSL
11518	25419	A	11618	94	2	CLTISWLGTVAHVGNPSTLGG*GCHITR SR
11519	25420	A	11619	381	9	FFPLPLPLPTVSLFPRSPDAEPKLDOT AAISAHCNLP*FSCLSPSACNCRAP PRLTASASRGAGIDGVFTQCSMVPRL ECSGVISAHYNLHLPAISLGLPKCRDCS LCPDEIVDPRI
11520	25421	A	11620	144	431	I VNVIVGKGEGKRIPE*LRNCGNW*S WDRWVAEDHVLKEPSENRRRLARVCLIP VSQHFORRRRLDHEVRSRLPACATWRNS VSTHTKSGWAC
11521	25422	A	11621	174	449	VFSLLDLAGASGLCYLEVRDPLEAAVCP FSDLKPHAGRTTTLFKAIRQCHLSLQRF LLPFWNLCPAPRGVYRQASLS*GGL HPVRASRP
11522	25423	A	11622	316	412	GGPSAVAHACNPSALGGGRGIS*QGEF KTSL
11523	25424	A	11623	183	2	PRQVYLENGLLSHSCKNKITHINRLKRE KIQPGVVAHAYNANTLGGGRMIT*QGE FENE
11524	25425	A	11624	355	168	DLLIVCYDPNAINL*SLLRRLKWEDEL SPOG*GYSEPRSCHSPAAAEPPDPVSK KDRNVEFYCC
11525	25426	A	11625	154	3	TADVLFQGGGRGNFVVMKNCRCPTVA HACNPSTLGGRG*ITROLEFK
11526	25427	A	11626	412	3	IFPPPPKDKRTRGGQKNIPFAPPRNF LGRGNFPFPQKPFPPPLF*IFPRPP*P KOSIPPLFLPLCQKKTPTSPFTLPGS PPICEKIFLFPKKGFLKFKKPRFLKKKG PFFFPFGHVALCQCPQWSAVAQSQ
11527	25428	A	11627	290	423	VFFFPFKFFKKNISWFGVVARIYNPSGL GQGGKIT*SQLRAP
11528	25429	A	11628	213	3	LSGLYSQNRNLVRYSKS/VSIHINRLK KNMIIISIDCKPLBQIQNSPNT*KN KLKNEHLRLPADA
11529	25430	A	11629	152	2	FQKRNDELPKSGWGMVAHACNPSTLS AKGQIT*QGEFETSMVNMVKP
11530	25431	A	11630	422	189	PLSGFCPTSWAQRALSKKKRSEAGH SGSCL*SQYLGLRLKQKDHPSPGGRGFS



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						LSDSPTS
11547	25448	A	11647	319	3	RSTKYSPTGWEPSMWFELFHVSLPFRS ILGPPILLGTPLRGSPPPPPFEGKGFY GLTFFFFP*RPCCIFFFFLDRVLLYCP GWSAVVQSAHCSLELDKVCVI
11548	25449	A	11648	165	2	DQSGRPRIKLCARHTTHAHMHTSLGQT* QDPV*THHTHTHTHTPLAAAAQRIN
11549	25450	A	11649	290	3	SKONTTHWATLSYIYPQGFVRLGSPSS RMQLDGLFVRLALFVLCRQPPSLRLITWW EKTEBKREK*DRERERNEBERNE RRERETQWY
11550	25451	A	11650	220	2	TPFLKGTGLTALRILPGRPQPRAGR PF*AGVAENCPDPAQSGSTRPLGAPGR GSAPP*RHPGAGGRR
11551	25452	A	11651	29	387	FLIFDVFIVIDLCKEPPSYKMAHLNV VCVLTAPTTYSYFPISLGPPVSLRNDI EIRPINNPTRTSQCSSEKSHTSLTNLQ KLEMTTLKDGMSKATG*EPGLC*TV SQAVNAK
11552	25453	A	11652	267	2	KFFFFVFSTSKLNFYAGTFPPLFLSFF FFFFFMMREGFAVTWVGNAPGAVLA HCSLELVGSGKPPISAS*GAGTTGMHYH TRMY
11553	25454	A	11653	50	411	EAVAGGMEKSMNLPKGPDTLCPDKDEF MNEFDVDFVSDCRNGQLEELRDNQ LYYKLLKTAMVRLINKYADFVNLSTDL VGMQALNQLSVPL*QLREEVLSL*SFV IRRSFSS
11554	25455	A	11654	303	403	VENVVWLGVAHACNPSTLGGQGEQT *GOEP
11555	25456	A	11655	356	653	SVSPCPFPQASTLSFLVADPFRRGVDV SQVAWSQKIDTPSSCCIINNSGNRTTV LHDT*GPRASPCYNPPISWLQFPHSPP WASQLPPSVASVYQK
11556	25457	A	11656	442	2	GRPILARPAVL*SEPTPAVDIQQIM TIIDVVKCAKAVQTLAPINSASRMQS IRHVYVILKDSARPAKGALIGFIKVG YKFLVLDREANNEVEPLCIDLFYIHE SVQRHGHGRELQYMLQKERVEPHQLAI DRPSLV
11557	25458	A	11657	109	474	DINCKGRVVLVARN*KKRDKRYNEET E*VL*KCVHSLQKENVAQNPVQNA AYIDQPSPAHVQQGLSKLPSRPGQGV EPQNLRTLQGRSVIRSATNTTLPHMLMS QRVIAFNPALQGGQRPPIGICRTTTP NMNPAVY
11558	25459	A	11658	342	3	ENQKNGEHSKQASGPPNDIMTSLAR A*WAGASRLALLTSAGPGRVHNPA ELKSHVVTQCKSAKHDKTQELLAGE RNITVLM*LKITPREPHAITSLNSRMA
11559	25460	A	11659	204	17	STCTPLPTA*SQSRHPPTPTTPAPWR SSNGPLSKGSSSSNSTSSWSLALATGW THRSKI
11560	25461	A	11660	505	514	GS*GNHFNPKGSHGQVQSDRTGPRGP CLPSPWGAQLRDWYQPEMGTGLQK
11561	25462	A	11661	80	374	FLFDIYNRCYLFINIT*YLSNFD*IF IIIVLVAIYRLCLGLFRAPROCKHPRP QPSFNKIQTR*ANPNAVATCNNTNLG





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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HCT
11576	25477	A	11676	305	698	SFMGRSPRKIDQPCNSRMVHGSVTPRD VAIDFSQERWECLQPDQRTLYRDVMLEN YSHLISLGSSISKPDVITLLEQEKSPV VVSKESTRWYPGK*E*SRQGEALIVPDS PCAQRGVTPLRGGLLENFLQ
11577	25478	A	11677	107	397	GGDGRETLRAPANDGCT*QERAEETPLAI SCPRSSSTCRGARARYDGCRTDRDGHQI IQRQQQESSSRRTAQPGSSKLCRGPGQHR PSLGTGVHGCSSL
11578	25479	A	11678	514	554	RKPTPTP*GGGEGQNGFLLKPPVSGLP LACPTPKKWKPKPPPPAPPHLFF*KK RGLI**PGVFNLRNWKLPSPFPQROGN KGRNQPPPGTPTMF
11579	25480	A	11679	266	3	GPFLRLGKLN*TFPSPKV*IFPSQVPS SPFQQLKGVREIFFFFF*DRLEQVNS ISAHGNRLNLPSSSDSQAASAGTTGVCHYT RMY
11580	25481	A	11680	1	408	NTCALRHRDHPSPFWSGDKTEGEBRTVQ ENWLLSWNNFSVPETLL/TLSCPLGKEGM PGEDGTAGAGKVPKEDKIPG*DOTAGED GTEDENGTGREDTAGVGKTPGAGGTG EDDTSEEDGTTGEDETAGKGTAG
11581	25482	A	11681	244	420	KDSBSTKAYIRDNISSTKKKKSWPGAGA HPCNPSTLEGGKG*IT*SQETETSANM VKL
11582	25483	A	11682	294	443	QMNTCTHIQPAYVH*EKYFRPSANAHAL NPSTLGGRGGWIT*SQEQTRP
11583	25484	A	11683	346	1	YNTNQFTLRGTQASVVTCLPALIVLKLL NQPTLSAVLLNAGNQPHAPSPPSLH PDAPHSKIMSHITLLIGPPLPASQS LTLSPSLERSGTLAQCNCLPGSSNSP ISA
11584	25485	A	11684	140	423	SSHQASSPPTTASHSHKISVAALPFPFL ITITLGTKESSSRGVPHPSECCPTVYT YKIPAQIRIMDYETNSQCFFKPGIVITK RGHSRWTFNK
11585	25486	A	11685	163	3	IKIPCNRLKFGPPSCCGFFFLPFPFF FFETLSRSVAQNLQWRDLGSLAL
11586	25487	A	11686	179	1	PIVPLGMLFVATAPRGPFESVTKFPNFF FFFMESCSVAQAGVQWRDLGSLQARPP RST
11587	25488	A	11687	192	1	EQGPDCHLASWISLQTKAKWNGDEI CSYYQSCCTDYTABCKPQVTRGDVVTMPED EYTVYDDG
11588	25489	A	11688	89	3	SGGYCCCLCCRCRSYSCCCCLREBGP TK
11589	25490	A	11689	168	2	QDRLQPHESKRKLGAPAPQLRRSESDTP SVNPFQSTESQIMSKGDEDTDRDSKETV
11590	25491	A	11690	301	397	HPVFSIVTGMNPLSPYINVDPRYLIVQ RLFY
11591	25492	A	11691	18	421	TKALQITCYLHSTMSSESDKLTLESLI QLRCHTFWKLILAPETLDELNVDREI QFLDTKYNGVHMLLAYVKILKGQNEEA LVSLKKASDLIQKREHQAQDTRSLQETW NPNANVYHMGRLAKAQTYLDKV
11592	25493	A	11692	188	3	PLQKKGWAKRRGQKRLPLRGQVHNSRP RPPFGPSLFFFFFFETDSDSHSAQDGQVQ CDLGS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US95/15,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=-possible nucleotide deletion, -/-possible nucleotide insertion)
11593	25494	A	11693	24	391	APRADAMGHPTFEEDNATITSLWGQGNVE DAGGETLGRLLDVYPWTQRFDSPGNLGS SASAIMONPKVKAHGKGLTSLGDALQH LDDLKGTFSQSLSELHCDKLHVDPENFKP LGNGLQTALQ
11594	25495	A	11694	138	425	NSGVKAAQFLNPGNPNLEGGKPGPGFKTH PGQLGETHFLKLHYLSGLVGKPKESQL LGNLNRHWHPTPERGGFRDLRHCHGIPQ WATNGHFPVLKKK
11595	25496	A	11695	158	838	CQTVHSCDAGQQRKATAPSHPCDHGNGQ PLLRVRLCCQLFWILCFVSSHINSTRKC PSSVPVSGEAKIKRATITSLKKTIAQK EGSPKVAIRKELGLAQSTSTILRDK QISDAKSSASVKSVTITTKRAGPIDW EKLAMWMDQIKIRIPLSLMIQAKAR SLPNMLKDRASDPTTQMFKAHGWFPQ FKRRHNFHNVKITGEAARAGNEGAIAPK EQL
11596	25497	A	11696	834	1431	SSACQGGSGQWPPRPQPPWMMGNSRRAPS VTHRTGERCTSGSAPFLLLSLSCSSL PRSWHSTLRQPPHPPILLPGCLPGRE AQRLSGAGHGPGPRPAAASVPTDQADR KQQQHHPGPDQHVCHREGLALEDAATHL GLVAALSCWLLGRAEAGYQVPHGHDHPK DQHPQADGGQIRIVRAIGLGLGHVHVSRR ARP
11597	25498	A	11697	143	1	TSKERGASRFSGPW/FFFFFFLESRSVAQ AGVQWNCNLSLQAPPGPT
11598	25499	A	11698	58	459	KGKEEKVKRKEASQNFSPYAKQKRIK GNENDEKTKQKQKTTIDILPLPKGLDETQ ENMDSTLTRTPPEPLENNQKILVLGLDQ AGKTSVLHSLASNRVQHSVAPTLGFHAV CTINTEYSHMEFLIGGSIPFRS
11599	25500	A	11699	215	1	GTRKALMAGGGGFFPFLPFWGFLPFCG GVGKGSPLGCPITFFFFFTESCSVA RLDAQWPDLSLQSP
11600	25501	A	11700	300	420	KPKLLFGNVFAAPHMHLKCRGETVAKE ISEAMKVIQAC
11601	25502	A	11701	351	466	RINKADLSQAQWFTPTVIFALMEAKVGRS LEVSRSPVN
11602	25503	A	11702	172	400	SNRLNRKIQGVFLNDSISIPFLLRKQSI GQAWMLTPVLPALWKAEASGSPENDSTT LLPSSSQVDSLVKMEKINYS
11603	25504	A	11703	284	408	ASVPSSTFFVCLFVFNESRSFAQAQVIL WRDLGSLQAPPPG
11604	25505	A	11704	20	447	LPGADYGGGHLSLRLPHLLASANWVFD ESQVTLNSALCVLSTVLMEFFDLGRHC SEKTKCQLDFPLVKCAKQDPCDKHFP YAAHKCPFAQKLDVHFVFCCLSTPLPV KKGQIPDVVVGDHIDRDCHSHPGKKKK IPA
11605	25506	A	11705	1	455	HSCSLQPTPTANDCTGVSSEQGERFAA AMKICSLTLLSFLLLAAQVLLVGRKKVY KNGLESKVRSEQKDTLNTGTOIKQSRPG NKGKPVTKDQANCRMAATEOREGLSLKD ECTQLDHEFSVCFAGNPTSCPAQDERV YWEQVARKLRS
11606	25507	A	11706	1	428	DARADKMAAAVRRGSRGSGSGCSGAGG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
						ASNCCTGSGRSLDDKWKIDDKPKVITDRWDGSAVKNSLDDSAKKVLEKYYKVENFGLIDGRLTICTISCFATVALIWDYMHPPFRSKPVIALCVISYFVWNGILTYTSYRE
11607	25508	A	11707	1	422	RSQARSSAAAAARASVPLRGSFGPSAIMPMFIVNTNVPRASVPDGLSELTQQLAQATGKPPQYIAEHVVPDQLNAPGGSEPSALCSLHSIGIKIGGAQNRSYSKLLSGLLAERLSIPDRYYINYYDMGAANVGNWNSI
11608	25509	A	11709	88	423	ADAMKQSEAGAPAFELAGTQELRSGKEDAKILLNKKWAKSAERLWGLVSRSSVSHSVLSLSEMLVIEHETPVSAKSSRSQOLDFFDDVGTFCSPGSKYTNPPSLWESIG
11609	25510	A	11710	393	130	NPSATAQSPFHAAKRLSTLDRPGSQAPCKMPSPKPGVVLPASTNAVPTPLAETATPKAHPALSLSTEGIFIAVPSPASGCSFLW
11610	25511	A	11711	331	440	KIFFLNPLISRAWNCAPLVLAWEAEVGRSLYPRRS
11611	25512	A	11712	122	478	SGLCPOQPPRANSCPPSSMASCAEPSEP SAPILAGVVPLEDFEVLQGVDAQGEEREDEDEREEDDLSELPLSDMGOPPAERA EQPGLAREFLANMEPEPGPSPVPKEWLDILGNGL
11612	25513	A	11713	102	2	TNLGNFRPPPPPPFFFTVSLLAQAGVQWCDLGS
11613	25514	A	11714	126	2	FFAPFLKIFPPPPFSEMESCSVLQAGVQWHDGLSLQNRSG
11614	25515	A	11715	178	449	LSGNLFGILLLYCATIGGKLLGLIKLPTLPPLSLLQMLLAGILITNPVINDN VQIMHRWSYSLSIALAITLVAGSLVLE SKALEK
11615	25516	A	11716	48	417	GGGONHSVCCDTMGGGGSGDKTGTGVLAFGFAGAGBAGYSHADLAGVPLTGNNPLSPYLVNDPRYLVDTEFILPTGANKTWGR FELAPFTIGGCCMTGAAPGMNGLRLGLKETONMAHAKP
11616	25517	A	11717	103	2	PKSPITOWLNAVIPALWEAKGGSRESRS SRPAL
11617	25518	A	11718	1	413	WPSGQVLVGLCSFLSYLCKRSLKRNPGFEVLLKIPLKNHPCHTRNMIQLTATPV SALADEPAHIRATGLIPFQVSPQASLE DENGDMFTSQHYRANEFASADLHAAS LGDDYLDGLALRLCLTKLPVFPQSY
11618	25519	A	11720	116	462	AGMLPAGVSVDEREDPASRDCPELVPIETQSEEEESGLGAKIPVTIITGYLGAGKTLLKNTLTBQHSKRVAVTLNESGEGS ALRKS LAVSQGGBELYEHLRNGCLCCSVK
11619	25520	A	11721	167	407	EIVSLARFIEVKGSKKISGCTVVEHGD EMTIRIRKTLKEKLPFVESHLSYDLGIENRDATNDQATKDALAFNKPY
11620	25521	A	11722	254	423	NQLSSINAHFKIKSPFVFNDEPKYVSGSKVAGRVIVEVCEVTRVKAURLIACS
11621	25522	A	11723	3	424	VSCDTMGGGGSGDKETGGIAGFFPGAGGAGYSHADLAGVPLTGNNPLCPYLNVDPRLYEGDTEFILTPTGANKTRGFELALET

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in U.S.S.N. 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						IGRCNTGAAFGAMNGLRVGLKRTQNM WSKPRNVFILDVTRQGLWANTLGALA
11622	25523	A	11724	2	343	AFGTNKWTVLVSFLFSSAYSRGVFR DAHKSEVAHRFKDILGEENFKALVMI QDLQCCPFEDDAFSTSEVPFATTCQDD DHFEDRCRRVHILVVVLQCTPATLLET DY
11623	25524	A	11725	1	359	HAFGTMIQVTVLVSFLFSSAYSRGVFR RDAHKSEVAHRFKDILGEENFKALVMI AFHILHQCPFEDHVKLVNDVTEPAKTC DADESNBNCDSLHSLFGDKLCTVATLQ ETYSBADC
11624	25525	A	11726	1	349	GAMSDRKFSAPRHGSLGFLPRKSTTR RKAKSPFKDDPSKPGHILGFLGVKAGMT HIVREYVRPGSKANTNEVAEAVTIVET PMEVADIAGYMETPRGLRTFNTAFAEH MSEDC
11625	25526	A	11727	81	349	TRGSVSVCCVCLCVCLCTWSHLCRLTW LPDMPDDVLWLMQVTSQVTRVLMCLLP ASRSQMPVSSQQASPCTPEQDWPWTTC SPBGC
11626	25527	A	11728	264	388	QADPFIDIMKFFGPLENQRSLFLLKAT TREAQNMKCNVVRKM
11627	25528	A	11729	2	471	PGCSASWSKRGSGPDMLSNAAAGSVKA ALQVAEVLBAIVSCCVGPEGRQVLCCT KPGVYLLSRNGRRLLEALHLEHFIARM IVDCVSSHLKKKTGDAKTFIIFLCHLLR GLHALTDREKDPACENLQTHGRHWKNC SRWKFISQALLPTOTDIL
11628	25529	A	11730	160	377	LQGRGRPSVYHAAIVLTFLEFFAWGL LTPMLTVSIAELGLCFVREDDKFLGT YTHCVCLDTCLGVALDSDLKQ
11629	25530	A	11731	45	438	KLGRQKATVTIGSCSKSRKRGSPDRF RSPQKRSKGRQDCPTLFCFMKVLDMNE LISPTVIIIGCLALFILLQRKRLRRPP CIKGWIPNIGVGFEGKAPLEFIEKARI KVCGGRGRLQRRQCFLF
11630	25531	A	11732	169	292	DSILLNLACSAVISHCNRLRPGSSDS PASASRAAGAHIL
11631	25532	A	11733	473	600	KFWEKRTSGRKSNSSETGEIVSISA LSTTEVAMRTSTSS
11632	25533	A	11734	19	349	AFSPDMNGHFTEDKATITSLAGTVNVE DAGGETLGRLLGDYPTWQRFDFSPQNL TSASALMGPVKVARGTKVLTSLGDAIKH LDDLKLTFAQLSKLHCXKLVDVPSNF
11633	25534	A	11735	234	359	FYHLKSTVSSVQSRMLTPVILMWSAE AGGSPFVKSSRPAS
11634	25535	A	11736	15	372	KLPLRALTGREKTHINIDIGHVHSVKS TTHLLITKSRGLDERTBIFEKAAEM GKGSFKYKALDKLKAAREGTTIDISM RKFTSKYVYITIDAGHRDFIKDNTTG TSHAJCA
11635	25536	A	11737	1	357	IWKAMASPAGSWARPPEPMHREPTLAM PTNAEDQKLLKRLMKSPDLAVTIPSK MSEWSPPPPPEFDRDVMGSRAGAAGEF HYVRLRRREYQRQDTMDMAEKRIILDA EFQRRL
11636	25537	A	11738	24	335	APNANANGHYTDEKATITSPWGRGNVE

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
						DAQGRITGLRLLDVYVFWTHRFDFRGNLS SDSALMGNPTDEAHGQKVLITSLGDAIKH LDDLKGTFAQLSKLHCDK LK
11637	25538	A	11739	141	335	MQPLFCIPILKSLKESVAHSHSQVHSOI ISTVFNHTGELLSTGDKGGRVVI PQRE QESKNQVHR
11638	25539	A	11740	7	337	APSPDAMKHFAERDKATITSLMCKNVNE DAGGETLGRLLAVYPWTQRFFDSFGNLT SDSALMGNRKNVAHGTQVLTSLGDAIKH LDDLKGTFAQLITLWCDKLVDFENF
11639	25540	A	11741	182	360	SRHSISPPVNIQLGASVTBELTVVTRT NRVSRQAQMLNPVILPALWEAEAGBSFEVR NSR
11640	25541	A	11742	174	1	HFSDRSLFVVCWGLDITLPLELCCSLLT AHCSLHLLGSDPPTAASVWSGNTGVHY HA
11641	25542	A	11743	75	218	KITLGRQAQMLNTPVILPMEAKVGRSPVS AQSAWDYRREPFCPCSTI
11642	25543	A	11744	168	2	LAPLNSLGPVLGGVQSSPGPGPPFPFF FFFTFETSCSVARLECSGPIIAHCSLR
11643	25544	A	11745	83	2	RBQRFLPFPVLCDAPEGVYRGRAS
11644	25545	A	11746	156	3	FESGSGRVRNENSPFFSFFETGSCSVTQD GECTGATLAHCDLFLGSSNS
11645	25546	A	11747	244	330	KDRAQWVTPVILPALWAAKGRSLRVRSS R
11646	25547	A	11748	201	1	TSQPLRITLSTLSTFFFSRDGGLMLPEL DPPLPGSSNPSCASRVDGTGMCHHT RLIFFSQITDKK
11647	25548	A	11749	262	3	VYTSLTFFPPISVNLLTQVSPRSVSYBON ILCLLPVYTYTCTFFVCLFVCLFVCFK MESCSVAQAGVRMRDLGLLQAPPVPGFTY TT
11648	25549	A	11750	225	3	PIINFSVPQFPLHLYNGILIESTPPSCCI LKQCSLGAQWFTPVITLWEAEAGRL EAWTLKITLANAKKHL
11649	25550	A	11751	185	2	VSTPFSFSPFPNDLVFLKGPFFFTFF FFTEFCSSPLRNGAPLAHCNRLRPR SSNSP
11650	25551	A	11752	261	336	DRVSLWSPELECNGLAISHCNRLRP
11651	25552	A	11753	282	381	TDLLYKKKCGLGAVAHAYNPSALGGQGG RITCS
11652	25553	A	11754	202	45	NPRKVKLQWALTLPPLNGLGGLKSRFQ KKKKKKKKKKKKKKKKKTLVVIC
11653	25554	A	11755	293	357	LTPVILPALWEAVGGSPEVRS
11654	25555	A	11756	264	1	TLPIINVCCDHSFGPSLISLPLSLPYS LRHNNIEIRLNNPTTACKYSCLKSHK SLTLQKLEMIKLGEGHLLKAQIQGLIG LHQ
11655	25556	A	11757	126	1	ILPGLKRLKIELFPNAILPLGIYPKE KKLYQKDTCTHMF
11656	25557	A	11758	399	226	IEKGTGRVWMLTPMILPALSEAKGGSPE VRSPPACIGLGLKFWYRCRCPQPARLS EI
11657	25558	A	11759	235	380	DTTVLKIGQLITLQWASKCSSREKSRSTS LTLTQKLEMKLSKEGWSKGD
11658	25559	A	11760	249	357	NRASGGTWCPTTIPALWEAEAGGSLEP RSRLTLWA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, = possible nucleotide insertion)
11659	25560	A	11761	168	372	KLEHLLCFYLSEFFVFCFLETSLSLVAQ SKCSGTVITHCSLKLCCSSDPATSDSRV ABTTGTGYHAGL
11660	25561	A	11762	303	377	QFAGCRWMPVIPA/WEAKADGSP
11661	25562	A	11763	135	1	ATTPGILFFIFYFFETESHSLAQAGVQCM ISVHONCLCPGSSDSPV
11662	25563	A	11764	219	2	KLRSSQLSEPEVRPDSTLSMLNHARAHT HTHTHPFLPHPCSRPHSTPTCMPIV TESPILYKFFHSHTYLL
11663	25564	A	11765	102	1	NRPINNPVTAASNCSSSEKSHKSLTNQK LEMIK
11664	25565	A	11766	245	3	POEPESDQLVKRFPESLLWFMFLFLRR SLAASPLKCSGVCESSVIAHONCLCT GFKQFSLCLSLGWDYKRVPPKPS
11665	25566	A	11767	350	97	GSPVASKQVTRPTMLTSLADKNFSLCLT SLRVNPGVALILSGSHSVQDTLLDLTL FSTHLGLPKCNDYKRVPCSAQFLVTL
11666	25567	A	11768	188	391	LGSVAGDLLCFPGGVFFPCSRNFMFLC YYLYIWNNSCVFLFFKTEPHFVTHSGVH WCDOLLQPPPPN
11667	25568	A	11769	131	2	YLYIYNKSPINQLSWAQNLPVPIPA LCGAETGELLEPRSS
11668	25569	A	11770	165	1	VLIFLTHLCTYYTYVYICVYYTRYPT HICHITHVYIHYVYIHYTYTYMYTY
11669	25570	A	11771	72	1	ILLFFFFFEASCSVAQAGMQWCM
11670	25571	A	11772	121	3	TSFVLPCPETFCSCCCGLEGCAILLAH CNLRLPGSSD
11671	25572	A	11773	152	3	HVCLNLTLPFLFKFNIPSLVCVVCVVC VCVVLCCKKCKDKFYFERT
11672	25573	A	11774	190	2	GFSPRQRGAPRVPPPLAGPFPPIFFFF FFEHWSHVAAPAGVQWCHSSSLAALTSP DSGDPP
11673	25574	A	11775	287	1	QMRRLKLPITPGKSLERQIAGFPHRGG EKKKTLFYKKKKKKKKKKKKKKKKKK LPKCNVYMQNHQVPYSIRPTECADLRV PFYIKFOLIKY
11674	25575	A	11776	121	3	KCAERDLKSKFFFFFLETESRSVAQAGV QWCDLGLQAL
11675	25576	A	11777	142	1	ERTLHVNTTHNSRGSLLVIRHGRLOVV AHACNPSTLGGRGQITRS
11676	25577	A	11778	179	3	SHQPVGTLTLPRGPKQSTSEARESEA SMSKASSEDLVPLLEAGNAPYREEEEA KK
11677	25578	A	11779	147	6	KTPGLKKNNSNFFFFFFFETRSHTIARA GVRGCDLSLQPPPLGLK
11678	25579	A	11780	184	3	GGPGFYIIPNYRLEFFSLIGPFFFLIFF ETEPCSVARLECSGVISAHCNIRLLGSC DSEA
11679	25580	A	11781	120	319	VKSLAKFLVNYQLHROTCSQAGRGALR QRFGRPROVDHLRPGVRDQGGHGETPS LLEVRKLSGG
11680	25581	A	11782	91	3	YICLSLIYTHHTHTHTHTHTHTIYIYVC V
11681	25582	A	11783	221	332	SLKLVNHPHRSVGRDHPGGHGETPSLLK IQKLARRSO
11682	25583	A	11784	243	379	LKYSVETIGICKPWPGTWHTNPSTLGG QGGNITLDQKFETSLAN



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, N=Methionine, Q=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						THSPLLAQNFRVGAVPSPRFSRFGSKG GOGFFFFFFFFFFESHVSVAQAGVQWCD LQSLQALPGPF
11702	25603	A	11804	202	3	WSVCCFKQQLGLSPRLCNGAQPFGKSF PLSLLSNMYRGPPRLNFFFFFFFEMRS CSLAQAQVQR
11703	25604	A	11805	3	315	FMLLTLLTFLLRNDRVQCDVRSSVCL GFLLGWSVILYPLMAAPMTMIFLFLIL FSMLFFYYVFFLFLFLFLFLFLFLFLCF FFCFYLFRRFFFFFLIFFSSP
11704	25605	A	11806	126	3	KRGFFFFFFFFFFFETSSRFAQAGVQNC DLGSLQALPGV
11705	25606	A	11807	130	2	QSTKNTCSSLYPFTTKKNVANKLTPVVA LWEAGAGGSHSPKS
11706	25607	A	11808	149	1	GGKKALLFFFFSLSPRLCSGALPTICK LCLPGSRHS PASAPRVVVTAG
11707	25608	A	11809	258	3	KYYVGNRQIKFVNASKNKLPSYSQKA SWFSSRNIRIMAGQWMLNDPTSFYKK LGOANWLRPVTIPALWAEAGGSLERSL
11708	25609	A	11810	153	285	CASPIRSHQKLNKNGVQWMLPVPVFN EAETGSLQLRSSRLA
11709	25610	A	11811	160	3	NHLFLLLNRYKSTPTGRVQNLMPVSSAF WEAKAGRSFPRSSRPAAQGHGKTL
11710	25611	A	11812	89	2	APFFFFETVSCSVAQGSVQLCHLSLQL N
11711	25612	A	11813	254	336	LLGQGPQLWTPVTPALWEAERAGRPSEVR
11712	25613	A	11814	108	2	CVGVIGFPVCLFFETSSCSVAQAGMWNH DLLGSLH
11713	25614	A	11815	166	289	SHSGWNAVWRDGSLOPLTPGFKRPFCLR VPSSWDHKKAPPC
11714	25615	A	11816	192	2	KDQPGKVTFRPFLLLCIFLYLFCFLRRT LAVSPRLSFGSGRCSEPRSHRCTPSKVT EQDSCK
11715	25616	A	11817	228	343	LIQSTQNEADGAWMLTPVTPPLWEAK AGRLSEVRSI
11716	25617	A	11818	322	407	VRLMLLHCLRECKLVQPLKWTWQFLEKD
11717	25618	A	11819	119	1	WEKIVRGKKCKENTHTHTHTHTHTHTH THTYRESKRERLV
11718	25619	A	11820	269	1	PVQVFIYLTQSCFLCTCCVFLFGYHLS SVSNRPMRSKGSTFFPMISEFFFPERS RCVQARVLECSGSIASHCKLHLDPGRH SPALV
11719	25620	A	11821	217	389	EHITVYVKGLESHHGKGLFNKWLTI WKKDYSQWMLMPVTPALWEAEGGSRV H
11720	25621	A	11822	188	1	GSHMPCRVISVHESMNEFPAPVPTSYP NPQPERAMRNQREKEDKKERSQSRVGR VQAGLV
11721	25622	A	11824	126	3	KLGQGVONLTPVTPAPWEAERAGRPSEVR SSRPASTWRNLV
11722	25623	A	11825	224	3	ALITKKEVSAMELEGSNRQIAYGVQST GARDYHAAASRPVPAIKGTHEARVIVP LVETGFHHVQAGLDSC
11723	25624	A	11826	3	364	HELPEPLRLVLTAAHRAVAMAPGSKTSLLL AFALLCLFWLQSRAGAVQTDPLSRFLDIA MLQASHRAHQLADYTHFESTETPIPDQK YSFLHDSCTTPFCSDSIPTPCMSETHQ



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, N=Methionine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
						KSNLELLR
11724	25625	A	11827	2	376	ARELPETPTVLRTAHLKMAAPGSRITYLL LAFALLCLPLWQAGAGAVQTDPLSLRFDH AMLQAHRAHQLAIDTTHYDETYIPKDH KYS ILHDYQTS PCFSNSITTPYKKEETQ QKSNLELLRISLL
11725	25626	A	11828	288	3	LHTKNPSVHHHHQRPRVKTRTKMGKQKS RKTGNSKKWASPPPKKEISSSPATEQSN TENDFDELREGFRNSYSELQETIQTK GKEVENFEKN
11726	25627	A	11829	107	1	KSGOVLQRSLVRLTPVITPALWEAEVGS GSFVVC
11727	25628	A	11830	220	354	CQNSPKNTLAPWLTVAHACNPSTLGG CQGRITGHEITETLLAN
11728	25629	A	11831	273	352	ENLRKGTQMLTPVITPALWEAKAGRS
11729	25630	A	11832	239	488	SOHCSGKRTENSIGHSNDRQVPTPALMK RPSPARPLTEAVPPPPVDYLQSVAAFA VSAAVQWERTGKPPFNPPLGETYELIR
11730	25631	A	11833	189	294	DOTRWLTTPVITPALWEAKSGSPVVRSSIL HFPLLF
11731	25632	A	11834	1	332	GTSPEPLTVLWIGDLLAVGSRISLILL AFALLCLPLWQAGAGAVQTDPLSLRFDH MLQDHRAHHLAIDTTHYDETYIPKDK YSPLHDSQTFCCFSDSIPTSPNMEET
11732	25633	A	11835	330	175	PRETAQLGSPNVRVSRVPRGQPMQPF FFWRQESCSVAQAGVQWHEPEQOE
11733	25634	A	11836	96	1	VFVETGSRSVAGDGGQWCDLSLQPCPP RPEA
11734	25635	A	11837	267	334	SRVQMLTPVITPALWEAEAGGSP
11735	25636	A	11838	180	2	SVLEKKERNLYKGLFTYKLLKVKQGRIT CBGRAQICSVVCVCVCSVCTCVHVCAY SSC
11736	25637	A	11839	183	2	AAPLTSSAPQAGWKPHLAPNSPFFNFT GUGAQWLMPTVITPALWEAKVGRSPVVR LSSC
11737	25638	A	11840	54	330	DPNQQLPEPLKGLTAHLVAVAPGSRITS LLAFGLCLPLWQAGAGAVQTVPLSLRFDH DHAMLQAHRAHQLAIDTTHYDETYIPKDK DQKNSFLD
11738	25639	A	11841	117	344	IQYVQYQINETEMGNNSYLAHNTSLTITY HTLCLMGSYLSEHFQNGCKGRARRLMPVI PALWEAKAGRSPDVRSSKPA
11739	25640	A	11842	750	968	RAQGRPWITKIPFSSPRLPLPLPLVFL YNSPLPLPPFPRTNATNSPFPPLPLPP LPSPPPPPPSPSRPPPS
11740	25641	A	11843	757	1000	VVELVWYCCLESFPFPLPSPLPFPPPP SPPHSPPPSPFRPLPLAPTRPPPPPS LPQADPLPLSPSCSPPPPPPSLSFL
11741	25642	A	11844	278	361	TLLFFFFFEMESHFVARAEVQWRDLGS
11742	25643	A	11845	260	2	GSCLLGGKLTNRKDITHKNPSVHHHQR PKVDKTKMGKQKSRKIGNSKKQSTSP PKERSSPATEQSNMENDFELRREGFT RA
11743	25644	A	11846	194	2	TSFAKRPSPPPCWQGVKPSPLGFFPCP RSFPVNGFPLKLNLPFFFTETSCSVQA GVQWCARA
11744	25645	A	11847	219	1	SLGHTLKQSESSLSPSGGTPLLSEFKPS

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						VYDPSVPPQVSKGGCVGFFFFQTESC SVAQAGVQWHDLSGSPRA
11745	25646	A	11848	126	3	RFFFKGLFLHFFFFFCCFLETSHSVA QAGVQWCDLGLV
11746	25647	A	11849	216	339	KCFKVGKVKLNKRETFYLAQNFDRNWA TQKMWVKTLELI
11747	25648	A	11850	190	334	VSYIHMSFFVYNEKIDHLLCKDENG QRKQPVRLKQFIIICEFEL
11748	25649	A	11851	198	352	SRQGTWSHGIECFVCLFVLPFETESH FVPRLECSGSAISNCTHLLGEL
11749	25650	A	11852	371	1	PPKGLGIQVTFPPAPRAFWVLVFKKKG FPQGMVLGFFFSKSVISQVPPFKRPF SGCBARQIGFFINRGKFFFFELGFFL KKVFLAKFLAKFFFFFETESHVAQ AGVQWRSGLV
11750	25651	A	11853	176	3	EKGFFLEWNSKVKNIIVKPGEDIQSKT LMTFFFLTESRSVAQAGNCDLSLHS C
11751	25652	A	11854	281	375	QLTPKFKYFLGWAQNLTPVLPALWEA RSP
11752	25653	A	11855	146	356	KCSALITAEIVDLFSLEDRDFLAYSRT EILCFKRCVPSLHHRALDAVDDCLHSC CTDYPINRSLMAY
11753	25654	A	11856	136	1	LSLLCEFFNWLTEMEYSVSAQVQWCD LSLKPFPFRLQOCHSC
11754	25655	A	11857	277	361	IVLKGAVMLTPVLPALWEAEGGSFEVR
11755	25656	A	11858	295	152	VVFGGFFETESHFVAQPGVQWQNLGSL CSLRLPGSSNSPASAPQVA
11756	25657	A	11859	1	342	GTRLPEPLTVLMTAHLGAWAPGSRSTLL LAFALLCLPWLQEAQVATPVSRLEFDH AMLQAHRAHQLADTYQSEETIYPKDH KYSLLHDSQTCFRFSDSIPTTYNMDTQ HK
11757	25658	A	11860	244	332	TIEMMLDIRQIVPLFEPFMGRKRIAE T
11758	25659	A	11861	1	339	GTRVVTICQVQLHAYARFLYFPEMBARS VAQAGVRWCDLGLQPPP PGSSSSSSSS S
11759	25660	A	11862	311	394	GMLGAVAHACNPSTLGLGQNTCSQEF
11760	25661	A	11863	130	1	VPPSVRTFFFFFETESHRSVAQVQWQH YLGLLQAPPGSTSC
11761	25662	A	11864	3	320	IMMYALFLLSVGLVHGFVGFSSKPSPIY OGLVLIIVSGVVGCVIILNFGGGMGLIV FLIYLGMMNVFGYTTANALIEYPEWANG SGREVIVSVLVLGAMVGLVIA
11762	25663	A	11866	165	309	GLTLLPWLECSDRISHCSLYLLGSYDP SDSGSRVAGTITGCHYAWLR
11763	25664	A	11867	208	314	GSRNKLSGQQLTPVLPALWEAEEVGS PEIRSSR
11764	25665	A	11868	102	1	KKFFFFFETESHVAQARVCNGLSLQA PPPRFT
11765	25666	A	11869	126	3	NNALQLHSSYCKKFFFLKTESRSLTK AGVQWCDLGLIQ
11766	25667	A	11870	1	273	KQLPVNPLGRVRLLELGLLCTINLSKPC NPLILLVIVKYFLLFCNI FKHIFPSQA QMPFVLPALWEADWGGSHGYMTTIVD FMCATIT

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11767	25668	A	11871	126	2	FPKALLVVFPPPPFFETESRSVAQARV QWHNPGSLQCPLR
11768	25669	A	11873	269	9	QVSGKFWPDI FYKTGEKGLQCPNPTQGH PPRGLKKKSPSKKKKKKKKSLAVGQAQ WLIPVIPALNEAKVGRSPVKSSRPACP TW
11769	25670	A	11874	114	1	LEAKPGVFQSGVLLVIFPPFFETESHVS QAGVRNCDLG
11770	25671	A	11875	146	1	GNHLSRRVGVDQPRHQKTLSTLQTKQ VAGPGGAHLQSQEVQVGGSL
11771	25672	A	11876	2	159	SLQPPPPFFFRMSFVLVACAGVQWHDLSG PQP PPGPKHS PASASQVAGRGGR
11772	25673	A	11877	124	240	FRAPSSGQAMLTPTVPIPALWEATGGSL EARGSPDWT
11773	25674	A	11878	135	5	QVLPFFPFSDFTLSPRLCSGVTLPHC NLCLPGSSSDSCASAS
11774	25675	A	11879	170	2	GFFPFEKMGYKNSFLCTFPFFFPFPRFC SVAQAGVQHLHLSLQPPPPVVKVDAP
11775	25676	A	11880	97	267	GHGATVGLICVLSLFFHTPAPSVSQTS DARECCLCVYRLICGVYSRNCILVPSDH R
11776	25677	A	11881	1	292	LPEPLARVMTAHLQAAPRSRTTLTLAF ALLCLPWLQAGADQTVPLSLRFDHML HAHRAHQLAIDTYQEFQTYIPEDQKYS FLHDSQTYFCSD
11777	25678	A	11882	93	2	KYQKSNANMLTPVILALNEAAGRSFET SC
11778	25679	A	11883	145	2	PPLGLRLQVQAPTGGFFFFETESRSP RLECKGAILAHNCNVCLLV
11779	25680	A	11884	202	1	TWRNRGVTVLVRLVINCRPCDRHKSASQ LIGRVQRQENGLNARVGCCS EPRS RHTP VNVTSNPSSC
11780	25681	A	11885	42	155	GRSGLSRGVQDEPGHSGTSLQKILK LHGIGQCP
11781	25682	A	11886	215	1	STMAHICTPSPMLFHSANVLVRLSQE KRIQGIQIGKEEVQLSLTDDMI FNLEK RKDCSKILLQVNLV
11782	25683	A	11887	214	1	GYFFPLNVLGLKLEKSLKVPQNPSPKR PFFLOFFFFETESRIVARLECSGAI SAH FNLCPLGSSSDSPVSC
11783	25684	A	11888	215	3	WGPFGFFFSFFFFFLRQGLAVRLKLCSSQ TITAHCSLNLFGSSDPPASVSLVATTG HEPSITQFHSHGSC
11784	25685	A	11889	118	1	RFFINGENPTKFFFFFETESLRLPRLCS GVISAHCNLS
11785	25686	A	11890	267	83	HCLRSVGVDQPGHGRNPSIQTKQKAT SPKKSLKIVIPPLPFPNDKTD SKSSCS LSPHS
11786	25687	A	11891	134	2	DRLAVLRLPRLCSGMI FILPLPSRPIRPS CLSLPSSWDYRGAPRA
11787	25688	A	11892	116	1	SKGVGHFLFFFFFETESRSRVAKGVQVQ CDLGLSLCLV
11788	25689	A	11893	397	475	RFVCSITIKVRLDLSRDNPNGRFLST
11789	25690	A	11894	115	331	KNVCLPVFVEMKNHLNPGDEGCSKPSR HCTPSMAAQQSISKYICITRYLHLDIY LSKLVRLRINQLPNS
11790	25691	A	11895	134	251	INPPVSRKKKKKKKKKKKKKKKKKK



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11810	25711	A	11915	274	385	IKPQRHGETRAEKLKSLKIRVPLLLQRN AAPHQQWKK
11811	25712	A	11916	259	441	DTKLPRKVNITKLNPHALKKKKKKKKKKKK KKKKKKKKSSSLRG
11812	25713	A	11917	254	402	LIVSVIDFLRWRLLPLEKLECSGNTSAH CRLRLPGSYHSPASGCQLLGR
11813	25714	A	11918	223	1	NTNSPRKCKFFYRVSVVVFVGFVFPSP LKGSFRAFLKLAWRPPLDPLFFFLMRSR SAAQPEVQWCDLGLSLQPP
11814	25715	A	11919	97	3	KPPFFPVQDFDFFETESRSVYTAQAGVQRD LCS
11815	25716	A	11920	154	384	KEFFLLMLFFLFPPPPPPPPPLGLKGLF FFPFGGGGGGFFS IGFPPFRGKKDFPP SPPKSGKKGTTPP PPTFFV
11816	25717	A	11921	225	369	GTLLNLLPYKIKSNQAVAHYNSPTLGGW GKWNITSQGFETSLANVUP
11817	25718	A	11922	116	372	MEYTNKMKANSYLNHTYQYKNSVTEHP TGVLPDSRVMVNTVLCYSKQJLKLRL RLMWEHLSPGGGCSDEPRSRHCTPAWA T
11818	25719	A	11923	271	409	KKKKKKKKKKKKKKKKKKKKKTGGGA
11819	25720	A	11924	121	228	KKKKKKKKKKKKKKKKKKKKKKKKKKKK GGGFKKKPWGGQK
11820	25721	A	11925	55	423	NKPKKKNLFLKKKKNNFFFFFLKFFFFF PKSLNFFRVRVVKISPPKKKFFFNKNS VFFFPDLKKNNFFFLPLKLGFPNNFFFK RPPLPFFFFFFFFFFFLSGNCKIKGL
11821	25722	A	11926	253	443	YQHQRPKVDKSMKGNRNCRKSSNSKNQ NTSGPPPKDHNSSPARQQNMWNEPDLGT EVGFRW
11822	25723	A	11928	175	413	KKKKKKKKKKKKKKKKKKKKKKKGGG A
11823	25724	A	11929	490	182	RKQKTKGCKKNNPLAQGVKKKAKKQPP FNFFLQKQDPLJOWNLQKKKIDIPP OVFSLRQKGAFFDRIFFFFFFFFFFESCS VAQAGVQTLGYKHNKIK
11824	25725	A	11930	110	2	KKLPKRPFFFFFFFFFFYKAGSLVLAQAG VQWHDLS
11825	25726	A	11931	169	987	YLEKINSRHSNSDQEBLLDEYNEDRI LANLSAEELKELQSEMEVQADPSLPGV MIQKQDQTKPPPTGNFNHKSIVDYMWEK ASRRMLESERVPVTFVKSEKTKQEBEHE TEKRNKNMAQYLYKSKIANEIVANKRESK GSSNIQTDDEDEEEDDDDDDEDDG EESBETNREBEGKAKQIRNCENNQQV TDKAFKQRDRPEAQOSEKKISKLDPK KLADITSFLKVSTRPSGQVTDLDGSLRR VRKNDPMKELNINNTENRK
11826	25727	A	11932	161	389	SVQTHPNLRSCSVLKNAHFYLLGYVIS GCTEPAKATKPTDKSVHQICSGPVVLS LSTAVKIKVNSLCAATNI
11827	25728	A	11933	134	289	ASTYKQKGLRLHASSFTLSLSLSHSTHI IKHTIRMIHTHTHTHTHTTPTLKV
11828	25729	A	11934	128	1	TKKGEFFFFFFFETESSRLOQSGOTI LAHCNIJLLGSSNS
11829	25730	A	11935	131	19	MYTGWQNLTPVTPALMEPRVQASLEAR SLRPARTSE
11830	25731	A	11936	104	3	LKQQLTRAQNLMPVTPSLWEABNGRSP



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						SAWPT
11855	25756	A	11963	43	2	COCYCCCCCYCC
11856	25757	A	11964	30	415	GLGPKRKIFFFFFLGGGNFLLLRKKR PFLPPPPFPKPNENRGVLLGPGSGVKKP RPRQGDVPPLKPRSLGVFLTSKKTPLGP WANPPPPPGDGP
11857	25758	A	11965	149	2	SKTNLKLAKLYRNTYPGVNRVLIPIVPA LMOAGAGELHEPRNLRPAWAT
11858	25759	A	11966	179	3	KKNIFPPPPVKFGPPQGFFKRPPLFFFF FFFFFFFFFFESRSVAQAGVQWLSIGSLQ AP
11859	25760	A	11967	245	382	DVTSKMHDPFESSHVRMLGSLVVAHCK PSTLGGSGGQGFKSLAN
11860	25761	A	11968	264	10	LSYLEKRGVSKRVSPKQRRKGLDYIFS PFLKKPHIPLGLISMVFFFFFDGVSAQ AGVQGRDLGSLKHLPSGGSSVSCASASLS S
11861	25762	A	11969	326	406	RLKGNLWMLTVPITPLARATVGRSPR
11862	25763	A	11970	120	1	KGYGFPFPKPKLGGPPFFFFFATESCSV AQDGVQNRDLGS
11863	25764	A	11971	84	370	RNGAELEKTPLAGQOTITINCRYSAVTLV LGLDLSILCWHIFPKKTNLFCGFSSFL LGAGRMKSHCVVLECRGMISAHNRVCL LGSNDSPCSAF
11864	25765	A	11972	196	3	SRGRMGEYPPVFLRNPSHARAGNGKNP FFFFFSBSCSVAAQAVQWNLGSLQAP PPRFTFPA
11865	25766	A	11973	559	644	KIGCSAYGVAILLFLYFNKLAFTLAKK
11866	25767	A	11974	3	391	HEAQLPEPLVLGTGLAEVAGGSRTYL LLAFGLCLPWLQAGAAQTVPLSRLFD HAMLQARRAHQAIDTYQSEETIYIPKO QKGSPLHDSQTSFCLSDSIPTPSNMEET QOKNLELLRISLLIE
11867	25768	A	11975	138	365	LKFECHSLCANRQKOTFTVFYKRLLL KTFYFSVLTYADNWIINLINVFKKKK KKKKKKKKKKKKKPKKKKQ
11868	25769	A	11976	275	433	MSLIDLSKARNFFLSPLTGSCTITQAG VQVNLHSSLOQPTGRLDDPASAQ
11869	25770	A	11977	108	3	RGLLFFFFETRASPGRGHNLSLQPLD PRKRF
11870	25771	A	11978	270	408	FENNVMLGRAQNLTPVIALNRAQAGRS PGPENQNHDPYKGNPWPY
11871	25772	A	11979	228	441	QALKFVIRMLLSLKKKQDVSVIPNRHK IELLQKKKKKKKKKKKKKPSQKKD SSRGKDS
11872	25773	A	11980	2	447	GALANIKTTADVRLNLFVSLGHWKRWL QQTSLSKMWXIKBCSLKKKKKKKKKK KKKKKKKKKK
11873	25774	A	11981	124	445	KYGMESQNPARGPKFSNQRYSBHLRI HCCPPFTFLISKKEIGDRKYSICKSGCF YQKKREDWFCCPQKTKISRAKSLKRP QKKPVAPPGGVKAPAKPSLPRF
11874	25775	A	11982	48	429	KESNGSQRLPLKILHSPIVSGKSGGMS QNPARGPKLSKNGKSSHLTHCDPL PFLISKKEIGDRKYSFGSGCFQSKKK DWICCPQKTKLKKLRPPPKNGPGGS LNGRTTWSGLPVLIN

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11875	25776	A	11983	419	500	SLLVKVEKQNPQAVAHACNPSTLGGPG
11876	25777	A	11984	362	496	LWSPIRILLRANWHVPTVPAINEASV GRLLRSLCKMVRPIS
11877	25778	A	11985	142	433	RFVCSSTIKVLEDLSSDRSNFQRLSTSN SSLKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKGGGVIKKFLGGPIFGGGG KKKFFFPGGGFIN
11878	25779	A	11986	177	2	QQRRTVTLSSHFTSITRPLGLKQKWSF GAVHTYNPSFLGGGGVNTYVHTRRR TR
11879	25780	A	11987	178	443	DKKKKKKKKKKKKKKKKKKKKKKKGGG LKKI
11880	25781	A	11988	329	410	LIFFFIFPERBSHVAQALVQWHDLS
11881	25782	A	11989	146	1	DKASALQPRCGKGNFVSKYNNVVIYII NTLITTLFGTTHDLSPL
11882	25783	A	11990	240	420	GVFAPLGLGVDSQSVGTFRDPLEEAVCL FLELECHARTTALFRAVRQCLSLQNL SVAF
11883	25784	A	11991	239	410	GTLFIYLLGLDLYIFRNKSLTLLPRLQC GGVIVAHCSLDLLGSGVPSISALPSSND C
11884	25785	A	11992	126	3	YTGEEKSFCRDKTCTHFTNALETIART WNKPNRGVGGGV
11885	25786	A	11993	300	22	SQLLGRLEQENHFNWGRCCSEPRSCRC IPAWATRANSIFCGPQASSVEVRSARK KLFSDDLKRHTISWRVSGLLLVDSYFG RLATPVRQAQ
11886	25787	A	11994	303	2	EGEEIPLSPSPFPFQENPGSNCSPLP PFGTFLDIRVAGSHKQVAGVFKRPPS LALFLIKKRRFFFFFETESRSVPQAGVQ WRDLGSLQTTPPGFKR
11887	25788	A	11995	171	457	SFSDELGLWIGPCNNLSKALCLSSPIK NRNDLQKKKKKKKKKKKKKKKKKKKAS SYQDS
11888	25789	A	11996	357	204	EKTGPPHVGQAGVDLTSRSTRISLPKC WDRHEPMRLAGHLVYYPQMK
11889	25790	A	11997	219	1	PRVFWAPPRIYPRGALPMAFPVGVSLG ARADPTKAGPRQGAAGTFFFFEMESHL SPRLCNGTIAHACNL
11890	25791	A	11998	254	1	AHLRGNRQLPHTFFQVMTINLCKAFSV GRQSYSLIPWSFYTSLFFKYSVCFHTHT HTHTHTHTHTLYFQIMVLLPSLRKGS
11891	25792	A	11999	167	2	NFKSEFQGLSRGVINPKVNLFFLETS CSVSQAGMQWGLDSLQPPPTRPPIRP
11892	25793	A	12000	104	3	RPWTFFFTSRTKRSVAQAGVQWRDLCS LOPPP
11893	25794	A	12001	178	2	KIFORGAKNSPWGLPFGNGENKKGAPP OKGGRFFFFFETESREFTOTGVQWCDL GP
11894	25795	A	12002	163	282	GIGGEWCLSRVYIVYVKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKK
11895	25796	A	12003	195	2	KWGRIPLEKGGFCFTKESGQTLILKSP PPAFVVFIFPFLLETESRSVAQATVQMC DLAGSIQAP
11896	25797	A	12004	152	1	CFVDSAKKLEPRDPMHTKDEAMATKAK IDKNALTKLKSFTAKRTIRV
11897	25798	A	12005	339	1	EVVPIINPPKKRVLKSVSKQFISAPIR



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
						KKFFFCQVGLILAPRVLLIGRPPFFFFFGVILNVEIQRMSEFISLVVVVRARIMMYALFLLSVGLVMGFVFSSSKHCVPVIGALVLSIGSRV
11898	25799	A	12006	189	12	DGRLPGSVCTYLIFLRQSFLLAAQAGAQWCHLGSLSQPPPPGFKGRVRVSRIRAVRGDQ
11899	25800	A	12007	131	3	KIFFFFFFFEMESHSVAQAGVQWRNLGSMQDPPPGWMLLFY
11900	25801	A	12008	150	2	IIILFLNPIEAVFFFFETVAEAGVQWNLSSIQPPPPGFKQSPASARVA
11901	25802	A	12009	305	3	KFFFSLKASIRGRWFGLFFTPPKKGFLPKPQVVEKSGPLWENLQGLKAGNLMLGPYKSPFGAARVFVFVFETESRSVAQAGVQWRDLAAHVASHASAS
11902	25803	A	12010	263	517	DKGFLQPPKRCQGDPLFFYGGIVPCKGQYGPPIFFFFFTAESRLVAQAGVQWQDLGSLQPPPCRTGRSP
11903	25804	A	12011	107	374	WMGTWGLPVLLITTSCTCPSPSRIRHRRTGATINILFRLAFTGTVLPLMRCSTVIMAHCRQLPFGSSSSPTIASQVAGTKAHLSDCFVY
11904	25805	A	12012	144	261	FPKRLNNFYPTFLQDPDPIGIFSLDKTIGLGTYGRIVLS
11905	25806	A	12013	371	3	IFHLRKIFTFPLPGIFWPIRLISEKKPKRFWVKIKKFKNGVPLNPIPKYKGRPRFFKGEKNPKNGVPLKIKKIPSPFSKALGFLQKQASKPFFFFFTDESCTVDQSGVQWCDLGS LQAP
11906	25807	A	12014	101	3	RGAPFFFFFETRSRSVIQAGVQWCDLGS LQAP
11907	25808	A	12015	205	2	VNPSGINVMVDAILLAKELATRIQQH IQRILHDOVGFIHQMGWFSIRKSNIVIQINRPKDKN
11908	25809	A	12016	168	1	GCVCQFQKRLANGGLNGFFFLFFPPFFEMKRSRVQAGVQWMLSLSLQTPPPPEFK
11909	25810	A	12017	311	2	RGLRFGQMKTKMENINTPFSALRPGQLSIRSGLLHTYPLGLGDHSPPLSCSLSSSKYVMQAVTSALSSNPKGASQGHKWDFFFLFFETESCSVTQAGVQWH
11910	25811	A	12018	383	247	LVEMGRFHVGGQDGLDLLTSSQAHGLPEKWN DYREPPRIATIEVL
11911	25812	A	12019	2	379	RVLMATHLAAMAAGSRTSLLLAFALLCLPWLQERAGAVQTVPLSLRFLKEAMVLAHRAHQLAIDTYQRFISSWGEAVITKEQYSFLHDSQTSFCFSDSIPTSSNMEETQQKSNLELHISLILLIES
11912	25813	A	12020	3	389	PEPLRVLWTAHRGAKAGSRTSLLLGFA LCLPWLQERAGAVQTVPLSLKLFDHAMVLAHRAHQLAIDTYQRFETYIPEDQKYSFLLDSQTSFCFSDSIPTSSNMEETQQKTNLELHIFVLIELMLDP
11913	25814	A	12021	247	386	PMLGHVSSQSGNGVRDLLEAVCPKLAKHCSGRSTALFRAGQKQ
11914	25815	A	12022	17	371	PLRDLWTAHLEAMAFSPRTDLLAYALLCLPWLQERAVQTVSLVRLSDHMLQAHRAHQLAIDTYHELEETYLKDKQKYSPLHDSQTSFCFSDSIPTSSNKEETQQKLYLE

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v =possible nucleotide insertion)
11915	25816	A	12023	3	359	LLPLSL LRALWTADLGAKAPGSRFTLLLSALALC LPWLSEAGAGQTVPLSKLPDHALLQARR AHQLAIDTYQELEETIYIPKQKHSFLLD SQTSFCFLDSIPTPSNMEETROKSNLEL FRTSLLL
11916	25817	A	12024	2	363	PEPLKGLNTHGLALAFSSRTSLLLAY LLCLPWLQEBAGAGQTVFVYTLFDHMLQ AHRAHQLAIDTTHLSDTYMPEDHKYSF LHDSQCFCEFSISITTPNMEETQHTSN VELLRSL
11917	25818	A	12025	314	393	QGAHWLTPVLPFAWBAKGRSLREAS
11918	25819	A	12026	80	392	PLIACSPFLPFLFFGKCLFLPPRNKG CGGTVNWNKPGRQAQAFIASSKKPKGM GGPPLTPGKRFVFLKKGFSFGPGGSGK FSAPGTPPTGPKWIEIPAK
11919	25820	A	12027	165	2	WQKLLFHFGTSCSVARVGVQNRIFSSP KPPPEFKQLSAPASRVADRRPDAW
11920	25821	A	12028	1	338	VFVALKFLMCLLSVCTFSLNLYNSLFP QKNCLPLIFPFLFEMEACSVTQAGVQW GDLGSLQPPVSHNLGGGCCPEPCCHC TPCSRPGDRDFVFNKTIQDNHIMEIT
11921	25822	A	12029	2	315	HEERERERERERERERERERERERER GVGETYKAEPLRVGGAAKRAHFARGR LFMEICGDMGEGKPKPPHSLTECLSR CGERFFDTSIAITRGCAQSV
11922	25823	A	12030	216	3	BRITPRGVQRNRLFSGRDTASFPFLFP PPRQIHKRGVDRHSHRRGRERERERE RERERERAPAR
11923	25824	A	12031	114	329	QTERNSININCKDIFKTFPSVGHQHRP KYDKTTIMKRNQSRKAMSKWKASSPP KEHNSPARBNWMS
11924	25825	A	12032	177	1	IKKKTFWQNIPLFSKKTCROKFFFFF FFETGSLLPRLVCSQAVLAHCSLCLPS AFL
11925	25826	A	12033	127	1	PSFFFFFNFNETESRSVAQGVQWRDL SLQAPPFGFITPS
11926	25827	A	12034	47	314	GAPVASVSIQSPSCSATDGVVNRKSTA GHQRYLCSHCRKTWQLQFTTASQPGTH QKIDMANVGVCRATARIMGVGLNITL RHLMN
11927	25828	A	12035	15	408	GATPGAMGHFTFEEDKATITSLMGVNAE DAGGETLERLLVDYPWTFPFDSPQNLG SASAIMGNPKMAHGKVLTLGLDATHG LDDLKGTFAQLSELHCDKLHVDPENFEL LGNVIVTGMATHIGKRFP
11928	25829	A	12036	122	2	KIVDVIPPPGGARVFFPPFFPLETHCS VAKAGVQWHDG
11929	25830	A	12037	154	1	GKPPPKLGFWGQPRQVRVGRGPPFFFF ETSPSVAIKGVQVCDLSLPL
11930	25831	A	12038	58	254	DPRVQQTATACSLNLRQRPSTSL PSQNDYHRAPLCATQKILAYRAQRERS AKGSYYQAS
11931	25832	A	12039	270	124	DGVLLHLPSELNCAISAHGMRIPGSS NSPASNKTQDNKKTLSNKF
11932	25833	A	12040	63	355	LGRGTARELRWRPLSPPASRVSYLSAAT NKRFSAPPSPRAFPNDKNWGGGYFFET GSHRRRPGRMCSGATTAHCSI.DFPGSR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v =possible nucleotide insertion)
11933	25834	A	12041	184	3	MGTFMFPSLVNS GVSRLLGGVSQLGYMGVRDPLAEAVCLP SKLKHHPGRTITLFAVRVGGCLSLQKFL LLFA
11934	25835	A	12042	118	3	DRVLLCYLQWECSTGTTSAYNLHLPESK RFSCLSLPSS
11935	25836	A	12043	40	436	LSBGLTKNRKDNHKTPTSVHHHHQPKV DKTRMGRIQSTKAKNSKSTSSPPKE HSTSPATQSRMENDFELREDFRSVI TNFSELKEDVRLCKEAKNLEKKLDENR TRINSMEKTINDLMELKMA
11936	25837	A	12044	101	2	HGGQVRWLTPTVPILWEAEVGGSPENRS SRPAW
11937	25838	A	12045	123	3	LTVIKELPLQARWLTVPVIALNEVKVG GSPENRSSPA
11938	25839	A	12046	3	432	PIFGGGGERIFPPFFPPFGGGVFFPKT KNKGFFPLFGFKKILPLANTFFLPPFF FINPFFPIFGADPPFFPPGGGFFPLFS RFFKFFQNFQFFPPGGGFFFFPLGFF FFFFFL
11939	25840	A	12047	325	164	KNKRNKQARWLTVPVIALWEAEAGGS PEVRTIGVSHGTRPHLLNTVSEYI
11940	25841	A	12048	187	381	LMDKRVSLGDDNTLKVSNSTGCTTLYL LVCFEMESRSITQAGVQRDLSSLQPPP SRFKRFSCL
11941	25842	A	12049	84	464	SYRVPSHPDITLVISRTSAQEAERKSPFC FPERVWPCPRPLDLGRRLKLECGDILL DSTFLSFFFGBLKTQSHSGALECSGVI RDHGLCLSGSGDPPISACLRVAGTTGV SHHCIFCRDPLPS
11942	25843	A	12050	232	20	LQCSSRAKHTSLTGNQKLEMIKLEE GMSKAEISQKIGLHHGLVANAKRPL KVIRSATPEKHA
11943	25844	A	12051	401	518	FFETESCSVTOAGVQWRKLSPLRA
11944	25845	A	12052	191	1	LEPLKKEKIFPLGPTNGAPPPFLKAP PLFFFFFFFFFFFPPFFVFNLLPL LSFLHILE
11945	25846	A	12053	12	369	PLPTYSACTEWSNPGQGDIDAKSVEN NCYLKKEKKKNSGSONLLPKIHTPNG SGKKTGEKIQNPPRGGPKLKNQKYSKN LKKHCCPRLTFLISKREKGNRYTFGKS GCFYQKK
11946	25847	A	12054	89	513	NFTVRSIPLINNTIPMANLLLTVPILT AMAFIMLTERKILGYIQLRXGPNVVG GLLOPFADATPLFPKPLTPAPSAFALC FAAPALALPFAFLCPPLRPLGR
11947	25848	A	12055	158	3	SQLTWPIMAQTDSMCLNTVYFDNIGWA WNLMSVIPTLWEAKVGGSLSHSN
11948	25849	A	12056	113	1	KSHGGHGVVLVSVLGLANEVGLVLWV KEYDGAALA
11949	25850	A	12057	44	263	ARIARSAHEGEMPRKTYGAKNAENRPQ RELQLKASSTYDIAHACALWYQLFL ISVSWWVLLPLTGV
11950	25851	A	12058	142	1	KKIFFFYKKGSPSPFKFIRLSLFFFFFF ETESRSVAQAQVQWRDLGS
11951	25852	A	12059	12	347	QTERNSTHNTKGDTHETPTSEGHQHRP IVDKSTKMRKNQCKKARNISQGSASP KDNINCLPAKBQWNTENEHKLITVEGFR

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11952	25853	A	12060	245	3	IINSVELKEHILTCCKEARNLEQRLEEL MPBGSGFFLEIPETRVRVVKPKGKPLGGV GPSLILFFFFFFFFFFMKQSLAVS PKLEEC NSAISAHNCNLCLLGSDSRSSGSR
11953	25854	A	12061	94	3	KGLIFFFFFFFFLRQSPSVAQAGVQWCD LG
11954	25855	A	12062	108	5	NNLSSGVRDQPGQHGETTSLIKIQIKLAR HGRHIL
11955	25856	A	12063	298	1	KKKIKINTHAQKRGPPFFFKPPEEKGEAP PQQRVTKKGGEKDSPIPKREKIKNPPL SFFFFLVRVIVREERERARERERERERER ERERERERERERAR
11956	25857	A	12064	122	1	VCBGVCQGVKDRERERERERERERERER ERERERERERAR
11957	25858	A	12065	126	1	ATCTKFRNDNRLALRVVFERERERERERE RERERERERERESR
11958	25859	A	12066	48	351	FFFFFFFKKGPKIVPPGGGGGGDDPIL EPPPPPLKKGFWGPILRGRNKGSGPPGW VNFGLIKKGLFWGPGGVKTPAFKGS GTPPKGNNRKNTPPW
11959	25860	A	12067	1	365	GTRLITVLTWHTNVAAPGSRSTSLILDFAL LCLFWLQAGAVQTVPLSRILFDIAMIQ AHRHQQLGIDTYQDEETIYIPKHEDSF LHDQTSFCFSDSIPTPSNMESTRQKYH LEILRISILF
11960	25861	A	12068	174	1	FAVMQHNPPVSLFFCFETESRSLTRLE CSGTISARCNVRLPGSSDSPVSPSRVA RA
11961	25862	A	12069	270	375	TRIKRCNGGAQWLTVPVIALWEAKAGE SPEVRSS
11962	25863	A	12070	197	350	KKIYIFLTINTINDLILPFLINDIILGPW LGAVAHACNPSTLGGKQWITTS
11963	25864	A	12071	3	378	HGQQLPEFLKILWTHLIGNAFQSRSTSL LAIDLCLFWLKRAVAVQTVPLSRILYD HANLQAHRAHLAIDTYQSBETIYIPKD QKLSFLURYQTSFCFSDSIPTPSNMEST LHKSHLEILYIL
11964	25865	A	12072	219	1	FSHPFPFGVQTPINFPFPAWVLSFGG GGGPPKQAGVQKVVFFFFFFFFFWMESC SVAQAGVQWYDLGSPRA
11965	25866	A	12073	134	3	VFGPFFFFFFFCRTESHVSAQAGVQWRD LCSLAQPPPGFMPSC
11966	25867	A	12074	175	357	MPINQPVKKMCVCVCVYIYHTPLIYI RVYMYMCMYICVYLHVYIMWCYIHTHV STYVM
11967	25868	A	12075	193	350	KIPHLTSLYHTQRYLYKCYIGQAWMIPTV IPALWEARAGGSPFVRSSRPAPW
11968	25869	A	12076	252	1	GVFGPFFKGGFFVWVKGIGTQQLFWVG VFFKKGKGLWVKGILGKPPPPPLFFFF FETESCSVARAGVQWRDSVKKITARA
11969	25870	A	12077	273	366	IFTYLFTYLFETESCSVQAGVQWNLG RLR
11970	25871	A	12078	127	2	KKKKTLEFFFFFEMESRSVTAQAGVQ CDLSSIQPPPLV
11971	25872	A	12079	206	334	HNRTIVASENLIYHFKIKRMTQWLTP VIPALWEARAGGSSSE
11972	25873	A	12080	135	2	KMKRKGEDSQIPKTLQTFFFLTESRSV AQAGVQCDLGSLSHC

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11995	25896	A	12103	230	379	KEASFPETESHVSQACVQWRSLNPLGS GNPFTSTSRVAGTTGMSHEVWL
11996	25897	A	12104	86	2	DGVSVLSPLRCNGLILAHCNLRLPSS
11997	25898	A	12105	116	2	SOKTPFFFFFETVSLLLPLKCNGLASR CNCLCPGSSD
11998	25899	A	12106	271	416	QFTFSKAFNLVFIKPSFPHISFYRTHSQ ANWLTVPVPELWEAEAGGSP
11999	25900	A	12107	194	3	HVLGTVLVARDTASNKIRSLQGCILLPL LFSVVLEVLRARAIQRKEIKVVIQIGRR VNRREG
12000	25901	A	12108	142	3	LCLLYNDCKRHAWNRQVRLWTPVIPAL WEAEAGGSPSEVRSLRPAN
12001	25902	A	12109	233	346	HQRSLGHWQNLMPVLPALWEAEAGVSP FVRSLSKAMP
12002	25903	A	12110	234	349	QSSFFDPLCFVPETESCCVQAGVRNH DLGSLGPPPP
12003	25904	A	12111	136	333	RLNFFYFFFFETASCSVAQGVQWHLA HCIPAMETEQDSISKNTVQKRKKVTRA GISKTKNENP
12004	25905	A	12112	345	110	QDGLCLVMTLQETPILAYSLNFFPIVFP TTKACINVQGDSKPLLLKKYLGQVQWMLP VIPTLNGADVEGSPLESLLEPA
12005	25906	A	12113	108	285	YNMKNRFLKTLNKNKSGWNRWLDV IPALWEAKAQRSPVKSRSRPGVAQV DAA
12006	25907	A	12114	1	364	RVAAREMKPMFGKALDLAAGRYSGRK AVIVKNIDGTSRDPYSHALVAGIDRYP RKETPMANGKKKIAKRSLKSFVKVINYH QLMPTRYSDIPLDKTVNVDVFRDPAL KRKARREAR
12007	25908	A	12115	120	3	TQIWGAFLTLTPFFFFFEAKSHSVAQGV QWCSLGLSQA
12008	25909	A	12116	120	3	TQIWGFFTLTPFFFFFEAKSHSVAQGV QWCSLGLSQA
12009	25910	A	12117	231	1	PLSPFSQSYATKLKLSGLSPILGLHLL LGSTPEAAQVQVQVNSFADSDIVPPAST WVPPILGIMHHNKQATENAKE
12010	25911	A	12118	216	1	LIFPPLLNFICYEVLQPGPLALFPACK FFWDRFSKPTFFFFFYKEPHSAQAQGV QWCDLGLSLPLPRGFK
12011	25912	A	12120	267	1	KKKKKAFPSPLLGCFIRIQKHLGLLV YRSHLSSILCLGEGILSLFIATLITL NTHSLANIVPIAILVFACRAAVGLAL LVLSIS
12012	25913	A	12121	167	372	ISGODLLKTKRVRKRPQDDVPFINIF VPTPGAPRSRLQILRLRGTDPSPVIVG DFNTLFSALDRS
12013	25914	A	12122	124	2	GLLKFNIFAPFFFFFSETESHSVTQGV QWCDLGLSLQPPP
12014	25915	A	12123	121	1	RPTAASANSQAVSAAGVMDPGSEIIE SVFPAGVSSVV
12015	25916	A	12124	176	2	RDLRGFSRFSNYKFWNPRGVGIGFKVF GGVKRFFFFFETESCSVAQAGQWNRD LG
12016	25917	A	12125	137	2	KLGFRGCGGKIPAPQNFPPPPPPFE NESCSVAQAGVQWRDIO
12017	25918	A	12126	103	3	LEENLGNVTQDIGRGKXPTSKTPKAMAT

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12018	25919	A	12127	212	351	KAKID LITFEILNICIGDENILDLGLARNLTPVY PALWEAKAGGSPVRSRLR
12019	25920	A	12129	187	3	RGSIMQQTINIRTPGVRLVLYILMIAIWA IPYIPMANILLLLIVPILIAAFIMLTER KILGY
12020	25921	A	12130	13	329	ASRVITRVMASNSTKSPFLADAGYGEQEL DANSALMRLDKGLRSGKLGECQCAVVRFP PRLPQKYPFPPIILNSAPLKLADVFRVGN NFLRLCVLKVCTQSGEKLEKI
12021	25922	A	12131	231	330	MDTDEYLGRAFWLTPVTPALWEAKAGS SPEVR
12022	25923	A	12132	95	2	KCKCPFPFPFPFETESRSVAQAGVNRDL SSL
12023	25924	A	12133	129	1	DLALLPRLWCSAMIAHCSNELSSSDP PISASQIPCTIGMCH
12024	25925	A	12134	196	361	TIMRYTAAKKKSESPILHFGQKGLNOD GGNANWPTVPIPALWAKTQGSLEPNS
12025	25926	A	12135	120	1	PPPPGLFPFPFPFETESRSVAQAGVQWCR LGS LHPPPPPEFK
12026	25927	A	12136	235	3	KKGIRIERDLRLKQLSVQCRPOLAKPFPF PSGVQGEQNFFFFKKKKKKQRAQMLTPV IPALWEABAGGSFVRSRPA
12027	25928	A	12137	185	1	IWCPFPQGPQICSFRCRFPFPFPFPFPF LEABTRSFAQAGVQWCDLGSQSSWVTE LAAS
12028	25929	A	12138	158	1	LRRGGVPSIFPCGGTIVLSPADKINVKA AWGKVGADAGEYGABALERMZLSF
12029	25930	A	12139	76	3	KVLARAIROEKEIKDQIGKEEVK
12030	25931	A	12140	157	2	FPSSPRLKRRPGRNPLGARENFPFPFPF ETESPSIAQAQEQWRDLGSLQAP
12031	25932	A	12141	234	388	LSQLMSANLFPVLLPEAFPHSVNRLCS GMIWAHCNIALPGSSSES PASTSQ
12032	25933	A	12142	112	453	LGRQAAASHREGISIHVGQMGVHIGNAC WELLYCLRHGIQPDGHMPSDKTIGGDDPS PNTFFNRGTAGKHVPRAVFDLEPTID ENVCTGYRQLFHPEQLITGKDAANNYAR G
12033	25934	A	12143	44	443	AKLGIRKLPLKAGAGKEITLINVVIGH VDWGKTTTTHGLIYKCGIDKRTIEKLE KEAARMGKGSFKYAWVLKXKADREGEI TIDISLWKLDTSKNYVTI IDAPGRDFI KNMITGTSHADCAVLIDAGV
12034	25935	A	12144	3	386	RSRATMRBCYCHVGAGVQNGNACWEL YCLEHGIQPDGHMPSDKTIGGDDPS PNT FFSETGAGKHVPRAVFDLEPTID EIVR TGTYRQLLHPVQLITGKDAANNYARGH YTIKKEIIDLVLDRI
12035	25936	A	12145	3	386	AGATYIDRLRVALFETATFTLNVVRPELS SGEATTMRBCMSIHVGQAGVQNGNACNE LYCLEHGVQPDGHMPSDKTIGGDDALAN TFFSESGAGKHVPRTBEVDLEPTIEIGER GHTYRQLFHPDQHM
12036	25937	A	12146	3	385	GRATYIDRLRVALLSATFTLRARRELG SREATTMRBCYCHVGQAGVQNGNACNE LYCLEHGIQPDQMPDRDKTIGGDDFFN TFFIETGAGKHVPRAVFGDLEPTIDIEI RGTYRQLLHPQLI

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
12037	25938	A	12147	11	381	HTPEGRTRVFLVLAUVVYQCEALRWGR VTASSTGNMAFLRSMGVLTALGRSGAK LCTGCGSRRLSPFSFVFLERWVSVLAR CEKKPVSSYLRSKQLP IFKAQNPDAK TTTELIRRIQAQR
12038	25939	A	12148	321	509	YSMDQYFIPFPYQIMHLCFFILKTRVSL FPWLSCSGATSAHCNFCLLSSNSPASA SRVTGIT
12039	25940	A	12149	51	400	AATMRCEISIHVGQAGVHIGNACWELYC LEHGLQPDGQMPDKTIGGGDDSENTTF NETGAGKHVPRVFDLEPTVILDEVRTG TYQLHFHDQLITGKEDANNYARGHYT IGKE
12040	25941	A	12150	25	399	EATTSITGLRLHQLGSRSTARECIS LH VGQAGVHIGNACWELYNLEHGLHPDGM PGDOTTGGGDDSFDTTFSETGAGHVR AVLVLEPTVIDEVRTGTGRLFIPEQL ITGPEDAANNYAR
12041	25942	A	12151	1	402	TKEEELCLACQRNRADQGWRSQNAQSD PVGIVSAARTIGSFNGALTAVPVQDLG STVIKKVLKRTAVPBDVSEVIFGHVLA AGCGQNPVRQASGGAGIPYSVPWMSCH ICGSLKAVCLAVQSIGIGDST
12042	25943	A	12152	3	400	TDLRLVALKTKTTSSFCFFHLLGSRETA TMRECEIS IHVGQAGDHIGYACWELYCLE HSLQPEGQMPDKTIGGGDDYNTFTTF TGAVKHVPRVFDLEPTVIDEVSTGTG RQLFRFELRTISKEADNLY
12043	25944	A	12153	2	398	GRCALDNTFFARFCYLASGHPGK LMDMDMS PLRPQNTYLPGCKLKAENDYH IVANDENBIQISLTTASLRAGANDMDNI VEAEANMYEGTPTKETLATLMSVQATD SLGGSEITPESVLRKCGSR
12044	25945	A	12154	203	405	FTCFSTRICVISRRISECCAPDINPLMS ANAMLDVFTVTFDEPGWDSKNLQKKMSH YSFLTGRPKI
12045	25946	A	12155	229	397	TRIAHHRKAGFALYSKRTTNLRMLFSKF LP IHALWVTGSSGQMPPLVWGHYDLGK
12046	25947	A	12156	2	399	GGVPHCVWATAGMRPGLEPTGLCQQT SSRGQKSVLQKESCGIWLQYHFLSRKQ EPRNEPCVSGSSGDBGAVADLADLRGY PALCCTPLVHSYRSWAGIRPQIMNGPLH PREPLVALLDGRDCTVEMPLL
12047	25948	A	12157	85	414	ALLPQSEALQGVATMHPHSYPALSAEQK EVSIDIALRIEAPGKSLAADSBSVGSMAK RLSQIGVNTENRLLHQVLFPSADRE KKKLGCVLFPHETLYLQKDDNGPVR GLLPHSESLQAVTRPHSDALYLBHKK DVSIDIALRIGSPGKGLIAPYRSMGSMAN PLNQMGVNTKQNRRLYQDLPSADRE KKSLAGVIFPHETLYLQKDDNGVP
12049	25950	A	12159	85	406	VLLPHSEALQGVATMHPHSYPALSGEHNK ELSDIALRIEAPGKSLAADSBSVGSMAK RLSQIGVNTENRRLYQDLPSADDRG KKSLGGDLFPHETLYLQKDDNGP
12050	25951	A	12160	275	146	EKTFIISIFTTTTETSESVAQIGVQWHD LGSIQAPPNPFERIA
12051	25952	A	12161	212	2	KRSRPPPPFFKSGSCYLAQVGMQLFV



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						GTITACYDPELLGSKDEPTASQVIGNT GTHITQLIFVFLV
12052	25953	A	12162	253	2	GRVDSECCLANGNAEKSTFCCLLVLFY LSSRQSHSVAGQVQMDLGLSLQPPFPF FSLLSRVAGTTGARHMDLIFVFLGET
12053	25954	A	12163	228	1	LLGLMFEQLGRFTKIATKGERSTQSG HSDMRVPQALLGLLLMFPGRCDIQM TQSPPAVSAVSGDRVITTCR
12054	25955	A	12164	122	1	ELLFFETESRVARLCSGATSAHCSLR LPGSGSSPASAS
12055	25956	A	12165	239	350	GQARWLTPVTPALWEAKSGSKLSEVRSLR LAWAGHGS
12056	25957	A	12166	235	359	TDKATSKRDLSEVIRETIFPMESESRVAR MECSGVISAACNL
12057	25958	A	12167	209	396	QFSGTLPDQYKSGFKNYIYIYIYIYI YIYIRKRYTRAYTKRIMCVSRATHNIV YLCAVI
12058	25959	A	12168	327	130	GGVGFLQGPGEKDPSPSPFFFFFEKES RSVPQARVGWPDFGSLPAPFPFGTFLR ESFLFSSIMI
12059	25960	A	12169	317	422	RGEKPLFFFLQKKKKKKKKKKKKIKKG GRRYKFS
12060	25961	A	12170	260	375	EKVTCSTWQMLTPVTPALWEAKNGRSL FRSLSANAI
12061	25962	A	12171	304	3	KFFFFFGFFFLGGVGPFPFPKRRFTS KIPPGVFFFPPLKKKIFFPFVPVILGPP RVFFFGAPLFFFFFFFFFTSTFRSC CDGRLECSVAVSAHCK
12062	25963	A	12172	105	3	LTFLRQSSALLPRELNGATSAHQNLCL TGSSD
12063	25964	A	12173	146	17	RIFFFFFLGQSLAVAQAQVQQRDLGSLK APPGVHAILLQEY
12064	25965	A	12174	234	2	LPREKPKSVSLSSLSLSLFRILKLLSS FMRHNIIVRPINNPATSKSSERKSL VSFTLANLKPQMTLSLEGMLK
12065	25966	A	12175	292	380	VRGLORVARTCNPTLGGQSGMTGGQE F
12066	25967	A	12176	109	1	GRKKVIGQQAQWMLVTPALWEAKVGG SPKVRSSR
12067	25968	A	12177	170	291	LINFYFYFLRQSHSVQTGVQVQCNLGL QPPPAARRRRRG
12068	25969	A	12178	260	380	LTYLALFTFLRRSLTLLPRLECSGMLSP HCNLCILGSSDS
12069	25970	A	12179	54	166	PKRGPHRVTVQGLNLLTGLSPRLGLPKG WDHRQDPLP
12070	25971	A	12180	273	359	APAGHGKSCLOSHQFGRLRQADHLGGV R
12071	25972	A	12181	27	225	IGQAQNLTPVILAFWEARAGGSTLEVRSS RPAMPYIFVLVLLASYLRFLCIQGHSDL LYTSSTRGS
12072	25973	A	12182	1	155	VHKIFLAYKYSQFOTVFRGRANWLTPVI PALWEAKNRSPEVRSSRSGRG
12073	25974	A	12183	91	2	FNLFFFFFTTQSGSRVARLECNATISAC C
12074	25975	A	12184	122	2	GQAQNLTPVILPPEWEAKVGKSPVEVRSS RTRGRTRGRTRG
12075	25976	A	12185	389	20	TDGRGRARRACFGKVFDEGLSFALKLA

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						RENGRPDWRAMLGMSSTYADWHRFYS THYPIDVILLDMIFSGLTYYTVLSLFFSDP DMHPLDPSLLNRREADSEFEDVLM/QKA AGLAGGVLFLLI
12076	25977	A	12186	180	393	LNPFGSGGCGEPRSRHCTLAVMTRESVS KNKIKIKINKQIEBGLFQFPFGQGFNC YFPAKEFILLALSKT
12077	25978	A	12187	37	443	PDPFIPPPPRKVOHLARPSKPTARPAWT IRRIILPPPPKKRHPGLARGKFGPRELA KAGLAKECPAGGPTPAVR FATPTROGGG KVAGPQTIMGIPMGKARLGILLITFLGFAS GWI GAKRPRETLCGGELNDVTLQ?
12078	25979	A	12188	3	411	APPERAKGSHFQDPVPSRGRREVQNM RLSVAAPTSEKRVFRBGLGPERLTHLL RNLTLGLVRHERI EAPMGARVDEMGRYAE KLIVYKGLGDTNQRAMRMAFDWLTEKDL IPLKLVQVLAPRYKDTGTGFTRLMQ
12079	25980	A	12189	2	414	QEFGRKRATFTSLILFFSSVYSRGVFR RDAHKSEVAHRFKDLAETLRALTLIAF AHYLIHQCFPADHVKLGNBATEFAKTCVA DESAENCDKSLHTLFGDKLCTDAPLRET YGMNADCCAKQEPERNECLLQHXDD
12080	25981	A	12191	3	514	PRLLMEAGPHPRPGHOCKPGGRIDMENG FVHHIRRNQIARDYDKKVKQAARVVR ERHTPAPTRPRKPDQLVYLPHRHDVSAH PRNPDIYESGESSSSGSELEPSGHLQF CLEYEADSGEVTSVIVYQDDPGKVSEK VSAHTPLDPPMREALKRLIQEIIAKRQS QH
12081	25982	A	12192	182	3	RGLFFIPPPPLKTKINGGPFMKVFMGFG PPLFFPFMESRSVAQGVQWHDLSGLQ ALP
12082	25983	A	12193	53	400	PETPSWLGVPVRRFYFTI IKSVMKKKKK KKKKKKKKKKKKGGGPKKTLGGDKPYW GVKKKIFFFLGGSKKHPMGFFEKLLFFG GGKCGAPPPKDISCLMGKJNFI LGAIGEK TCCC
12083	25984	A	12194	182	3	KGIFIQIAPPKKKKNGFLWKVYFKGFG HPIFFPFMESRSVAQGVQWHDLSGLQ ALP
12084	25985	A	12195	200	378	KSSRSQWLGYLFI GLLIYLPFIKFFLETR SCFVTQAGI LAHCNKLKLGSSD PPTSA QAA
12085	25986	A	12196	341	54	SLSFHGGLSVLCTFSTYKKSQEQWLT VTSVLAEVKVRS PQVRSRLPGDPPASA SQSAGITGVSHARPHLNLPRLMIKIL SEEGMLKRMTC
12086	25987	A	12197	1	462	GGPRPRFRKKAANVLTLAVLFLTGSQARR FMHDEPQSPMDVMDLATAVGLKLD SGRDYASQFEGYALGKOLMLLNDWS VITYTFSKLEQLGVPVTOEFNDNLKSTE GLTHMSKDLLEDVNAKVQTYLYD/PQKTW QKSLTFTARSEPVP
12087	25988	A	12198	80	1	SNKVFFLETESCSVAQGVQWCDLGS
12088	25989	A	12199	221	3	TMGINLDKKIEIQAIFSPFKMGHVAEET TCNNINTS GPOTANKUTVQWFKFKCKG DESLDEDEHHRLEEV
12089	25990	A	12200	239	336	FGALPTITCKPKPKKKKKKKKKKKKK



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12107	26008	A	12219	171	365	SEI ALVQPRNGREAVIVFACSCSDVFLIYET NKVARIQS LNYGTFKFFHVIVFVSYSKE HLKRLKLEK
12108	26009	A	12220	171	452	ARYKFLHPKFARGLYPSSSQIQAARHQL WILIKCSFYLLFLRQLCTLPLQLECSNM ITAPLQPLQLPGLKQSSHLSLPSSWDYRH EFP
12109	26010	A	12221	323	458	FRVQSLFLFIYFFETESHFVYQAGVQW HDPGSLHRIAP
12110	26011	A	12222	189	56	DRVSLVQPLBECSGTISVYCSLNNLLGS DPTTSASPVASTGGI
12111	26012	A	12223	246	494	FLCSSAYDDELRFFPFIHLILDYTAFA SQDTTISLNNLFDQACSPKCAKNGQAQ WLAAPVIVLWEAEVGRLLVRSRRPAW
12112	26013	A	12224	55	353	RTQGCSGVVQLCKPVEKVVQRTDAEQES QTAEITQDMKQLSAVNMDFFPARSARL ERKINKMKNKLTHTVKTQAQSGMLKVV ISVAFYKLGTVLRL
12113	26014	A	12225	199	23	LKLSIYVYVPGTILKYPTGMARWLLPVT PALWEAEVGSPEVRSRRPANSTWIER HQ
12114	26015	A	12226	369	14	DCVRVGLSYPTVCPSCSSVRKAPSSSR PHRGVLESQQPRCKSRKVDIFFSMERER DRERERERERERERERERERERERERER KLGYSHAMWRGRGLQWGMCGIPPPC TSDVHQ
12115	26016	A	12227	206	2	QNGHMNGPCRVSLSLFLBETRSPLFLFLA SLSLMLBESGAILAMCNLRLPGSSNSPAS ASQVAGITGACH
12116	26017	A	12228	231	501	ESWEOALHESDPLKSCRTQSNYHALQ RTNQRLDKLYRMQGHYEEKALSHSEI VALSHLLEAKVTIDKLEDIVSAAHTW PMEDCR
12117	26018	A	12229	86	455	DLPTFFVPVPHKGFSGPLGQSELPSNQC TGGRSHLSVSVLCPITLATTPLGLDPTTC GTSQPLPLGPIQLAHSELAGLSLPLSLT NCTSQRLPDRPHRSHDAPHTHTHTQTHT HTHTHTPATVT
12118	26019	A	12231	211	96	KSHFKAGGGGPPRYSFPPGGGGGVPRV GGFPPPGLTQ
12119	26020	A	12232	228	3	KRWPIRGPLSKGLGPPPPKLFKLGFFFF FFFBQS FVLVAQAGVQLBCSGTILVHFN LYLPSSSNYPASASHPRV
12120	26021	A	12234	137	3	VPLFGTILKNSNVCPFLVCLFVCYETE SHSVAQAKSCGATSAH
12121	26022	A	12235	139	1	FKLCFGQAWFKPIIPALWETDASRSL VRSSRPADAKADAKADAN
12122	26023	A	12236	80	1	VLLIFIFLEEMGPRHVGQDGLDLTL
12123	26024	A	12237	187	494	TERNSFMINKEDTHTKFFVGVGHQRPK VQRTTKMGRNQSRKAENSKNSTSSPPK DRSSLPATCSWENQDELTEVGFRRS ATTNPSRLKSHVLRTRTE
12124	26025	A	12238	252	503	CQGVADDLQSQARYQCELCASITDAPD ILFFFFLGLGPHKPNPPTPKQKMKPG APPIALWOLIPGKAGPGQPGRPALHTC
12125	26026	A	12239	2	471	RIALCPAVERIPHEERERERERERERTP GHTQLSPGARRTPLERERAFNDFSLN

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12147	26048	A	12261	125	3	LFLIQKYYITGQERALTPTVIFAPWAEAG RSPKVRSSSPAW
12148	26049	A	12262	228	385	SCLYLMQIPSSIEKSCQYKATRGRRAR WLTPTVLPALWEAGAGRSPEVRSSR
12149	26050	A	12263	227	369	MLKHKSNNKTQDLGQVGLTPVNPVLWE AKVGGSPVEVKNRPAWPTW
12150	26051	A	12264	102	487	QONRRFPTGERGRTRGRGVSSFPQSLSPGS LELASPSPPSVGRGLGSAASQRSGGQER PKAQLRRPFPSSSPRLRGRENCAHHR TPGGTLDRRPPTPLGTNLKGGPRPAWAG NPPEAKTANGPQGA
12151	26052	A	12265	391	476	PRSRYRVCSSGSISAHNLGLLGGSSNFS
12152	26053	A	12266	378	476	MSSRLGSLGVGLGRAWLTPTVIFALWE AKEGG
12153	26054	A	12267	166	58	NFFFFFFFTDSCSAVAQGVQWHDLSHCN LCLPASSN
12154	26055	A	12268	209	49	TPPNFYTKIRSGQAQWLTPTVLPALMCA EAGRSPEVRSSRPASTPRTNSISNS
12155	26056	A	12269	127	1	SSSFFPLKTFGLFFFLCFESESRSVA QAGVONCHILGSLQA
12156	26057	A	12270	154	27	IQTPGKKKSPFFFTETKSCSLVAQAGARL CPKKEKENSFVL
12157	26058	A	12271	180	22	VLKIHNGRAQWTVTSVPELWEVKAGGS QALRSSRAARTWDAQNGVEKTVQY
12158	26059	A	12272	207	422	GDSSIRGADEKPKGVKTNNNLINLKV MGQDCSMEQFKIKSHIPAGYGGSHRESQ HFVMPRNADHLRSGV
12159	26060	A	12273	59	479	NSLGGGGVYGSFRFTFPGCRALSPNRV RVQRRCRCSTMFADTLTVFISVCTAL LAEGITWLVYRTDKYKRLKAEVEKQSK KLSKKETTESAGRQQKKIKRQEK KNNRDLAMVRKMSWAIGICPTAKMK
12160	26061	A	12274	354	439	VKTGKSLAKTNGQKQPTTIDWIKGW
12161	26062	A	12275	366	499	TRAQYVVVVVGIGSQCVLECSGMIAH CSDLGSSDPPTAS
12162	26063	A	12276	136	37	KFFGVHNLKPVI PALWEVAGGSPPEVR SSRPA
12163	26064	A	12277	419	48	DGKLVNSFLTVSSSGCLPLLTIVRPPY FLRYNNEIRPINNPWTCKSSKRSR ICLTFNQKLEIKLSRSGSKIKTGQNL GILCHVSQVVDQHKFVKATKSATAKIN LSISKYIMSGA
12164	26065	A	12278	190	1	RKGVSPQMGPLGKGSPLAKINPFP KKTFFFFFTGSCFVAQAGQWLDPSPP DAWADAN
12165	26066	A	12279	276	389	WFNLSFFCFCLFFETSCSVARLECSG ATSAHCNLT
12166	26067	A	12280	425	1	PHHFPKGKFPFPRPELTFEKTNKRR VLFFSPPPKKNFSLITRFFFSPPQKK KKKLNPQKGPFPVPIKPPPLFFFF FFFFFFFFFFFVFVFVFVFVFVFVFVF FFFFFSGLTIVRIMTCWLVNDIGLL I
12167	26068	A	12281	253	90	INPQGSFKTAAPFFVFLVYVMECH VVOAGVKLLTSSPPASASOTAEKLF
12168	26069	A	12282	61	387	PKSSSSAPFQISWFLDASTASTVSI RVTQPYKVNNGWAFSSSSSYMRPSA HSSILVSRVGSSTSFQGGAGMGLP

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12169	26070	A	12283	186	305	LHSSIANRARILOKKKKKGGKRRFP
12170	26071	A	12284	2	190	LHGSTVQVREERHKKSLTQVHTHTHT HPHLVIMSSHS
12171	26072	A	12285	17	197	PRVRFDVRNNRSLNPLRSTRTTETFE NPKPSVKKKKKKKKKKKKKKKKKKK KKKKKKKKKGGGA
12172	26073	A	12286	158	405	SLGVGGGQQGGGVHPHPCPFVILSPVS LSKHCSYLPKKKKKKKKKKKKKKKKKK KKKKKKKKKKK
12173	26074	A	12287	364	142	GVASYABQRKYLEMEYFPGGEAISIVE MTTEDLHYSINLDDKAPTGERVYSHEE RTCTDDKMLSYCTCYREIFCRNKI
12174	26075	A	12288	171	380	GCAFFLGGGLKRRRRRAVPLFFNF FETESCVTAQVQWCMNGLSLQPLLDIM WQGGTVVAHACHPOTLGG
12175	26076	A	12289	194	2	VPEAGHAWLQENLTSPLFWGFSFFTTDT GMLKKKKKKKKKKKKKKKKKKKK
12176	26077	A	12290	179	416	GPRGFWQAVTQGFPPKKGFVFPV DAG GWHFFFFPKRGFPFSPFLFFDVRWLCHP GWSIVARS
12177	26078	A	12291	3	408	LIFLFTFACAVCPQLARHPFKIHITALL RCLIIISCPETHLYKCYRQQAARWLTP VIPALWEAEVGGSPVRSRLRPAC
12178	26079	A	12292	119	278	LAVGFHDRTYYTDSALMVLVDELIT GNKNGSGEAFEYLPEDFRDGEDDAAVTL EKQEDLTTVLTVLPGHQRQRETQLE AKLLKKRLELGLLDLVEDLELIIQLKK KKKKKKFLMGAPFKGPIGAPI
12179	26080	A	12293	119	3	PKSIEAGVKSVLDHPLPNKAKTHLSCKK LKKKKKKKKKKKKKKKKKKKKKKKKKK KKKK
12180	26081	A	12294	205	1	MLFTGPHTKVMSLNSITGNAMWFTFVIP ALWEAEVOKS
12181	26082	A	12295	215	1	LHFFSTETKQPKGLFLALFYSDCQEKK RKGGKLIKFKKAQGAQAWLTPVIPAFW EAKVGRSPFVGS
12182	26083	A	12296	185	411	APKIKLTMHIFSSPLCLFQDEHPHFTEA LLHVRATAYTFNQLQARKYFKKHGK RMSKEFHGARLBGNQ
12183	26084	A	12297	281	388	DVPLNPHALHLSDFRTISTETGVETVG KRVLHRIITLLLLLLLFFEMESCSVTHAG VQWCDLGLSLQAPPFGPTTF
12184	26085	A	12298	178	3	RILFFFFFETTKFCSVPQAGVQGRDLNSL QPPPPPGFM
12185	26086	A	12299	199	450	TLSSVTQVPLFGSASSPLLFSRKDIKI PTVSVFSPQTEPRSVTQAGVSXCDLGLS QP
12186	26087	A	12300	3	407	TLIRHMCNYFLLSHRSPFSSVDYFLCY REIYSLIKTLNKLQIGGFLLNIIKVMYD KPAASIIRESSEKQKAPLRSQTRIRCP L
12187	26088	A	12301	227	3	EPFDHSTAMDTSPNPOTSSVSTTSSTT TTTITSSSRMQQPOISVYSGSDRHAQV VIQQAHLRPPSSAAQYLQOMYAAQQQL MHPTALQQQHLSSSGLQSLAAVQASLS SGKPSSTPSGVYQGSSTQPSI
						KKGTGQGLTFEAPRARKSEFPDKKHKK VKKEFPKGGFFFFFTTESAPSPLECS CAISACSLNPIAGAIAS

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12188	26089	A	12302	292	380	KCYRWANLMPVPIPALWEAKAGGSLER N
12189	26090	A	12303	13	186	VDERHILRLSRNMAVALYLISLLWATAQT STQTQSSCCEYDVFRRSGKQLPWRGRC DL
12190	26091	A	12304	253	409	ITAVIAAAAAVVGVTITIMINERSLERLE CNGAISAHRNLLLLGSSDS PASAS
12191	26092	A	12305	153	64	GRAQWMLPTIPALWEAKAGGPTDVRSSR PA
12192	26093	A	12306	265	420	GTLSNRNTKLQLCRMNGKRTLGQPWMLT PVIPTLWEAKAGGSLERCSRPAW
12193	26094	A	12307	295	1	RPCLNKKKTSPIWKKGFANPLPGKAAPVF PLCKKPKPKHYRESIRPLKKKNGPKGFF FFFETESCSVAQVQWRDLGSLQAPP PGGVHSPSKLTIKV
12194	26095	A	12308	247	421	SWCCLKKKKKKKKKKKKKKKKKKKKKKK PGGALKKKKKTPS
12195	26096	A	12309	168	3	GOALLLCITVAFSKTIVVCHAPTILGWA WMLTPVIPALWEAEVGRSPVERSRP
12196	26097	A	12310	117	3	VAYNTAVPRGGVSLALPRLECSGVISAH CNLRLPSSS
12197	26098	A	12311	256	101	EPPTPTTTTTTETGSCSITQAGQRDHSF PQSPPTGLSNTAPASRACESGR
12198	26099	A	12312	146	3	FVALCTQLFLPVNIVCFRKHKTGRARW LMPVIPALWEAKAGGSPRV
12199	26100	A	12313	207	3	VRVRTAGVINALRGFLCSVRESMTKDEL IARLRSLGEOQLNRDVSITGTKEELALRV AELQELDDSR
12200	26101	A	12314	282	2	NCLAEKVKPMVSATSLQPGQISILFLSF FFEKESCSVPQARVQWPNFSSSLQSPPPP FKLFCLSPGGGGCSEPKSCRCIPGWQQ NETPSQKKK
12201	26102	A	12315	298	84	KTPQPVFALSKNFGPPKTAIPFFFFFF FETKYSVAQAGVQNRDLGSLHSSLGHR ARHLKKKKKKSINL
12202	26103	A	12316	124	1	SKGHFFFFFSETESCSVAQAGVQWNL GSLQVPPPRPTF
12203	26104	A	12317	132	398	VVTVNAVESIVTESPSVCHSEVALAAKYW LVCYLLRETRYQKLNQBIKPTLSVPKXK KKKKKKKKKKKKKKKKK
12204	26105	A	12318	262	392	PHYQONQPOARRSGSHQHPKQRRDEHL SLGVQRDQPGYSETP
12205	26106	A	12319	168	3	EAPKASINCTALQPLQGNLSQNKEG QVQCLTPVIPALWEAKVGSPEVRS
12206	26107	A	12320	48	385	DLGSLGHSTLASSFISLLLSYKCKLSP STMIMRLPLPGSPPIKPPPLPKKKKKKK KKKKKKKKKKKKKKTGG
12207	26108	A	12321	218	83	NLSPIFPBGNFVFFFEVESRSVAQATV QWRDLGSLQAPPVRRPK
12208	26109	A	12322	197	1	KETWFPFKKEGLEFSFKKIRIFFFFSK KIPSPPPPPPPPPETESCSVAQAGVQWH DLGSLQAPP
12209	26110	A	12323	128	36	KGLFFFFEMGVSLLRLECSGTTSAHCN LP
12210	26111	A	12324	140	3	ILNSNLKPKTKNTFFPETESRSIAQAGV QWHDPSKQPPPLGPKR
12211	26112	A	12325	273	369	RKEWFLKKKKKKKKKKKKKKKKKKKKKK



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, -possible nucleotide insertion)
						KKK
12212	26113	A	12326	140	415	RTGLLSPGRLGPPYGSREYKSGLLDL NASLLDPEVNAPSLSGPETKPAHSPSD PGVHSSCSASQSGQGELPTPSSRIHP KPSPGPFKK
12213	26114	A	12327	2	506	FVPLSETEAPGCSGSRPELEPERSLGR FRGRFEDKDSLEEESELESESESESESE MSHFSRLLEGGQDSESEERLINLSEL TPYLICSICRGYLDATITTECLHTFCK SCIVRHFFYSGNRCPEKNTVVGQTPLEIN IRLRQGLQIVKLVINLESEKQGD
12214	26115	A	12328	1	419	FVPSVCAKCYLLDLRSGSOLYSQVDF PVEEAVCPFSDLKLCAGRTTTLFKAVRQ GHLSLORFLPLFVWLCAPRSGVYRGRQ ASLSCGGLHPVGASWPCPLPTQASAMAG TTPPASLPPCSLIGDCCASNERGSMGV
12215	26116	A	12329	259	414	NMENSLECVVWPKLAQVLFSGASLLSAIL QVTFGQIKAFATLRFLESPSDAVT SCYRVSVISQARWLTPVPIPALWEAEVGR IPEVGS
12216	26117	A	12330	302	404	SRDMSPLLTTTRKALMAFRDVAVAFTQ KEWKLLSSAORTLYREVMLENYSHLVSL GIAFSKPKLIEQLQSGDEPVRSEENHILL DLCPGWSNMA
12217	26118	A	12331	94	375	NTFVDSFGGIRVTRPAGRGPPALVR PETWEAGEKMPSESLCLAAQARLDKSN LKTDIQCNCFTTRKISLLPLFCHHL
12218	26119	A	12332	7	246	YTYFPHLVRLPGSGGYDETFVVVVVNTRE SPSTVQAGVQWCHVSVQKPP
12219	26120	A	12333	150	1	EKGFLVFFFLIKSGKTELEFMTGRNPF KSGKPLFTTPKSGSPSPKSGGFLFQ TRSRLTPQSGWFGAPKPLAGEPPKWE AGLGDDPPTPRAPHADQTLQPIQAPT RTIQNBQKAIKFPQPMGG
12220	26121	A	12334	34	426	TVITPLHFSQHEARLWSRVPAPALNR SMEGGLGRAVCLLTGASRGFGRTLAPLL ASHE
12221	26122	A	12335	185	3	GWGPIPSTDVTVLSPKPFILLQGHERRAI TQIKYNREGDLLFTVAKDPVSVGWRSGG ROGILLPGRWDTFVLELQGNQRASHE K
12222	26123	A	12336	60	316	SFRIQVQGNHISKYFKIQZSDQAQMLT SVPALWEAKTRGSLVRSLEAFRAP
12223	26124	A	12337	3	167	RPLSVMOGRLTSIRVDSGARCWYFLFI YETEFRSVAQAGVRRRLDGLSLQTPPSG
12224	26125	A	12338	238	401	GWACQWFMVTEPALWEAKGVSEPVRS LLIYVNMWLLPDAVAPTCHSSILGGQGR RTRRQGEFETSLANWVKPHL
12225	26126	A	12339	354	433	KTKQTNKRTSRVQGTWFTPIIPAYWEA QAGEL
12226	26127	A	12340	238	382	GSCLLEKLTNRKDLHTKTFPSVEHHCQR PKIDRTIKGRNQSRKASKQSSSP SKDCSSLAATQSGWPHDFDELKREBGR
12227	26128	A	12341	101	1	YNOVNERGCSQSTIFKSSLSQLWWRAP IIPATQSAEAGW
12228	26129	A	12342	276	23	LHVYVFFSVGDEPLTPPPPPDLDSALFS LSGNPPPPPLDEEAFKQVQVREKVMKL GKS
12229	26130	A	12343	122	1	
12230	26131	A	12344	180	360	

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12231	26132	A	12345	35	411	TMTIVDKASBSSDPAYONCPGSSBRAVS PGMDMAGSAGWGVSSINDVSKHTLSLG VPVGA VVYSSSSVPDKSPQKQDALG DGIAPPQKVLFPSEKICLKWQQQTHRVGA GLQNLGWTCFANA
12232	26133	A	12346	278	386	IIYCYKQTIIGQARWLTLIPSLWEAKV GGSPEVRS
12233	26134	A	12347	111	2	KSQTQGVOWLTFVPALWEAEVGLLEL RSSRLAWA
12234	26135	A	12348	215	316	LNRRLNLSF I KKKKKKKKKKKKKKKKK KKKKKKGGFL
12235	26136	A	12349	265	404	SKISYFLANSFSAKLSLNTKYNISQARW LTFVPLWEAKVGGLEPE
12236	26137	A	12350	372	1	PVFPFPEKKLQSGLEPPALRFANVSPLP KAHBEQELKEKVLAVHEKNP IDPVYGPFP KGPTNFFPLPQRFVFLGAQKGVSWFG FVYKGLSLAPLKGPPPPFFFTETRSRV AQDGVQWCDLGS
12237	26138	A	12351	318	416	QGRAGNLTIPVLTILWEAKAGGSSSEVRSS RPAPP
12238	26139	A	12352	144	1	NGYAIVECVVLFCFVFLRQSLVAQAG VQWCNLGSMPSTSLWQAI
12239	26140	A	12353	116	1	SGRYSFKKCKQGRKWLASVLPALWEAE VGRSPSEVRS
12240	26141	A	12354	102	2	ETRYKQPGQGWRLTLPVPLWEAEV GSPSEV
12241	26142	A	12355	112	294	LISPSCEMPSPHGPTWLSRLISQHSFS NLKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKGGGAP
12242	26143	A	12356	138	2	SFFLKVFVFFFTFEMESRSVAQGVQWGN LGSQADPPGSRHCFVD
12243	26144	A	12357	148	394	PGEFPFGKSGKGGKGGGRGWGEPFPCR GQFKKFPAGSKAPFLKNSRNLGWC TKLIPDGLKKKPPPOBOENILGPPOF
12244	26145	A	12358	97	3	EKFSPCFVRARHTHTHTHTHTLSLSL GFH
12245	26146	A	12359	204	2	KRYTPACFPACLPDEAPYIATAKPAIT TSEQMAVFPKYANLKSARVFNKGVG YGLINLLTKTS
12246	26147	A	12360	156	391	NRGLEKVERSPSIPCSVRCSHPSALVS PTPTPTDTTNWALFFETESCSIHQGNR WRDLNLQQLPFGFKRFSCLNL
12247	26148	A	12361	179	1	ALKKLLIYDENSEHKTNLVGHFSFRNFTF LPLLETSSRSIARLECSANDTHCNLRL SGP
12248	26149	A	12362	218	391	TILKDCPTFKNCLSGAQWHLPPVPAWE AESRGILLEPTS
12249	26150	A	12363	2	356	TNSHVNSTQKPEPCIPRCGGYIVCOL QLVERAFIPFNFFFLKRSFVLLPLRLEG RGAI FRVTOGSSNLLTGLPAPLGLKGV NYRGDHPGPAYFYFLNGKRLLIQGGSG LKENLL
12250	26151	A	12364	94	1	KNPPLFFFFFBSSESCVQATVQWHD LQL
12251	26152	A	12365	237	2	YSSLLPKPAESARGILRHVTPSTSAI SKILFCPLFPVETEFSLSPGLKCSGAIKV HCSIALGSSNSPTASQVPGS
12252	26153	A	12366	340	442	GLFVCFVFWFLETESCSVQAGVHWCCL

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						SSLQPS
12253	26154	A	12367	208	45	EGGRTFFFTSVFFVFRAGVLPCCGWS ETPGSSDPPALASQAGITGATVNST
12254	26155	A	12368	60	443	CSSCVSSKPKQS PHLKQDDRMGAHLISG GCTRTATAGKMKR KCLVAVSTCAGARFES RNRGSQQHSARFQGRPLPTVVRLPPFP QAKPFCKKRWMLGGP LSLPEKQHPGPGG KKKMWAGKAAPRLVPT
12255	26156	A	12370	341	421	SGWVRMLTPTVTPALWEAAGSGSEVGR
12256	26157	A	12371	280	393	NTLDHYVTQWLTPVLRITWEAAGRSPE VRSSRSAMPT
12257	26158	A	12372	268	399	TLCSSLSAESLIHSYPEFSCKDNYINTH NEAYKACMRAPHLPL
12258	26159	A	12373	209	468	EAVIDETSHSPADSFSSTSNLACQTHI LARLLKLVBEELIYYPRKIQCFHSPFF PFESRSLLLLPRLECSGSLSAHCNLCIL GS
12259	26160	A	12374	381	488	TITCLFQKQCRGRKMLTPVLPALWEA AGSGSQGE
12260	26161	A	12375	276	395	GHVVTKTKLRLIYVFFEMESCSVAQGV QWHDLSLQPPP
12261	26162	A	12376	295	472	VYSSVALNTPTLLCNHHPQSPVILTP NKKCRGALLAHNCNLHLGSSDSPTASR VAG
12262	26163	A	12377	390	511	PGAVAHACNPSTLGGRRQQLTRIPSL
12263	26164	A	12378	417	511	AHRSSFEMESCSVTQAGVQWRIGLSLQ SPP
12264	26165	A	12379	133	406	KLSLNRDRYKQVCKETKKKKKKKKKK KKKKKKPGAQKKSGGSPR
12265	26166	A	12380	247	345	HMWSSQLNKLGLINKKKKKKKKKKK KKKKKKKG
12266	26167	A	12381	156	15	NFFFFETESCSVTQTRVQWFDLSLQ GKQBQNYVSKNQKQLH
12267	26168	A	12382	275	1	KIVFLKGPPLFFPKKFFVFLKVGFG GLNF LKTFPPGKPLSKRQLFFFFFP ETEFHSVARLECSGTISPNCNLHPSSN DSLASTS
12268	26169	A	12383	43	379	LLGYDESRSLSYICLCLSCGLQLSPIN LLVXVPCQCEVCHYFPQYTSLELIL FNDINVLNIRHFGIVDQVLDLIVFSPN KEITLGLQGLMMPVLPWFEPDAGRSP
12269	26170	A	12384	303	1	KQPPFFFLGLSPFFFLKKVFFPPFFFLRT PPFFFPFFPKNFFPPPKKKNPPFFFP PPFFFPFFFFFTETRSRSVQAARMQMG HGSPQPPQPGSSDPTDP
12270	26171	A	12385	141	1	KKEPLRAPPPFQLFCFFYKSTTPCSVTQ ARVQWCNLSLQPPPLRYK
12271	26172	A	12386	31	417	CRPADSPSPNDTGQDSRGRAGTIGHTPPL KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKSGGGA
12272	26173	A	12387	291	412	LSSEMLLFCFVYLRNMSPTFVAQAGVQW CDLGLQPLPG
12273	26174	A	12388	310	1	NTPCPLFFCPKKRQAGQGFIKALFFN PKQSVFLGPPPKGPPFLGFQPIPPWGGK IPRLNLFWRSSJFFFLLDGVSRLPR LSCNKVLSAHCNRLLAGS
12274	26175	A	12389	117	2	KRNFGGGPLFFFFFTETESRVVQAG

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						AQWHDGLGSLQ
12275	26176	A	12390	117	319	SPLKKPKDSTGNLKLLENEFSKSGPKI TIQKSVAFIYPNGRHSKKIREVITFTI AAKTICKPQA
12276	26177	A	12391	95	2	SKSHTSLKRLTLGWARHLTPVLPALWEA KAG
12277	26178	A	12393	127	395	IPGSGQFCILKQSALHLNKSFSFSLF IETQSLSVITQAGVQHCYLSSLIQPPPRF KLRQRNRLNSGGRCNKLRAHHTYTPWG TEKDS
12278	26179	A	12394	252	391	FFCFVGFVLLCFPMESCSVAQAGLQWFG LGLRLQGFAMLARLVSS
12279	26180	A	12395	275	3	TLRVLILAKSKETVEINCLTEKSHSVAR AGVQWCSQDWEEKAGPMWRPSKARCCP TSVLKCHLGAQWMLPVIPALWEAKAGG SPEVRS
12280	26181	A	12396	111	3	GNNVKIRGLRLRPLKGWCHFTPVLPFAF WEABAGG
12281	26182	A	12397	124	1	VSRGRTVHQEKPTERAASPRLECNGTIS AEHNLCLPGSSNS
12282	26183	A	12398	259	387	VQESFSCILFIFLFFIFYDTESRVA QAGMOMHDLGSLKCP
12283	26184	A	12399	103	1	KGRFFFFFYETESRVAQAGVQWRLD SLQAPP
12284	26185	A	12400	308	416	CGNPFERAGRVRLTPVLPALWEAKAGG SLEVRSLR
12285	26186	A	12401	92	1	HTWGLTQWMLPVIPALQEARVKGLEPR SS
12286	26187	A	12402	265	388	GLSHLFRPQHLFFYPFETMSVSITQA GVQCDDLGSLQFP
12287	26188	A	12403	279	1	SLSKMESGLTPTSTIDTWGILLTSCC PGHCMPSSIRGLNPLDASSTSSSCNN QNSPDWGTCSLWSQLLRLRLWEDCINTG GRGCEPGS
12288	26189	A	12404	387	152	NPPPGFNFGPLKCNFFSPRGEKVFPL KRPPPPPPPPPPFFETESHVAQAGVHN RDLGSLQALKSFCDLVSAFKGF
12289	26190	A	12405	262	464	IIFHWLACTLVTHSSFPDGHGLPLDLAVA DSAAVKHSTSCICNTRYIPGNGIAGSC GISVINFLRNC
12290	26191	A	12406	204	67	KCFQGAWMLPVIPALWEAERASQRLR SSRPANAKELIANRTRAS
12291	26192	A	12407	134	1	IQRFCILQFSTFFLLFLFYIFTSIDSCS VQAQVQWMDFGSLQP
12292	26193	A	12408	145	403	TYMYSILINYKAMSHPIRVKNHNTARFL ESLILCAHPNPPILKILSLILREKKKKKK KKKKKKKKKKKKKK
12293	26194	A	12409	65	415	ENKRLISQSWNGPSRRKQSSALLQGLGH LTSQVRAVSPVQGCIVRIKGGSGPSKPK KKKKKKKKKKKKKKSSKKKKAQGG ALKKK
12294	26195	A	12410	124	404	PWFFLEHRNQMWPVIAHTNCPNPTLG KKKKKKKKKKKKKKKKSSSSS
12295	26196	A	12411	164	2	TGAGLTIMQVGVGFDLQLRFCEVLVFC FLVFFFTKSDSVQAQGVQNCNPSLL
12296	26197	A	12412	114	3	PGVAHACNPSLTGGQGWITRGQVYKT GLAKTVKP



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						LRA
12318	26219	A	12434	193	3	FGAENPPPKGGPPPPPPPPRGFPFGVFF LKKKGPPPPPPPPPPPPPPSRVAGVQW HDLGSLQ
12319	26220	A	12435	321	422	NVEGDPLQRHNIIRYPPGVAHVTGPFST LGGRRG
12320	26221	A	12436	116	2	HDRFCLFVYDRVSTLSFRLCSCSAISAH CNLRLPGSSN
12321	26222	A	12437	302	400	THHTHTHTHTHTHSGLLYLPRGKQSH BFCW
12322	26223	A	12438	329	399	LALQARLECGNIIISAHCSLCLFP
12323	26224	A	12439	310	2	KPLISRGFLFCARPCPRRSNMSFNPQS YQVGNDTGGFTYVTKLVKLGSPSRGPKG AKQVUKKCLLTLPKMLRFLFFPETES CSVTRLECSGATLACNL
12324	26225	A	12440	151	401	EWMHPLPSSHSSTNLKRGRESGRKAGR KGRKERRKGRERRRKEEKGRGKTRR RKDRGENEENNLSSKVSLEISTCP
12325	26226	A	12441	276	1	FHFFGRFSPVSPRVQPKIITHTCVARI EKGGSCKALSLCPQYVGSNFFFFPETRS FSVAGVQVQRCDLGSQMPHPHFGSSDPP APASRVAG
12326	26227	A	12442	140	1	NSHFPPKNLGSPSSFFFFFFFYLETSRVA QAGVQNLDLRSLOPPPPG
12327	26228	A	12443	310	3	LPCCSWGLYGAFARCPDLDKQLSVPL WACPLSTAGRTRLCVACIKAAKGAGPFF FFFTESHSVTQAGVQWHDLSLQPPPTH AKPKHTHTHTQTHITIPDT
12328	26229	A	12444	337	2	GFFATVPRKQKQIMFSPFPKEGIFSGPC FISSTPTLLGVKKILLPPNTSEIRPVLS INTSVHTRBQKKTYYGLFTGKSRFFFF FETDSRSIAQGVVRHRLGSLQAPPPG
12329	26230	A	12445	112	9	GRVWLTLPALNEATAGRSFVENS PAMPT
12330	26231	A	12446	172	3	TPGELLIGRAKFAKNWPAAPRGITPLGR QKFSFFFFFFFETESRSVAGQGMWNLGS
12331	26232	A	12447	221	418	RKAERLEVFRRRLCOENLEPFFHCLAA PMPLIVLKKPILGRANWLTVPVLPALNEA ENQGWLESRS
12332	26233	A	12448	280	392	PLGRVRLVTPVPAHNEALAGSSPEFRN LRPAWEDMA
12333	26234	A	12449	410	129	PSQRIFFYPGPPGKTFFPLKXKKKXRG GGGLPFPDPQKVKKKFFYPGRGRFPKQ KFNLPPPRGEKKNKPPPPKXKKKKEK KRKEKGLVT
12334	26235	A	12450	159	1	KKKRGGLGLTFFIKTGDEFFFFFFFETE RSRVAGVQWYDGLGSLQAPPPGLM
12335	26236	A	12451	270	1	NPLKFFFFSLEQNLKKCAPLNNFFFF FFRIFWPPFGVGSKAGIWWFFPPPPFF FFFFFFFETESRSVAGVQWYDGLGSLRT RGRTRG
12336	26237	A	12452	249	33	DKLVCLPLILKKLNSPPPPFETESRSVA QVQVQRNLGSLHPPPPGPKPNAANAYAN AHMWVPSLEAGNLR
12337	26238	A	12453	190	86	TNDLGWQLTTFVTPALNDAEAGRSLEL STRKA
12338	26239	A	12454	318	2	PPFFPLKTLFFVFPLKLFSTLSPFKK FSNPLVSAPPPFFTLTIGNSQVLLKGGP



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12359	26260	A	12476	364	234	ERMGFHHVSQDULNLNSWSACLGLPKCWDYRSSTSRSLASLPF
12360	26261	A	12477	288	450	PGTVAHACNPFSTLGGGWSRTPLGLKRIICLGLPKCWDFFRELLSLPCLLIPL
12361	26262	A	12478	271	396	TISPLSFFFFLFLFFFPFWRKSGRESRF SQKKKKYKKKNIYY
12362	26263	A	12479	289	2	GSCLLRRLITYRKDIHTRNFSVPHRHQR PKVDKIPKTKGKGRKTKGNSIQASAPP FKBCSSSPATEQKWMENDFAKLRKRGPR RSNYSLSQELI
12363	26264	A	12480	323	1	YSHVTFYPLTAKKDQLVNNITQLTCKSYQLVHCINHSITLCHNLSLAILGHIPGLCIPVNLSEAMATPALSHVKKLLTLELTHHVCRALDIIILAIIVSLVALITS
12364	26265	A	12481	279	429	MNGQCKCYVTVVTVTVTVTVTVTVTLKRRK NPGTMAHACKPNTLGGHGWIA
12365	26266	A	12482	308	423	LTFFKNITGFFFFFTFETFCFVPQAGAQ GDLSSLKAP
12366	26267	A	12483	272	474	MVSNGLSEAKIPVWLSFPFFFEKRSHPFF EQGGGGGDI.SNEQPLPFRSGKGFSCPTL PSTRDYRPAQP
12367	26268	A	12484	84	229	LFRSVCHLLPLSCSSSHVQACLPTTFC HDCKSEASPMLPVQPAEL
12368	26269	A	12485	392	3	TGKKKRFPPPPKKRTFNSRQPSWRKKK LFKIFSPGGGAPFPVGQKKTFPPFPYFSPRTPFFSIFTPGKPPGGGLGPPFFPQKRGGOFPMKSWETNEKFPPLFFFFFF ETESHSVAQAQVQWHDL
12369	26270	A	12486	76	1	KLISWVWHNPVVPATNRASAGDPS
12370	26271	A	12487	204	8	FTTFPPPPPPPPPPCFKTKGSHSVAQAQEQ EKHDDHSIQPQPQSFHLSLPCATMNGL FFLFLPLT
12371	26272	A	12488	96	3	KKPLGQANFFPPFETSSCSVAQAQVQNC DL
12372	26273	A	12489	126	1	KPPHPPLFFPPPPFETSSCSVAQAQVQNC YLGSQAPPPGPTP
12373	26274	A	12490	107	2	IAGRAWIMLAIPLINEARAGGSLEPDS SOPTCAT
12374	26275	A	12491	302	2	GGFGFFPPREKGFQTVLGGVPPGFFS PPVFKTGPGVFFLGAQKKIFPPPPGGK IMFFLEAGAPLFFPPPPFFFTENTSCSV AQAQLQCDSLQLQHP
12375	26276	A	12492	248	398	PTQVTLSTTAQSYSEVHTNNRVYDLAV GSGHPDGAIAKGSFVQLKSY
12376	26277	A	12493	341	1	KTSHPRETYPLERHASSIKLETGALPC SQRLINSQNSVNNKPPCLNQLPFPQVNSCIIRPQTKDLKHTAIQPEACTLSLPCSYTHTRTHTRHTNNHSIPELLCMQCDSY N
12377	26278	A	12494	95	3	PLFFPETKSCSVAQAQVQNCNIGSLQPP PP
12378	26279	A	12495	62	420	CAKLCETAEHTASALDHTSPHGSVSGL FCHTFPIERRKRSRKPFGAHLRAGRALSQKPVGSCATPHNLHQIKTQNGLI QLLGURQAPWTVPLVLINEARAGGSLE ARSLRPA
12379	26280	A	12496	58	492	NSPPPPAPSPORTSPPAALASPTTGSSEA PCPASSWPRSSIALITFYPPQPCGLSF





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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						LLFRSSSSPTSAKSVAGITGACHHACCLRYFLY
12422	26323	A	12541	314	402	NLNSGPAMWLPVTPALWAEAEAGGSPVVG
12423	26324	A	12542	339	3	GSCLLEGKIPNRRDTHENPSPVHSHQRPRVDKPTRMGKKQNRKTGNSKTGSVSPPKRRSSSPATBQSWMENDFDLREGFRRSNYCELAEIDTGGKEVEIFENKFRV
12424	26325	A	12543	31	365	RSAMVPTEDRATKIFNYFLKITQLLDYPRCTVGGANDVGRGQQLRMSLRGKAVALRGWMMARLCALRCDFEENPALEKLLPRLAGNESVFTWEDTETRDLLGNKV
12425	26326	A	12544	278	410	PSKRVTAZRWNLNPTPALWAEVGGSPVEKSRITLANMVK
12426	26327	A	12545	88	276	KYFQAHKRLPSAIFRPLQATSTKGPQPSQPSRPRBGSSAHSRGEKTRTERGKEKRRKK
12427	26328	A	12546	251	3	PVEDNSRRRFQTGKEKVVBEQALTPWRTPNFPCSRDRVGAQVQCDSGSLQQLPGSSDLPTSAQVAGTNGRHAC
12428	26329	A	12547	106	2	DEHLFFLTSTFTSCSVAGQGVQWDLGSLQAPP
12429	26330	A	12548	225	1	GFFKKEPHPRPCKKTPPKLKPWGLNKKIPLSPVFSKGLPLPKZFFPPFFFTGSCSCHPAGVQWCDHGSQ
12430	26331	A	12549	218	3	VPPGGLVGLPQIIPKGFPTKGPSPKGPFGDQKSGPPNKQNFPPFLRRSHSVAQAGVWCDLGSQ
12431	26332	A	12550	276	24	GFLRMVEAFPQNLSPKRIIPFFFTBESHVAGQGVQWNLRLPSSDPASDSRGAGITQARPHVGLIFVFLNKTGRIR
12432	26333	A	12551	331	440	KSASSGYSKSGHGWMLTPVTPALWAEVVGSLVR
12433	26334	A	12552	136	1	RHTGSKTTATALVDVLLLPETESHSLSRLECSGTTPOGHNLYE
12434	26335	A	12553	84	1	TPFCLFSFEMESHVAGTGVQWCDHGS
12435	26336	A	12554	3	349	HASGPRLSKDPSVLSQGPRLPGLKRCSSRPLGPDVLGGSGQLGLGFTMLWSGPIKPCDDEENKKKKKKKKKKKKGGGPFKKLPLFPFGGGRNFFLGAPKFFWAGRP
12436	26337	A	12555	257	417	QQLHLQGLRFSFSLPSISLFFPMEBSVTVAGVQCDLALQAPPQGT
12437	26338	A	12556	268	403	YMRLSQDLVMPKGVADPSQEWELNSYQRHLRYDRLLENTSN
12438	26339	A	12557	286	426	DMLIKTCHLVCKKKKKKKKKKKKKKKKKKKKKKKRGGALKKRPLPP
12439	26340	A	12558	114	1	PLKEIANRIMKCCSSLAIRQMQIKITMYFYTPVIMA
12440	26341	A	12559	106	1	FFFFFFFFFFFFFFFFFEMESRSVAQAGVQWCDL
12441	26342	A	12560	118	2	KNYSHLKFKNAGRAQLTPALWAEAGGSPVRRW
12442	26343	A	12561	196	2	MCCFSKFWGSAQMTPTGFPFQDSEKTKLSYDRLFFFFFFFFERSRSVAQAGVQWCDLQAPP
12443	26344	A	12562	128	3	RAPPPFFFTSFDLPLRBCNGAISAIR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v =possible nucleotide insertion)
12444	26345	A	12563	277	370	NLRIPGSSDSPAS WSFTLVPOAGAGQCDLGLSLQPAISRFRK FSR
12445	26346	A	12564	55	251	AMVPTVPFNITINSKPLGHISFQLFAD KFPKTGENFHTLNKDKGFGSCPHRIIP EFIQGGDFF
12446	26347	A	12565	129	3	KYSVLIRPGTVARTCNPNLTGGRGQITW GWEFETSLANVAK
12447	26348	A	12566	172	1	PPPKKKKPRPPKKNFFFFGAI SAHCN LCVPGSSDSPASPSRVARITGSRGIARF Y
12448	26349	A	12567	257	380	GICRPLGLGVLSGATGVDRDPEAEVCP LAECLKCAGRSTA
12449	26350	A	12568	120	1	GVPFPCFVLFPETESCVARLECSGMISA HCNRLGLSSRS
12450	26351	A	12569	250	2	ICKPKTQFQFLTKRGGRNABSFRRKF FPOLKPPRPVFLKIPSCQKLIFFFFFPE TESRSVQVQARVQWHDGLSLQCAPPPGF
12451	26352	A	12570	338	3	VSTPEKNVPHTRGFSKSSKYKCNFF FQKKLGSPPPSLKKVPFGKPPVYCCSGR VSTAPYFLNRGISTKILPPFPGLPGPEE KPLSFFFFFFEMECRSVQAGVQWCDLG
12452	26353	A	12571	5	356	ICCLCFKINIFQHNKINFFCVTRSG PVTQAGVQWNCNLSGQQPQLSSKQS
12453	26354	A	12572	115	2	DRVSLVLVACNCLDRGSSSPASASRV AGITGARHD
12454	26355	A	12573	279	377	GQVQWLMPPVVPAPWDEABGLQLQSSSR PAWAT
12455	26356	A	12574	117	1	KTPLFFFFFFFEMESRSVAQAGVQNYDL GSLQAPPNGFT
12456	26357	A	12575	253	374	SLPGNVVHACNPSPLGGRGRRITWGRKF GTSLANMAKPL
12457	26358	A	12576	130	2	KFGSPPLGSPFFFFFEMESRSFAQAEVQW RLQPPQAPPPRFT
12458	26359	A	12577	132	3	RVPGLPLFPFFFFFEMESRSFAQAEVQW RLQPPQAPPPRFT
12459	26360	A	12578	3	370	LRNCNLNGRRCSFLRSHMCTPAWTE RDSVSKKTLTVLMKQWNTPLRPLALS RKKPRGPFQVTHLVKEVVSILTGPCCA EGADLDYDPRTSPLPAKSWERNPPFPV HRGPVEGCPK
12460	26361	A	12579	131	2	FIYFLFYFLFLETSSLSVAQAGVQWHDV GSLQTPPPRFTPTRA
12461	26362	A	12580	202	2	RMKKNQHKRAENSKNQNTSFPKQHNSS QTRQNMWNEFDELTEVGPRRWVINS SNLKEHVFC
12462	26363	A	12581	109	2	KIFFFFFFFETESRSVQARVQWHTGSL QAPPPGF
12463	26364	A	12582	105	375	LIMILLPLQILLVSGTFCPLFGFSETF HSTPRLECNMGVSAHCNCLPVKTSPAS TSQIS
12464	26365	A	12583	106	3	RPIFFFFFFQTESRTVARIGEWCDLGS IQPPFP
12465	26366	A	12584	484	700	SSSWRAFSKKDKTWMHTPEALSKHFI PYNAKPLGSGTEVQPKGTEVVRDAVKL KFAKPKKSGGKKK
12466	26367	A	12585	301	1	TPKVKRTQKQNIPEHJLSTSPFWLP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						NLRADPYSATSGTKPKDILQSMQKAPKNS GIGQAWLIPAI PAALWKAEEVGLLEPR NLRPAWVYGRKLSLQK
12467	26368	A	12586	76	379	PLHPPASCPAPSLSCILIGSPSDPLFSD SARPGWGRGWGRAPQLPPSPFLYNLIK KWSRPFCHQKKKKKKKKKKKKKKKKKK KGFFFWRAPPPPPPGGGPPS
12468	26369	A	12587	109	376	LEFFFMSSGVPTAPEOPAGEMENQTKPP DPRDAPFEYNSHFLGPGGTAVPPTTG YGGGLPMGYYSQPGPSTFFLYQPVGGIH PVWYQ
12469	26370	A	12588	323	1	KKPKPRFFPPLPGFKRGNTNIPSPFSG GFKKNLGGFPNDPRPWPSPQIGPFLRS KBLILIGLFFTRIGIGGPPSPFFFCETKS HPVMRLCSGVISAHCNRLRLVS
12470	26371	A	12589	262	1	GDFPTTSPTQTNQKEHNNFKSDQLY EDTLAGRSVLKNTPTQLPRAWTGPLY VIYSTTAVRLQDPPHWHRSRIKLCPS EKK
12471	26372	A	12590	284	374	TESRNWGAQWLTPVILPALWENAGGS PE
12472	26373	A	12591	297	387	GQAWLTSVIPAPWEAKGGSPDVRSSG LA
12473	26374	A	12592	206	407	VKPNPRACKRLGLVYTHIVYIVYVY YIYIYIMYICRYISLTVVYVNSKEKG LDTAHTCNSR
12474	26375	A	12593	222	379	LTGSGIMGNFSLILVYIRKVMGVSQWL TAVIPLLWEAENGSLGSRSSRPA
12475	26376	A	12595	301	189	KKIQSQAQWLPPIPALAEAGRSLEL KNSRSAAWS
12476	26377	A	12596	209	3	SVKPLFFIFQSGVVLFLFGRGLKRSQ TISAHNCMLHLPQSRPSCGLPKCWDYRC ASPTLKIDLTQ
12477	26378	A	12597	306	3	NGKGTYYNAPEPPFFHFFFFSPLPPL FFFFIFPLDFCPALSPLVGGSSLSPLLL CPMQHYFCDAWNTFDALIVGSIVDIAI TEVNVSTWRLSLTVV
12478	26379	A	12598	1	249	NTGAQCPLEFSQELQLLFTGGGDEGS LLILRLCNGAISAHCNLRFPQSGDPPA SASRVAGITGACRDHTECPRPVPPSS
12479	26380	A	12599	228	404	RLSSLSPVTEFGCLSPDLLLKCDDWPG TVIHTCNPSLTGGRGWITRGQBFKTS VNM
12480	26381	A	12600	101	580	LSLTKNCALLGEETMEQEMTRIMRRVS EVRVAVLSQKEVELKASERTQSPLODLA TYITECSSLKSLSEKARMEVSEQEDDKAL QLLHDIREQSRKIQETKEQEQQAQVEEM RIMMNLQLEEDLYSARRRSDLYSESELRES RLAASEFKRKATECQHLLK
12481	26382	A	12601	464	3	CAIQGTLVHHPKSSRIEPLQKLEPCKE CNKVVYFKHSLQALHLLNKKPYKCD QCSYASAKNLLVHLRKTGEEKFADY CSFTCLSKGHLKVIHIERVHKKIKQHC CKKKYSIVNLIKIHIRDAHDQDQMYCGR SRGSARMSRALPS
12482	26383	A	12602	140	1	WIGSFLSSEEDGTVVQKISGVQRSLSLY VYIHTHTHTHTHTHTV
12483	26384	A	12603	112	2	ESLRFQGAHAHTNPSTLGGRDGWNKKDK

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12484	26385	A	12604	139	1	EFKNCERV KKRVKRGPGGQFGKGLGGKFFFSKTFPF FFFTESCSVAAGVQKRR
12485	26386	A	12605	204	460	SGQNGEICHPRGFTCTPKALSSLLIAR VCLGHFNKGVASLSQTANGCFEFGFSBT ESRSVIAQGGQGDPSLQPPFPGSCILS L
12486	26387	A	12606	317	1	KRPLFKNIPOKPPKNGAPRRKQPCIF GPNQKNFLFTEAPLSPPFWETKKGAGGF FWGFFFFPTKLGGQKVPFFPTTFPFFF FFETESLSVTSLECSGASIAH
12487	26388	A	12607	248	367	TQLSSGVSQSSLRHPPICTPLHTHTHTH THKRRHRS
12488	26389	A	12608	2	387	QKQQAAGRETFSTCSLRILSAPIMATPV ELSTKAQMPIVGLGTWKSPLGVKKEAVK VAIDGAVRHIDCAVYVQNGHEVGRAIQR KIQEKAVIKREDLPIVSKVQWCIWLAPNT IVPKSQWQSLQTFQR
12489	26390	A	12609	258	23	WMERGITRPTQTILTEPEGLDHRGIS PNSVMNGIVPHISILTLNINIGNALPKR PGLAKWLRIRYQTSMLQETGR
12490	26391	A	12610	176	433	DALSSAWGTVLGTQIPSHPTILMLSPF AWGSSSLTQTLFYVPSGAIRGTSVYLAR VGQKYKTLMLGAVAHACNPSLGGGRW IT
12491	26392	A	12611	312	410	AHHYRTCSRGWNSWLTGPIALWEAEAG GSLEP
12492	26393	A	12612	3	289	VFEPLSRKSLYSILRMFWTFKFWPLERF WLPTIKNSDLEDHDLGVFKPSHLVYT IPYAFLLLIIRVFEKVFASPLAKSPGI KETVAKVTNT
12493	26394	A	12613	294	432	FMKLFFFFFFFERRSGCSVAQSGMQGYN ASLQPLFPSSSNFSGLPL
12494	26395	A	12614	138	375	SPNATCGHADPELQCHICQALKKPTF QTFFFGKPYGLIILYIAVFFTLRLSCS VAQAGVQPNLSSLETTPPSA
12495	26396	A	12615	232	1	GVFORAKLRAGLCPPQANDTSTKSLAL QAQKILLSKMAKAVANLVDDTSSEVL DELYRATREPTRSRKKAQKML
12496	26397	A	12616	236	419	LEMRNGNVWFFPPVNPILNETHGRVQDP GOHRETLGLKILFKLSRHGMRLGSQLL RRLRQ
12497	26398	A	12617	197	1	LCHESRGFLSRVSALEPLTLLVLMRSP PSVSPGVQWPHFSSSLQPLLRFPQFCN TLPSGMDYK
12498	26399	A	12618	132	3	NSPMFPLFTYFEMESCSVAQAGVQWRDP GPLQAPPERVGGRV
12499	26400	A	12619	255	2	MNSLNSFTDIAVILPLAYNRILPHPKILL SYPLKSKFQVKGIGRVKMLTPVITLWE AEVGRSLERPCPAHQPGQKILLYKK
12500	26401	A	12620	141	2	PHFTYILISCVCCVTESRFVARLECSG ALSACCKNHRPSSNSPA
12501	26402	A	12621	274	421	TYVNCVCYTFPLQVSLAFPNFYIIR PDRPTDRPDRPDRPDRPDRP
12502	26403	A	12622	132	2	NQSIKKKIELQCFQKRSQRCQKQVQMLT HILPARWEAKVGRSP
12503	26404	A	12623	390	86	IFPFFYQNTNGMAPGNQIPQCFSSRFF FLRQVIALWPSLEYTGITDQCRLKCSS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US95/15,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						SLSLCSWDRCAHPPVLNLFYVETGS HYVHIGLKLHLSRYPG
12504	26405	A	12624	297	396	LIRVGRQAQWLTPVLPALWEAKAGSGPG VRKSR
12505	26406	A	12625	303	381	KFHLVPS LNTMSGSG QRLQWVQPHFL
12506	26407	A	12626	318	152	GDKRLRLVS KKKKLNWFGRIQWVPFVIP LLEGEAGSG PEVRS FRPTGQOSMTFP
12507	26408	A	12627	48	388	QLNGKVLRLYLQRHSSFFFFGSGGFPF GPQGGGGGPNLQPRSSPPGVKGTTPPS LLEGGEGPPGPPFPCHFWGKGGGLPL YGGPPTS GPGKEAPTPPGGGGIGKL P
12508	26409	A	12628	116	3	KVATNQQLMPVLPALWEAKAGSGSEV RSSATAQW
12509	26410	A	12629	227	400	VLPVLFFCKKMHVFLPLPVYSYKKKK KKKKKKKKKKKKKKKKKKKK
12510	26411	A	12630	182	3	TNHLFPFPKFGVPLFPPLPFPFPFPFPET GSHTVAQAGVCSGAILAHCHLRLPGSSN TPA
12511	26412	A	12631	134	473	ASTINDLLFGRRKTPKELLQONORALNR AMRELDRLERLKELETKKIADIKKAK QGQMDAVRIMAKDLVRTRYVRKFLVLR ANIQAVSLKIQTLKSNNSMAQAMGVTK A
12512	26413	A	12632	100	462	QLLLCCCCCRONTAFNVPSAPPPPPAWA HMAPSLLEPPSLLVTOICLSAFSGSPSI NAPLLSKKKKKKKKKKKKKKRGAPLKK KK
12513	26414	A	12633	313	441	CWELLKWLVCPLCHIKTNCAQWLTP VIPTLWEAEVGGSL
12514	26415	A	12634	129	400	VSQQCWPTFPALYSISRCALASPOKRP WLOPMPSPSLLPRAFAWPKPLRAL PPAPRCIGPSTAQGLRSAGAWGTGRHL HLRPOC
12515	26416	A	12635	308	399	BIRGWTQMHVPVLPALWEAKAGGLPEVG SS
12516	26417	A	12636	285	390	TFGVNLINSFTYFETESRSVVRAGVQWRD LGSLOPP
12517	26418	A	12637	260	2	GQGPFFFGGSGSPKKKPLKQFFLVGGS KTQFFFRPKKGGPGVFFFSQTASRS VTRLECSGMLAHCHLRLPGSSDS PASA SR
12518	26419	A	12638	76	3	ALQVQWLMVPVLPALWEAKAGGSL
12519	26420	A	12639	219	484	LGLQEPDLDPKPILEPLALAQQLQTE ELSLIES ILCS YLKQALKVHQEVNCLMIF LGECEBELALALKKSKERGLLYGVMS LKDT
12520	26421	A	12640	33	462	BGLSWGYREHNGPIHKEFFPIADSDQ SPIELKTKKVKYDSSLRPLSIKYDPSSA KILSNHSGHSFNVDFODTENKSVLRGQPL TGSYRLRQVHLHWGSALDHGSHLVNGV SAPAKLHVHWNSSDKYPSFVEAAHEPDG LAG
12521	26422	A	12641	2	414	SGPAPATPMSIFPELYPNVDNGYLBGL VRGLKAGVLQADYLNLRQGSTLEDLKL HLQSTDYGNFLANRASPSTVSVLDRLK EKMAVEFRHMRGHAQPLASFLDFITYS YMLDNVILLITGTLHQRSLASLVPK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12522	26423	A	12642	161	463	KRRKRGKPKPLLLFTISATTAMGLTIS SLFSRLFGKQKMRILMDGLDAGKTTIL YKLKLGKIVTTIPTIVENVETVEYNNIC FTVNDGGQGERIRPLWN
12523	26424	A	12643	124	2	TVVGGGAQWLMTIPTALMRKAGRSPKV TSLRPAWPTRG
12524	26425	A	12644	258	454	NRPRICDYQGLREDSKRGRINOTACQF LWPROKMSQTKFKKDKKILAEYBAQIK KIRTQLVRO
12525	26426	A	12645	636	182	APLRKPSMIFPRCSGGQPSDLRSSPAQG TFRPALGDRKGTPTRIEPCGAGRAEAPP PRSGRQFGPQRKGTGNATKIVETRLSA APARSHAFIACRQVGRFRLSARRSGKK PHLTVWCPSFQDPIDQTTLQITLLSL GGDTFSDFFCS
12526	26427	A	12646	199	414	IYHTSRSLDKRLRAQRDELPHYQCMD GVGVPSMVGDPHAPGPIPPVPHNLNHP PFHAKQNYGAHAPFN
12527	26428	A	12647	130	3	DGFLCVITPLKKKNFTHTHTHTHTHT TNHTHTSHHTHTTK
12528	26429	A	12648	192	443	LLLCWAQKSLGTLGENTASSHTACLEWE SPLFACWFFWGFCLFVNLVFNVEPKSGS VLTLSCSVITAHCSLDLPGSRDPASA
12529	26430	A	12649	393	179	LHSRVQRSGCFCSVSNVPTVGGMHPTRS SPQSNQEDGQARM/TPVILALWEAKAG GLPELKSRRPAWATP
12530	26431	A	12650	263	2	KAPLLVYKWEKPNPGGNFSPGMOTENTF GVRFGQETKPLFFFFFTQSHSVIQAQV QLCNLDSLQPPPPSVKPSQYSMDHKKQS NTK
12531	26432	A	12651	355	111	QDFCFIRLRLPLSLVSLFLECKTSLLED WRMLFPLLDGPPHLLSLSLVSPINTWNY SFOOLMFRDVAVDFSQREMECLDL
12532	26433	A	12652	271	3	ROLKNILTFSSHNMLSKHYIYNYVTF LKSAPIFNLSTHNLNCFPGSISAKSYFI LFYFFTEPHSVQAQVQMDRLSTLQPP PERFT
12533	26434	A	12653	333	2	PFSQVFCNFPSPGCDPLGKTFTFFPRGPP PRFWGGGFFILAPFPFGLFPPFPLEP SQGPPPPPPPPPPFFEMKRSVSQAGV QWRDLSSLQPPRARFSDSPLYFLEGR
12534	26435	A	12654	310	444	TVLSNTIFYFLPLVETSPGVAQDCVRW CGLQSLGPPPPGCGRFS
12535	26436	A	12655	336	411	DOFGQGHRTFSLKIQKLVKCOGAH
12536	26437	A	12656	114	2	GIFFFFFGLSRSVAGAGVQLCDLNSLQ SPDPGFKQF
12537	26438	A	12657	191	1	KNFILTFSPGAKGVDVFFPPGYIQTG ENFFFFFLKWSFTLVAQGVQVQCNLSS LQPPPPR
12538	26439	A	12658	1	445	LRGSKFSGRDSKGLAARPTANPGLLL ASINDQAGGGYCSGRQVGRGLRNL LVLLTQACVAGVALLQVGRAGACAL CPRLSAPFFPGKLLRLKMTILPLVG CSLTGANSLLDPGALGRIGAWALLPFLG TTLLASAL
12539	26440	A	12659	2	224	ESTASRIAPQAMQPTPLPGLNYSQSP VVINAVLPLKKKKKKKKKKKKKKKKKK KKGGGVFKKKKIKGGGG



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
12540	26441	A	12660	96	1	GLKDRGRQVQWLTPTVTSAPNEAKVGGSP EVMS
12541	26442	A	12661	1	457	CWVHLQKGCPTLGRLEHSGQAEALLTSQ TGRPGRGAPHIDGAARQRSSHPRRGG QAEALLTSQTGQPGRGAPHLFDGAGQR RSSPPRRRAAGQGGSPRRWAGQRLS SLPRQGGRAEALLTFQTRGPRGAPHIP DEAGAGGGAG
12542	26443	A	12662	175	351	KGIFPPFPSSWAGGAINFKGTFAFRGKG NPPPNPSGGGGKKKPGQPIFRGPFLLG PPV
12543	26444	A	12663	247	401	SSNQBPCKGKPCVLTNFPYLLGRAMWLM PVILAIWAGTQGGSPVRSWRPT
12544	26445	A	12664	152	251	RNSCCPIKKKKKKKKKKKKKKKK KRGAP
12545	26446	A	12665	2	365	APTRSRCLRHASCTACRTVSTDTSSLR ADPKRSALADIQQGTRLRKVTQINDR SQAQIESKGTNKGGSANTRGASTFP TLGDLFAGGFPVLRPASQRDVAGKEEPI LPLWTVSP
12546	26447	A	12666	179	1	LELSKSGSHMRHLFSLRSPYSLTSPQLN TTWFTIITPILLTLFLITQLKILNTNY HLP
12547	26448	A	12667	279	35	NQAPFFARFFFTFRNVLFRKIKKKKCNWS GAPPIIPPPWGGGGPPWGGNLSPPGP PVSTPFPFGAQKHKKKR YGGACL
12548	26449	A	12668	299	399	ISIKKRGKPVQMLNFPVLPALWEAKVGS PEVR
12549	26450	A	12669	1	385	KMONRGFFFLTFLLGLTSGAARKKNG GKAGPSSKSPNWPWGP CPSSKDCGGV FRKGTWGAQTHSLRGSGPCNWKGFEDN CKSKFNWAGAGGGPGTKVRQGTLLKAP SIAGQGTIRVTKPCT
12550	26451	A	12670	357	1	AGKIAKICPVSSWQAPGTFVGGNCNQ GGAPDQQPQPIQLQNTSS PDPSNENSP ATPNEQQQGDAPPQLEDESPAFPHDTL AKLDDMINRPRNVVPLPKGELEVLLKK GIDFSKK
12551	26452	A	12671	107	373	TGNTYPLEDCABQMRLLAQVHLETRV KQQQVKIKOLLORNEVQLDKGDENTVV DLGSKRQYADCSETFNDGYKLGRFYKIK PLLNP
12552	26453	A	12672	196	45	YLYFHSGREKRLAKCTYDKLFKECCIAD LSKYKKNKVCFPHYGRKFLFK
12553	26454	A	12673	33	448	KEGAERAGAAAPVMSFLDDRDSARTRS GTSLGSADMGDMKTPDFDLLAAFDIPD IDANRAIHSGPERNDVPGGPGKPPQCVG SREHTASASAGDGGVPAIASDHGLPP PDISLVSVIVHTGLSRGRWRPWVDV
12554	26455	A	12674	250	29	RKGNTNWSQPYEDYRFTTSSSYHLS IYPTLSIVLSIVLSLFTPLSLITD YVSLIHELRLPNIQ
12555	26456	A	12675	377	442	SDRONWCFIVITATWEASGES
12556	26457	A	12676	1	533	RIFPGRFRVLKPCPDPMGTLLAWV AFCLLGADETHGAGVSQSPSNKYTEKGD VKLRCDPISGHTALYNYRQSLGQGLKFL IYFQGNAPDKSLPSDRFSAEFTGGSV STLTQRTQORSDAVVLCASSLATWHS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/155,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y Tyrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RLLPAMKPHPSLSLQLDLINRGFSLLL PPHGKQVDLDLSLSFG
12557	26438	A	12677	232	3	GWSSDCQQRARVIEEKHSKQKGIKENP SVRRHHQRPKVDKTTMGKKQKNKTKGNS KTQSASPPPCKRSSSSPATCI
12558	26459	A	12678	134	3	IFIVRFPGGKPFSCSTISLSQWLKCLFTG IGELLMQGVSTGTLTY
12559	26460	A	12679	212	47	NGTHPHGYTLHTRKLTHTSCAHTHTHTHS LLLVKRSFLPKQNTTISFRSCCKLGKF
12560	26461	A	12680	224	2	MQNASFLAFLNFRVCLLLQLLQMLNPHS AQFSVLGSPGPTLAMVGBDADLPCHLFP PMSAETWELKRWSSSQCT
12561	26462	A	12681	35	397	KPLISQNKLSHSVSSSQTPFFFFFPGFE KKVPAPFGGKGPFPPLPFGGNAPFP RGEKKKGKGPFPKPNRGAFFPQKTKKTFG GGGGKKKT PAPPTKEVDQPLPRRSRG PGRLLPRGA
12562	26463	A	12682	188	514	HTHLVYVLSGAAPFFFFFERNFLFAFR VEKRGKDLGSLKLPFGFRHFSGLTLQG SGNNGAPPSPVILFVFFEKRGFPILVGR EGLILPPLQPAFPCLISFTGADNGPS
12563	26464	A	12683	366	3	ISQIQTQMTDWSLELQCELAHRDTVA IPQTRSFPFPLMISCNLFSILLQMDRAF PPFPQPTITIQGQISTSPATWPLTHIH STPGLSVEYSSNTHKSSLSPTSONLRVD FMLASPTV
12564	26465	A	12684	99	1	SSCIRFFLEQAYGQSQSYGTYGQPTDVS YTAQCI
12565	26466	A	12685	247	31	FLKEKNQPFYLFIPQRWLDNPKPIRKQL KRGSPYSLNFRVRFVSDPTKLQREYTR WVIGYIFLENVKTLL
12566	26467	A	12686	416	253	FSPTIPIWTAQFADADLMSHAKMLAQ LKSDSEVVRPLGSSQIPLCHRPSFTL
12567	26468	A	12687	116	3	CLLGRNMLRPVIFALWEAKAGRSLE SLRPARPMY
12568	26469	A	12688	380	1	SPSSKLGMSIHVSPLCLTG/CPPFVS MAELRQVPGGRPTQGLERPEVVEDEV RSPVAEPPGGGSSSEALXLSPREEDL DPRIQEELEHLNQASREINQVELQLEA RTTYRRIQLQESASV
12569	26470	A	12689	157	488	REFVSGGSHLKAQVRLEALLTIGTFP NAHLSILHMTAMQQRNKRRAASRRIQV LLNHSQAIKQESIILFTFRESQVWRPQ YSRMSASCTFLSGSNSSNPVSAPRI
12570	26471	A	12690	514	3	PSTRAGLLOGSARNATPFLCQITMAAGP LYTYPENWRAPKALIAAQYSGAQVRVLS APPHFHFQGTNRTPEFLRKFPAGKVPAP EGDDGFCVPFESTAIAYYSNBLRGSTP EAAQVQVQWSYADSDIVPASTWVFTS LGIMRHINQATENAKGECRPLRVSSSLV GP
12571	26472	A	12691	304	4	AESLRVARIERLDTSSSEIENFPQFQS NLEMNSEILESANVQSSTYSINTELS LFSKVNGKFSFTEFQRMKTLQVKDQAITT RVQVRNLVYTVKINPL
12572	26473	A	12692	221	2	VGPATRDLCFADEPVVGGKQKQKQWVVL CLSPNRGLAGRPDTLHITCASAHNRHTH CMHTRHAAHVAHTHC

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12573	26474	A	12693	3	205	YMLCSILSTQEAASICLGRKFTYLFYTL FRDGVSLLLPRLSCNGVILAHNCNLRIGD RARILHLSKKQK
12574	26475	A	12694	233	3	IMGPAHLPGKNHNGWGLMYKAPFFLF FFICTGSHSVAQAGTI PVHCNLRPGSSD SPAPASRVAGNTNVPHITLY
12575	26476	A	12695	408	3	PAREMEKFRVCRKRLPLGVRVRGEIN IITVEDKETLLVHEKKAVDLTQYILQH VFYFDEVFGEACTNQDVMKTTAPLIQH IPNGGNATCFAYGQTGAGKTYTIGTHE NPLLYALAKDITFGLVYSQV
12576	26477	A	12696	123	631	REAVCGKRGSGGGFSGRDSRSGGAVSAA VQDMCDPGSELTIESVPAGPEASESTTD ENEDDIQFVSEGPSPLVLEYILDVCGDD ENFSAYYSD ILFFPKMKRQGDPLHFLNV KKVKTDITZENNEVSKNHCLSKAKKEHFE VIRQPIIREKPSLSSKKRINDLGASDCW D
12577	26478	A	12697	429	629	LALLYPLKAVGKPVNFNEED ILGLPFPF LNEEEEEAEEEEEEEEENPVAKIPDS HEITLKHGTKT
12578	26479	A	12698	158	404	LPLLSVERLIVETIYATFIQDLFASNTIP YSSSVFRIEMDQPRTHSGPTTASNPAPS STNSSAPSATNSKQRRSSSLSKPS
12579	26480	A	12699	185	3	HRFPISIPSSVTHPAMVRLGLQYSGLV SGSNARCIALRLALQVCFILLSLMIQP HLVY
12580	26481	A	12701	181	3	TVWASMFLSAALRAAAGLAAHNGTHVR HLHKFDMDQNGAGGALFVHRD FRENNRDT PCI
12581	26482	A	12702	373	1	LLVQRDSQRVIRIMDKLVSSRDRVGRG VEKQWTDHRTVIVSVKLIKQRTTPEFFIP SRTTTPKLLFLVLPSCGTPOHPVSRSTI PEPPLPTEP LERLPEHVPVSGTIPKPPE PPLPIEPHETMY
12582	26483	A	12703	272	508	TKLGKRNKATGNSKQCSASPPFKERS SPATEQSWMENDFDELRESGFRSNYSR LREDIQTKGEVENCEDNLEE
12583	26484	A	12704	341	1	VPQHPHPLAPPSLGFQSNWPLMGSRFR SSLSLASSASTISSLSLSPKPKP TRAVN KIHAFOKRGNALRRDPNLFVHIRGLWDLH QDSSGLRLWKRRNPFVLSGHCLFYKDKH V
12584	26485	A	12705	187	365	WEPSCRGPSAKPTRCQSYDNACMOGAE GRSAMEQPOESPEVREEREIEENAHAE GTF
12585	26486	A	12707	238	596	LWLIVVKYSTINGGAAGLEIVPVFFLAL FLLRHYGDFKQHLVILGTLNAYLCLF LIVFLPLDVSTTIRNKGHAANSSFP ENSNTIGLYATANPVPSPHCPTKPSYI PDGIMPI
12586	26487	A	12709	131	2	DRVSLSPRLKSGTTLAQPSRLKQSSHIL SLTSGMDYTHAAPCI
12587	26488	A	12710	151	2	YRQGLITLPRICRVMINALCNFESPL SDPLTSASRVASTTATCHTC
12588	26489	A	12711	151	1	NFPFDDHPTVGLRAGSSLIHWWEKCL VQSLKAVWRFIKDLKIDPLVY
12589	26490	A	12712	28	411	RUVFARPAGEPEPRHVSVMKLNPOQAP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, -possible nucleotide insertion)
						LYGDCVTVVLLAEEDKAEEDVWVYLVFL GSTLRHCTSTRKVSDDLETAPGHDC EIMKVQLCAFKGLPVFVTEKYFLLPR MYYYRCLTYTPSAV
12590	26491	A	12713	351	675	ENPRHTPIYSLPLGLQKQVLTVDIGFG GTAIMTVGKSSKMLQHDYRKRNLQDG RIFIGTFKAFDKHNNLLCDCEFRKIK PKNAKQPEREEKVLGLVLRGEN
12591	26492	A	12714	326	457	ACSHHQKQAPFPALHPCDHPGSLP LLNFSVCNPGREVSPT
12592	26493	A	12715	200	1	TITRVCVFTTRICGLKGLSMAKALPDQRK DRESETECQVWMLTPVIALSBAEAVGL LEPSSRPQV
12593	26494	A	12716	208	405	KKEBENKHTTKKGRKKVHVLCOMHSSL HRKFGQYRKTGTGMAQWLTVPVIALN EAEVGGPPEV
12594	26495	A	12717	157	3	AKETPTHGSKCKKFTFFFPETERBSVA QAGVOMRGLGSLQADPPGFTPCI
12595	26496	A	12718	1	472	SPAILPRLAFLPYLLDWSGTGRADRSA LWNYFTIHLPRHQWCEVQSQVDQKN FLSYDCGSDKVLWSGHEQLVYTDANG KQLEMLREVGQRRLRLADTELEDFTPS GPLTLQVRMSCEADGYIRGSQWPSFD GRKFLLEDNSNRKQTVV
12596	26497	A	12719	537	1	LHTMNGNNESSGADRAGSPVATSVPIGW QRVREGAVLYISPSGETLSELSQTRSY LLSDGTCKGLEGFLNVEKVPNFDPLAP VTMGAGVGPASEEDMTKLCNRRKKA MATLYRSMETTCSSSPGEGASPGMHT VSPGPGAPPCRVPTTPLNGGPGSLP PEPPSVQACI
12597	26498	A	12720	369	3	AAKIIIPATRKFKASLELELPSSPDSTGGT PKATISDNDALQKNSNPYITPNRNGH QNGASYAMHFEARKSQILKCMCEGSSHD TLQELTAMHNVIGHFKIVTNSAMKKGK IVETPTVTV
12598	26499	A	12721	230	3	KFFWVLNAGLTGNSDASASLNQVHSFP LPSRHHPLSLGLSSPVLQSGKRRL ATLRALESASLSQHPHVPV
12599	26500	A	12722	26	110	REQYABENMRGPAFGKRTSLGQQRNEV RYGDVQIRLGSCPVVNLGERAILQAM VQQGSAPADRFAPASPRV
12600	26501	A	12723	224	1	WQNDQASDPKPYSPSTCCCLSPARLAK RYGDVQIRLGSCPVVNLGERAILQAM VQQGSAPADRFAPASPRV
12601	26502	A	12724	120	530	KKVARCRSRSRSRSRSRSPKAITNR T*GTRCTPRWRSTVLGRSCTRAR*QR RSLGRGHYRSAGLCDHGSVRAGSDGA DGTGGGDRRIIGRHSLLSSSQSAAPS SSAGSSSSPSATQPLRMLEYFVL
12602	26503	A	12725	434	222	KSEKSRGVEKQD*EKOREEVEKRE/ RRSRRRRRRSGVYRKGRRRREDIL VARSRHSPRNSLPTSL
12603	26504	A	12726	268	370	SNILTHIESFFPFGTIDPSV*KSLDA* KTPGPDGFDIKLYITPCELTFFPHLL H*FTGAVLWNSFSKAAISITLTPKNY DIMRKKNYSPLSSYINWQCSFFLQDIPP LSFKLNCPLIIPH
12604	26505	A	12727	103	636	VCFISMKQPKGSRHPPCS/PPRPGS*VC QQSRPLGQPSAQQLAHRRLGLLQCG

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in US 9,951,512	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
12605	26506	A	12728	1193	1638	PRSPNQPVPRHGRVSGQTLPKPTPKRP PGPAPRHGGHSMILK*LVCAQFP*P* *ASQAVFTLQVPGKQVMTFCPPVVRAP TP\PLSNGGLGVSEH*DG*QAPTSP* PRCQGGAGEGPQ GLGFAMLPRLALNSWPQGDSPVAFSRAA GTRGVHRTQLQVSPNYKVLAMHSGSQ L*SQHFRKPRSDHLSGVRDQSGHQHE TPSL/LKNTIRISWAMHPIPLVPATREAE ARELPE\PGKQKLASEPRVKP\ICTASLG NTCTPPOK
12606	26507	A	12729	304	101	BHLHWPCPSPLAFTPDISHCEPFPKQOT SP/CPGT*CLGFLKPCSSCHFA*K/PLH PSEPARKSLAPDTCF
12607	26508	A	12730	91	264	SORSISGLRVKENLIVFMIMFPPIYSSQ TFWSQTFMLKIVFMGISISICYIL/NT EKNLGGQWNLAPIIPALMEAEAGLL*L RVKENLIVFMIMFPPIYSSQTFWSQTFML MLKIVFMGISISICYILGKRI
12608	26509	A	12731	1026	406	LAFPRSQTFSSHILVHFERMVINRYRY LACVRRVVFRLHVLAYFGRIVLYKRYF LVHFRPREVFPRHMLACFRMVLYCYPL VLKILILIYVPLTYPRKIVFLRHNFRLG GY*KKYGYAPRNLSSFLYRQCFILAYF LFYIWLRLHLQF/CCFVVSFCLFPDFPL FSAACVPSVLQIAIVMFFHALQLFFF* VVLCPSSNRQ
12609	26510	A	12732	1508	157	QDVGGSGFKDTHPRGRVASTFSKLLTG RNASLLFATMOTSVLITTYGLLNQKCA EVREQPRLPFPSSADYDRIKXNNCMAREC LIPATYAKLRNKVTPNGYTLDCQITGV DNPGHFFIKTVGMVAGDEESYFVADLF DPVIKLRHNGY*PQG*LIGHTDLDAKI T\OQGFDEHYVLSRVRTGRSIRGLSLP PACTRABREVENVAITALEGFKGDLA GRY\YK\LSEMTQDQORLIDHFLP\D KPVSPILLTCAGMARDWP\DARGI\WHNY DKT\FLIWNED\HTRVISMKGXNM KRVLRS\FCRG\LKEVERLI\QERGWE F\MMK*AP*EYILT\CPENLGT\GLRA\ GVHVPDQSPSQDPTAFKILEKPRTPR KRSHKVVWDLAA\VAQVVD\ISNIDRIG RSBGL\VOLEDSVNYLVCEKKLERSG QDIK\VPFPLPQFGK
12610	26511	A	12733	261	487	TGSEFDCAKQGSPIPREVPTVAEMKKE LLKNNQPM\RGVVAHCNPSTLGGQGGK IT*QGFETSLANMAKPELY
12611	26512	A	12734	382	668	YKRITDIFVDSHTVHLLNKRQSCRTFG FTIOLVQLISHOLAAPRDITYSHSVAQAG VQM/RNLGSLPLPPGFRRFLCLS*HAL KNLSSCDTFPQY
12612	26513	A	12735	401	27	GDRAESAEPRAMSHSDNSHRYTTLFIC LTHTVHNPVHS\HTHTHTHTHTHTHT TVSHRHTETPPLLKQTKLKYF*NSRDD TPRSRPGSSGLQLRSSSPVPPQPGTVB ASADFCGHDLTT
12613	26514	A	12736	202	182	KYLPFIINLITNILLFFETHSCSVQGA EVH*S*LKPMPPG\SSDSFASAFQVSGI

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
12614	26515	A	12738	319	2	TGSPSSSWLL*PFLKIGPTKKG QNTPHLYBYIPKVDAPLFLFKSYSVY VVAVLSPLYFVNGJALTLKJLAINSLF HKIQEPS\LGSGSG\PLSCITII*RLCL RSLHLVFRSLWILPICDSSSVF
12615	26516	A	12739	1363	2000	DRVFVIPGWKCSGTIKVHCSDLDPGSSN PSTSAP*VAC\ATGTYPCCGLNPLYF* MEERGFTQVA\QAGSQNSWGSKNQTSSE ASPKVLQMNKP*NLNPGRSILN*DGSI RYKDNYP\WEPKRSIKCLQKKS*+L SAQFDYEAQPKRKYFISLLIFCTSS LHFNPTLTCSCQLQYSIRKLSSEESC PPLPACSLKHTQAIKITF*RLWRTA/L FVLLK*NCFRN*+*KYFLSVSNLKI/ QWVRSSLHPGAGVYPTV*RPKHKSIVL I*IQS\ITRCLFYILVVRTIFPLQLFL SKIPSTYKEDFA*VLPLSFFFFMESRS AARRSLSSQLPLPRLKRFSLSLSSW DYRCAPPLGLASPLSS*GSCCSIQFIL RMSTISHAINVLVLKNTVLVLV/SASEHS LKKKPC
12616	26517	A	12740	1696	743	GGQIMRSQVHDPQHQHETSLLKIQKS AGPGGMHL*SQLRRLRQENRL\NRGCS EPR\SRHCTPAMATSQDSVSKIKK*KK *NHLESKQGGPALEPPGQAGQLRKE OLOGRRELAADMT*+QHSKRLGALPR FLLSAYFNKHAARRQAYLETPPTFS YQREGEQALILQVEQAQASPTVIRER RQSQALCHSRKSQEAPEVRPAHPPRVRG LGKPSQGLSAHLQODRAPAPRRASWDQ RSQAPISVTFPSVLKKEESVPCGPFPG HAPAPRGIHGATWGAHSRGYPGFIALL PQHSDEQRPN
12617	26518	A	12742	2473	445	RGARRSRRSRRRRRRHQSRPVRAAPRQ PEQGRRRGAPTHGPQLMMDLPLPPGL PSQQDMDLIDILNRQDIDLGVSREVTFD SQRRKEYELEKQKLEKREBQLQKQBE KAFPAQLQDERTGEFLPIQPAHQISE TSGSANYSQVAHIKPSDALYFDDCMQLL AQTFPFV\VDNNEVSSATFQSLVFWYSPG HIESPFTIA\TNGA\QSPETSVAQVAPV BLDCMQDIEQVBEHLLSIEPLQCLNIE \NDKLIVETTMVPSPEAKLTVDNHIFV SSIPSMRKEVGNCS\PHILNAPDSFSK HPLHKNPNQLTVNSLNSRM\PTVNI GAWNIFILV\MAKPSIRQQWSPATLS HSLS\ELLNGAHGCFLLDLTL/CKAFNQ NHPEGTA\EFHGF\DSGISLNTS\PSVA SP\HIS\VESSSYGDTLLGLSDSEVEL DSAPG\SVKQNGS*NTMYSSSGDM\VQP LSPSQGAHFCTMDAQCESTRGKDLPV \SPG\HRKNPISQDKHSSPIGLISQR DEL\RAKAL\HIPICRKKSPNLVPG\G FNMMSKEQFNEAQL\ALIR\DIRBEGV RNKS\AAASGICRKNKNENIVELEQDL DHLKDEK\SKLLK\KRGENDKSLH\LLK KQLSTLY\EVQHAAYDEGDKPYSPE YSLQQTRDGNVFLVPSKKEDVKKN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
12618	26519	A	12743	6	457	RPNRRFGIRVDFVRVGRVGHAPHEGLVP ERMYRGSPTACETQAAA*ERAPGPSSTP C/RLPIPRMSTSVPGQHTWTQRVKKDDE ERDFLDQLISRSGCCASHFAVQRCMAQH QDWRQCQPVQAFKDCMSEQQARRQEEL QRRQEQAGAH
12619	26520	A	12745	297	12	QERPVRLVHLFGRLRLADHLKLVGRDQ PGQYGETPSLLKPKLSGN\WAP*IC
12620	26521	A	12746	98	428	YNISFNETVILLTFTTTIDCLEYTRKDAI APESACGVCPCSLLGVA*IPKVVIRLD LSKXVTTTAGGHMCAVCVLDINAFPL IDEHKIVPVK*KLSSGSKACEHET
12621	26522	A	12747	3	638	LMLSLGFWVAWSLFLQPTLLGSLHPCGG QASMRVOLLHFGSGRASSKPSGSGVVP GLLLDQEMVTLFLVCTGILLHQMVSVP LLVYTRGILLHQMVSPTHGLYPWDSPP LDGHSPPGLF\RGAAFPS*GG/PLPVLV YTRGAAPSGDS\PPPGLYPMD\PPS GDRHSPPGLYPMDTPSGDHSPPALYP WDSPPSGDHSPPGLFPRG
12622	26523	A	12748	2	333	DMVLCHGWSAGSTIKRTERERMRNLE HR**IDRERERERERQIQ*KE*KRINFP EGSKERFTQSVQRNK/ELEKIRTLDS ETIYLSIYRN*SLRRQQRTERERMRH
12623	26524	A	12749	30	333	KTSYLLPVQWQANDNERYSSTNTIMA LPLPLPVFPSPSDAERKLDCSAISAH CNLEPAVDSFASACRVPAIAGARRHA*LV PSFPHWRRAFAVAGLV
12624	26525	A	12750	231	39	INDLL/CLF*EKLLTGRV*LMPLTPA RNEAKAGGSPEPRSLKL*AMITPMYSS MGREGQDPVS
12625	26526	A	12751	49	273	HLQVTEVPWFVVCVFFRRMGSHCV/AQ AGV*WLTGTGVVPCSPBELLGSRDPAS AS*VAGTGTGACLAANCRGF
12626	26527	A	12752	505	897	SVLRVQFYSAPSLFFHBEVLPCWGNNA VV*SLTATSN/CLGPSNLLKAPHLAN* KKIT*RGQLSMLPRLVINSWPHMLLP* LPE*LGQLARATAPSGGFTCLTQDSIL MCSPTVHKLSDSLALERTQ
12627	26528	A	12753	335	542	CCNEFFLSQVWMLMPV/DATR/SAEAGG LPDGGQRLR*ARSKPVNSHCSAGGROG IDFISIKQKNNR
12628	26529	A	12754	356	72	WHRYTLLMERTKCHLS*GLYGLNN*Q /WCTHPVVFATWRAKAGESLEFRSRL* CTMITFANS HCPFAWATARSCLNQSINQ SBNWQGMITGCK
12629	26530	A	12755	340	127	NLYLTIYPRUSITNLPRIECSN*PTGSI VHITKLLSSLP/ASASVAGTGTGRH HVOLSNEYFKIKIKPKP
12630	26531	A	12756	290	511	KGNQGT/CSSRL*SQRFGLRQADHL/ DQLQHGKAPSL/LNKTKISWALMRTPV FPSSQKABMKELIETPSRLQ
12631	26532	A	12757	254	549	YDGAKQRPGGDSVGRTHQSRNCWLL HNCO*PKSNQTQTP*PKNIRE*NAT*KS TDL/WPGAANHLCPSTLEG*GEWIT*G QEPETSLGNIPRPQIY
12632	26533	A	12758	617	451	NKKRRGLTLRLKCNVITIAHCSLKYP GSSEPTSAF*VAGITYGT*IHAWAY

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12633	26534	A	12759	91	393	KWYTKCECLYLLVSI FSRYLLSIYYREVL AQTIAGKLSKTVMPALEETVAVNGLQIK SKK*/WLGMMVTHACDPSTLGG*GGWIAW GREFGTSLASMAKPCLC
12634	26535	A	12760	10	221	QSHNTNGCLDLHPQKGP/QSVGETLNL* TIFLCVVCVVCVVRHVYHM/CYIYSDP ICPSICEYFSFAHR
12635	26536	A	12761	309	55	IIRYKNYISIKLEGNKKLYHATHEKKV GVAVLISKEVDPRKN/MYQDKGRFLL *R
12636	26537	A	12762	640	896	TIVLKNVFLFCGRDEVPLOCPS/SAVA /QSQTQLM*TTQPLQSSCLLSLWN *RHVPPLAMPLEKTFTTLLYTGHLETN IC
12637	26538	A	12763	1	357	IIVPLHSSLDGRVKKPHLLKKKKCTSLV IRETQIKITRYTYSNG*S*RNKAGNNK CWHGYTATGTLIAD/CKSKQMLWKEP*Q FHIKLNHY*YNSIEIQLGLYPRDKNIA ROGGLRL
12638	26539	A	12764	129	320	RWECVLRNIGQAWLIPVIALWKNQ/ ABGSLFARSRLQ*TLIAPLGYSLPG*W SGTSLNKK
12639	26540	A	12765	617	435	GVEGLILFLQKLKLEST/E/I*E*KLPS FYDASLTMIPKLKHD/RPISHVKIEARI LHKISINII
12640	26541	A	12766	243	5	QKIKERI KENKQNL*EIDYVK*PNL*I IGLPERGEKVNTSEMIFGSLIQ/ESVFN L/AYLRSVGMQIQEIGCTPPIYITK
12641	26542	A	12767	101	16	RQLPLSVFNRFCPLFCFSSSCSTQVG VQWCHLRSLQLPPPP/GSRDSPPPSSQN RG*TNII
12642	26543	A	12768	362	92	RVPHNGLGECTSPYMYI*PMTCVPRHG *DGNFCVITYPATIIIVTYI/YLSVCVSI *I*CYLCVCVYIYIYIYIYIYIYIYIY MKERRL
12643	26544	A	12769	1161	824	QAKDLSTHPTKNN*MG/NKQMKRLSES LVISEMIKITHMRSHLTHRTITIKNTS DKICP*RCG*MRA/LLQC*WKYKIVSPL WKIVWPFLLT/INWNISCNLMILPLGPI PIY
12644	26545	A	12770	241	237	K*RIWA/GVMAIACKPSTLNGCDWIA* SQEFTNLNNTNRPCLYER
12645	26546	A	12771	326	6	DTVSRNKGSGKIFQLSSRV*TYERSQG VKVYCKTFGRAPTQ/HF*AHBMYTGE KPKY*BOGKFFILVLLLLIMIQYFHL IKIVRLYLIRKKVSCQPSNKLIGS
12646	26547	A	12772	413	1	KRTYVFFFTFQAGV*/CDHNSFW*P P*SSMPLTSAG*MA/GSCMHILQAL S*/PVFLRAGSHVYAGTDKDSPTSASQSA GITAVSHHTRPILXYILNVLSPALSFSI LYSAYFLQPHLPIDHNF/LSYISSCC
12647	26548	A	12773	2	1055	FFFFLRLNLTLPRLP/CVILLACNLRHF PG*SNSPASASRVAETGSRHQARIYFV FLVEMGPHFHVSAQLE/SPDLK*SAHIG LPKC*DYRRDITPGHH*SF*RYFLKTY ISRVL/WCSLLGTFMFMAFDM*TW*H *QNHPHFLQIKWLISERLSAQQQQAL KTVTSTFSSKYVCRAFLRGMIAILYV



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						TF*SLDSRRRTCLVVAVSNNFFYSTLFLKL RQQVILITG/PYHLFSARPSSQSDKKAR ELNLSLSL/CPFFFGKKVSGTQAGVQ*H DHSSSLQMLPMSRLKQCSHLSLLSSNDYRS ITPHLANF/CNPLSGWSRTPLGK
12648	26549	A	12774	315	98	FRCLFNSINPLSPHVRKTCAGRAQMLA FVIPPFWAEBA/SQMPQVHHR*LEARS SRPAWPTVQKPCLEKYN
12649	26550	A	12775	275	59	NPSPTKIQKISMAWWMFVVLATRRLQ *SALAPLHSSVDRAH/CPLMKKQKYNKQ TKTSQEPVLVGGATVC
12650	26551	A	12776	73	381	SLANSRLSSIPRPTWESPSTSDSAWPNQ NLASEPLPLP*TPPDFFPALSA/VE/P LPPTPSPRDLPPLSPSYKQAPVLSVH PPVMPKLYVPSPLLSFLYL
12651	26552	A	12777	274	342	LNCVIA*WLMPTISALWEAEVGVSPA/P /RSLRPAMATW
12652	26553	A	12778	2	478	TIYYTYTTRVFNGLQLLPAFCPCVCV CVSLNGFNKAKDYGSHLKYSVITGFL LQFSLKFDCLPCVCVCFP*MA*KMPKI M/RGSHLKYSVYMT*FLP*PSLKLKYP DPIILKKRI/WPGMAYTCNPSTLGG*GG QIT*AQEFETSLAKVVKPCLY
12653	26554	A	12779	680	453	SETDWRNKFPSPNPNLNRINSNINSC SKKTPKKH/RVGLGVLAHTCNPSTLGR GWSNP*QGFENSLTNMNHFS
12654	26555	A	12780	59	487	SLHKHPEKGLQSPQCVTQEMLGGSHVQ QRAWELCAPPLTICPYLSFFAQDQAL LSKLECSGTIPAHNRPLSPQLEKNSH LSPPSSWNSRCTTPHQILLLF*DRIRL FCCSWNSVAQSQPTVT/SSLPSPLQKVS SHLSFPSSWNSRCTTPHQILLFFENFL* RQVFTMLPRLVSN*VQAILPWNPPKVL RLQA
12655	26556	A	12781	109	361	LSPNHSRNYTLIYPYTLNFMWSAFPTP KREFFSPFETPHSVAQAGAH/AIIA HGLDLLGS/SDPPTSAS*AGTTAIIIP G
12656	26557	A	12782	3	204	LIDGSLALSC*LFQCGATIAHCSLESLG LQ/SVPSATRVAAETGVCHHAQLAPVN LHLRTSEKHCH
12657	26558	A	12783	2357	6366	LTGS\NSHITTLTNT\NMGINAPI*RH RL\ANWIKSQDPSVCCIQETHLT\CRDT HRLKIKGWRKIYPSPMGRQKKKAQVAI\ LVSOKDTPNPTKIKRDKBHYIMVRSI QRELTILNIYAPWTRGAPFKVQLSD LQRDLDSHTLI\MGDA\NTPLSTLDST RQKVMKDTQRIANSALHQADIA\DIYRTL HP\KSTYTF\SAPIHTYSQNWTTIIVG SKALLSKCKRTETIT\NYLSG\HSA\IX LKLIKIKNLTONHSTT\WKLNNLLNDY\ WVINEMKABIKMFETNE/NKKTPTTYON FWDAPKAVCRGKFI\ALNAHKKQE\RS KIDTILTSQLEKREKRSKHSKARRQE ITKIRA\ELKEIETQKKILOP\LKKISE SRSWFF\ERINKIS\RPIARLKKKRRK NQIDTIKNDRGDI\TDLTLEIQTITREY YKELYA\NKLENLBNMDKFLDTYVSPLR

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						<p>                     INQBEVESIARNP\ITG\SAIVAIINS\I                      PTKKSP\GPDGF\TAEF\YQRYKEELVP                      \FLKLEFQITEKEGILWNSFYEASILI                      PKPGRDITIKKENFRPTISLWIDAKILNK                      ILAKRIQQHKKLIIHDDQVGFIPG\MQG                      WFNIRKSNVQIHNIRAKDRNHMIIISID                      AEKGFDKIQQPFMLAKTINKIGIDGT/YI                      FKIIRRAIYDKPTANIILNQKLEAFP                      KTGTRTOMPSLTSPLLFIIVPCPIVFWA                      RAIRQKEKEIKGILQKHEEVKLSLPADD                      MIVLENPVTSQNLKLSNFSKVSICY                      KINKQKSAFLYTNQQT/EEAKS*WMS                      EIMSELPPTIASKRIYLGILQLTRD/KD                      LPKENYKL\PLIKEED\TNKWNFIPI                      PCLWGRIS\IMKMAIL\BKVIYRTNAI                      PIKLPMTTFTELEK\TTLKPIWQKRS\                      RIAKSILSKQNRAGGATLSDFKLYKAT                      VTETAWHMYQNSMVLVPFQRYIDQNR                      EPSEIPIHIYTIILI\FDEPLEKNQW                      GK\DSL\FIKW\CW\ENMLA\ICRKLNL                      \DPP/LTPYTKINSRWIKKRDINVRPKT                      IKTELENLGIITQIDGVGKD FMSKTPGA                      \MATKAKIDKWDILKLSFC/TICTAKE                      TTRVNRQPTKKEKIPATYSSDKGLISR                      IINELQIYKKKKKTPSKGWTR\DNMR                      HFSKEDYIAA\KQMKK\CS\SLAIR                      EMQ\IKTT\WRVILTPVWALIKK\SGN                      NRCNRGCGEIGTLHCWDCKLVQPLWK                      SLWRFLRDLLELIIPVDVPLLGITYPED                      YESCCYKDTCTRMPIAALFTIAKTWNP                      KCPMTIDNIIKQWHIYTMYYAIIQND                      FMSFVGTWMLKETIILSKLSQEQRTKPR                      IFSLIGGN                 </p>
12658	26559	A	12784	787	926	<p>                     FQAIRRPRPPFALG*HNSVDLGWAWMT                      PAIPTLWDYTHEPLYLAKIS*CFKKVYK                      FVLNCIQNCIGPHAAHS/SGKTS*V*S                      NYLFFSPCFETKFCSVTQARLQWHDLS                      LQPPPGFKRPSCLSPGWDYRRLHTR                      SANFCIFSRNRVS PSNPGWSPPTDLRS                      AVLGLPKWWDYRSPPCDAKIYTMAPQ                      KNSHSSQPI/FLS                 </p>
12659	26560	A	12785	248	285	<p>                     CVVIF*CGMLLVLLVFEKITSRLAVY                      VV/CITRLRVK*ICSCILGC*FLFNV                      C*LYPIIFVFFFFFFFVFELN                      ILY                 </p>
12660	26561	A	12786	243	37	<p>                     RRSAGHGGSC*SQYGRPTRADHKVRS                      N/RGETSLVKIKVQAWN*EPVWV                      RQAEAGADAWDR                 </p>
12661	26562	A	12787	75	289	<p>                     DYRHEPRFFFLYTTFFEMDSHVARAGEH                      WCDLGLS*PST*GSSDSSASTSR\GRH                      HAWLIGFL*RRGFAC                 </p>
12662	26563	A	12788	83	256	<p>                     RKMZVUGLFTVQNH*E*PKYPSTEE/YI                      K/RLWYLHTMEYSAIKIEKLGTRQNR                      LILY                 </p>
12663	26564	A	12789	197	499	<p>                     QSLKSVEETVFRNNQ/SIPTFQVILMP                      WWLIPII*ATWEG*GRRSPLNPGV*QDP                      GQHSKTPSLQKTKFS*AMNRVPVWPA/                      IGEARVSGIPLSPRSRL                 </p>

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12664	26565	A	12790	394	91	FYNSTKFEKWNQIQLITRCRGDQIQVIR AHAVQLGFHVIYF/CISQNLISYLYISI YVITYRYINTHMCIIH*YLYITYTYIVI KH*KEHWIKGCFPTERK
12665	26566	A	12791	735	75	FFFROGFLSPPKRGVPPPTTKRYFSP RGSFLWNGTSRPPPRKCFSPPPPPVFL PPPKKKKLIISFSPTKLAPPETFKSPSP PS\PPPPSPSPSTFFFKFIFPSPSSP SSPPFFFFSPANEDPPVQSRRIY*FLPP PF*IPELPR\RVLKKKPGEGRWGLFPF PKGPKRRVPLGPEFTRLGHKTKPRFFK KKKKKRLISCLWHEPALPSTLGG
12666	26567	A	12792	482	342	MGVVFVFFETGSHSSVTAAGVQFCHLSL LOP/PASSDPPTSDSRVAGST
12667	26568	A	12793	405	169	FYKKKKTGSLGALSFRLECSGTLDNEN LELLGSRSLRL\SNTPTLAS*AAATVSV CHOTHLIF*FFVETGSCIVASA
12668	26569	A	12794	270	94	YVCISYKQIKISHSVKRRE*NTPTKTYLL KYIALGLTHGFPL*TFSEKTYTLNPGAV AHACNLSPLBQGGWII/R/QGEIKTIL ANM*IPVPLHVNIFLSVCSYSINTLDY LFYTCYILISL
12669	26570	A	12795	284	415	NPIKTIKKKVMGLFYGKTFPLINLKKKK KKK*WPGTVPHA*NPST\LGGLGGWITR GOBFETSLATN*NPTKISIRSGF
12670	26571	A	12796	1387	32	APSSFAIRSFSSGPNNAFFSSHWKRPW PNLEVVSMLNRSIFSRARRFVCTSCIDLR RVSTRFLVHLTAPLGKAGMTHIVREVD RGSSEVKKKEVBAVTIVETPMVVGVI VSYVETPRLGRFTTVPFELISDCKCR FYWNHKKKKKAPTCKYCKYNQDEGKKO LEKDFSMMKKYQVIRVIAHTQMRLLPL RQKKAHLMGDQVERGAPVPEKAD\WAPR EALSSKVLVTQVFNAGIK*SNFIGGDPR AKGYEGGQPVCMANPRKLPORPHPRAL RKGGPVLGAW\HP\ARVA\FSVARRNGR KGLPFHRTINKKIYKIGQGYLIKDGKL IKNNASTDYDLSKYSINPLGGFVIYGEV TNDVFMLEGGCVGTYKRV/LTLRKSLLVQ TKRRALEKIDLFIDTTSKPGHGPFQTM EEKFAWGLPKKDRIAKESGA
12671	26572	A	12797	86	364	EQDNRIFFSFLSLFFFPGFTEFGPFAQG GGQGAILGLPKPPRGL\SSFT*GSQE VGTTGAPHDIFCFNKKGETPRLYKKNK NNRGGATP
12672	26573	A	12798	101	440	HCSYAVKSTPFWYSGILVLLLRFGIYE PBNLNDQPTDPSPLIKRRLRERAK SLIEVLSKNSHPWGLMAHACHTRLRG IGGRIA*TWGFAKTSLSGHARPHLYLKK I
12673	26574	A	12799	364	195	NPPGDLGKRTLLNGGIMGTTPP*FPPP KEGFLQDPPGGFNSPI/QGRSFSPPP PGKFGPPQGFKRPDPFFFFFLNNIQ
12674	26575	A	12800	86	489	PTMAAREGIAAGGVMDINAAQLQLLKT LIHDGLAHGIRKATYALDKRQALCVLA SHGDETIVYKLEALCAEHQINLIKVD /NKKLGSEWGLQIDREBGRKRVVGCSC IVVKDTGKESQAKHVRNPF*CKK



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						VTEKFLFMTLPLTY*NMNRPMQVAHCN PSTKLTPGSGGRIT*AQS*TSGLNLVIPC LYQLK
12705	26606	A	12833	654	321	LVGIRFLRVKYFYNIKFPHLLATISPSLE VENLQHFHYLVLFILYF*ETSSSVAF LECSGVLIIVICSLIKLGSSNPPLASQV AGCTIAHHCAQQHFCILEXSNLCITVPFL
12706	26607	A	12834	867	201	RQMSPFTLATKSRDVAKESSFSANWAKGL FTTFDFSMLSVLISLQPGQPHTSPTQ* TQ GR*VENNQEP LATFPFGPPERSLPQQRL EPALISGKRGRGLEPIRFPVFVSIDHGPD SQACNLVRGVEAQPVAVWGQQA*\SBQ* SPSPPLDVSDPGSSLPRSSP*MDLR.* LSLTF*TPQKGSGN/DPAASSPA/KGPQ* EWRIKIGPQQLLLGHMWSQARVLS
12707	26608	A	12835	328	1365	YAFCLMLDLKKQT*AVFLPEFFOMVHKA AKTTQNISNTFGPGTANKHTQVWLKKPF CKEBSLEDEERDMHGKVDNDIP*EAY* *TT*KITBELSDVYSTVTRVVQHSRQIG KVKLDKGVFHELSSQGVNFRE*\SSFM LENKNPLFIARIVTCTEK*\ILYN/RDAP LGPBGQLQSQFPKPNIAPKKRSLVWH/ SPVGLLAPLDPTYFLNF/GBGTITSE KLCSGKLGHGHLQYLPLLAVNRKGIPI /LLHDNT/RDCVFAQPVQLKIKELG/YK VLPHPPYSFDLSPSDYVLC*HLDNFLQG KH/SQHGAENAFQEFVK*\STDFVATGINK/ LFSHMQKCVUDCNNGSCFD
12708	26609	A	12836	7	328	RRERREREEREREEREREEREREERERE REREREEREREEREREEREREERERE REREREEREREEREREEREREERERE RYKSPPPRPPLRL/RKV*RKHPHARAL SFPLYKKTCGGGRAESSVCWGKGFVT
12709	26610	A	12837	219	350	PNHITYAWTSILISNVGVCFWRADQIYL LILFEAGSCSYALRELCSDMIIMHCSL DLPGSKNNPITSAT*
12710	26611	A	12838	189	359	LGLDGVMVRVGCRCALMGTS*BEKSARVQC LTWTVIP/LLEAEAGGSPEVRSISRPAWP TW
12711	26612	A	12839	368	77	KNPINFLKPGSKMPGPPIYSYP/LEG*AG GFINPGF*TPGYMGKPPFFLYKSNLPG LAAPGCGSPFPGLGRKISFTPEMEVSI NPGSPLSLPPGBQN
12712	26613	A	12840	16	173	KTDVHSKTCTLFTAAFLVLTKWKHKLP P*VD/EINKMYZNHIVEYLYIAKS
12713	26614	A	12841	425	45	NSFFVFFFLPENKRLVTPAPRLE/CTGV LI/APHCTLPALBPFKRLVPASALLSWS DYRVPVMPWLNFCIFVBTGHI/HVAGS VLKLVSLKL/PSPSTDWDVKC*DFRYSVR COGLGF
12714	26615	A	12842	237	375	LLLWVYVILLKLV/LGVVAHANCNPSTLG GCKGHL*GRFVPCGVV
12715	26616	A	12843	21	325	TSEFFLESYSVAQGGWCDCPGELOPQ PG/SG/DNPTSG*VATTG/VHHHRL IVPFFCRDGLILYCPGRSKIIPSISCIRE LFKKILDFFLLTMLICNSNKG
12716	26617	A	12844	369	58	PISPLQFMLPELKNSPYPPFWMKKNRP PPFPLGAVLTPGF*NFLFKKIQRF

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						PFPPKKKPRRPPKPCPPKFG/SDPPFFFY PGPPPPKKGPPPPPPPPPPFF
12717	26618	A	12845	211	409	NALKPRTHFFFGGGLKGVNGNTLLDI GLHKTFFF*\GDPYYAL*I=AENALPGG GGDCAPHLQVK
12718	26619	A	12846	200	33	QKTNNTRCWQGMATGTLHF*GEFTRV QSHWKIVNKL*/SLNLI/P/SSSSSSSS SSSSSSSVKNC/LHKACTW/FIALLL AKTWKQP*CE
12719	26620	A	12847	416	125	KPTRPKQGGPPLYPRPFRLGNQKIGLT PRGTPLGNKGS FFFGQNKNA\NWRPG GGTGPSPGQAVPGLTLKGEVSTKLD PPAPPQQQKWLPL
12720	26621	A	12848	85	397	KIHFFIFLVLKGLSLPLTFSEKNVVF /SFIDPLILCVVCIEFYCFILILFHYF CLFGFCLFLMFVS*/QSLDPYFNS*/YI F*YKIQCYKF/CILIF
12721	26622	A	12849	1	246	RPRHLVASLVLQINGSSPLPKITISW ANWLMPIVPTFWAEAVGGLLEPRSSQ* *AMI\SPCCPMAAT
12722	26623	A	12850	161	1	NKTTSSQIW*PMPIVSTT*EAVVGSLS PRS/L/KLKAMISPVNHSCTPTWTTK
12723	26624	A	12851	65	244	STYYLHSLPFLDISYKWHHTC\GRYFM GALFLIAIK*KQKPRPSADEQI*T/IMW YIYLTLEYDLAIKRNELHRAATWVNLK IMLSKRSQTKT\HVV*FHL
12724	26625	A	12852	235	34	TTIAVSVLILKELMEF*TLQPDFLG/WS LITRSVDHVQMHAPVIPALNEGEVEGLL EPRSLAPMAATW
12725	26626	A	12853	168	453	QLKRGKSTGQGLSSEQCQPCP/PC RPSKPRPCCRI*SPARSQPSPASIM ALP/NERTPPPALGW*PK/CPKQSPQSA KSKSPVKSTERTAK
12726	26627	A	12854	244	3	ELQVYMH*YIY/C*SYTPKANTYIKYM HMCVYIYTHHVVCHILHILHLRHFQ CWLMLGKVRGCGAGLAKAQOQNGW
12727	26628	A	12855	376	428	KWEPGGHTSFFFFFKGLVNLFGRGVLQK RP*GGGQGGKFNPNFSGPREPPPP/ppp GGGKGGPPPPPGVFVFFLEKGGPILPR GVLMGAPKQVYTORGGIKSGNQCATPL SFFLKVWF
12728	26629	A	12856	129	395	APFNTHPFLSEAFQSLSEARPFSAFNS SSSR/PPVWRASQTHPPQDNSSHCSPPW GAPPQI*PFSDSLAHPQDNSSHCSPPW GAPPQI*PFSDSLAHPQDNSSHCSPPW GAPPQI
12729	26630	A	12857	363	97	GLATLRRLVNSQAQVIRFPQPPVLSL PKC*DYRQRPASLIEVNSRQT*KVAP /CSKPLAAAHQSGPGATETTRCPSPR CGPIF
12730	26631	A	12858	322	361	KSEKQS*VMLAVCTDWMKNTLFGVVF LPKTHN/LMSNYKNTQIPMGHSTIY LTRLPCNQCGHQKQ*KSEKQSQCSKKK
12731	26632	A	12859	88	417	HFTFFFFFFFFFFKGGGFFSPRLKRLGKN FFFLDDPPPG*RDPSPFKEGGF*TP/ SPDPLVFFFF*KKKGFFLAGGGF*TSF PGETPPLYSPEVWFYGGTGPTTSG
12732	26633	A	12860	217	2	LILINKLANNHCFLVFBTSLT*AGVQW

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Yeastine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, v =possible nucleotide insertion)
						HDL/GLLLRLAFPRFKQFFCLTLFSSND YRCALLHPATREDEA
12733	26634	A	12861	375	145	LSFFFFF*KGSCSVAGQGVQVHAHSSL QLQTP/GFSDSLNSAFSVPVRVHCHT RPLSPFFNICNRARPKQKQVFL
12734	26635	A	12862	525	852	NLLSTYPFETESRSVAGQGVQVCHLGLSL QPLPFRF*IKKPSNTALFM*NLLSIYFF ETESRSVA/RLECSGAILAHONCLPGS SDSFASRSRVAGVHSHSLSSWDYSCAP PCLANFFVFF*VETGFHVQSDGL/DTS *QVVCPSRPVKVGLQA
12735	26636	A	12863	3093	204	EPDKTQPLVLRKVGQARVGHARTLSGL GDGGAAGAALSSASSETCTRLRLSRLV IDLRAELRKNVDSSGNKSVLMRLKKA IEDBGNGPDBIEITSBGNKTSKRSSKG RKPFREGVEDNGLBENSQDQEDVETSL ENLQDIDIMDSVLDEAID/NGSVADC VEDD/DADNLQESLSDSRELVBGMKE /LPBQLQ\BHATEDKETINLDTSSSDF TILQIREPSLEP\ENEKTLIDLGET* RSEPVN*ESSELEQFPAQDTSSVGPDRK LAEEEDLFDSAHP\BEGDL/DLASEST/ AHAQSSKADSLAVVKREPAPQPGDGER TDCEPVGLEPAVBQS/SVAASELAELASS RELRAPTEAPSPPEAROSKEDGRKPFDF A/CNEFP/PAKESSTSEAD/QKMSPE DSDTTRKLSKEKRSRSCARKTGLGV LSSTTRATDLK\MLFRQIWRGVGAFL WTMARSPGSPAVYGVFVYSTAEBATCKI NHLKHTLHGMI/SVEKAPNEPVVKTS /PKRGSDGKKEKSSNSDRS/TNLKR/DDK CDRTDDAKRCDESVESK/DKNDQK/P GPSERSRATSKRSRSGPIKRTVV/MDKSK /GVFVSVKTSKSKERA/SKSQ/DR/KS ASREKRSVSPFDVKPEKRSRDS/BSHS RVSERSERQR/MQA/QWERERERLEI ARERLAF/QORLERE/RMEREERLER MHVEHRRERERQET/HRE/REELRQCE LRYEQERRPVRPRPYDLDRDDAYWPEA /KRAALDER/HSDFWQGERPHDFHDDR GRYPOHEV/DRREGSRMG/SIRBQGH YLEHRA/SDEPH/QQSDLR/LWGYEL* Q*RLS/SGRLSPFP/PGAGDMGTWLE DRDDP/PWKGFTARGPMMDR/DHK/RWQ /GGRSSMSGHSGPHMMNFGMSGROSF APQGASRGHPIPHGMMQGGPGQSRGR PSDARFTRY
12736	26637	A	12864	2	456	THLGSSEGGDSSGGLGRGNSNTR/SS SSWARGDNVPRPPPAVCNSI/SEGDVQ PGLGAGAGSSPTPGDGELRY/WPLGLG A*GRGTGGDDDLRTGLAGVQQCGG/ RRGPRGPRGRPRPRDLGLRGPRRAQ GAA/SATAAPP
12737	26638	A	12865	388	1	LIRMTVKKKAITECK*RGWGRGTAFTHC SWECKMIQPLWQTWQLKLNILYLWK QPECPML/VKWKGLYISMDYSINVEKK ETLWYTTA*MTLEVALLSERSQTKRGER GHTLWDSYINFGQMQTH



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, - = possible nucleotide insertion)
12738	26639	A	12866	198	3	KKQKQTFKNPKKIS*ALNCVPPVVEATWCA KVEGSP\PRNSRLQ*AMITPLHSSLN RVRTGRGTRG
12739	26640	A	12867	415	973	NPVNCQFSLPPTTETMGRHVRGAIGHG TCPSVPPNTHLHTGMWCLQHRRSCRANG RGGSHTRCTPQRVPDGEHP* IYIAVHGE PP/ESPQQPSPLSCPPQNYIALREEP QQLPLPOTLPSHPPPFWHICKTHSSBSR HPPFPQFCOLELEKGVDFIHHPLPLTP KCLPMLKPEPTPTPQHL
12740	26641	A	12869	715	893	PCVAFHSIREERFLTSESTNQKVLNWS ID*Y/VILITLGNWQKRLHLSFFLQKQP GGMAP
12741	26642	A	12870	342	58	KKKKFKRENEQSINDMNDNFRISDI*TTG VLEQPRE*GRKII FKELVRNENSNLTK /QINLLTQEV*TTT/HKNMKNSTPHII IKLMKTTTKEKI
12742	26643	A	12871	110	401	SPFSVMILKASRIYICLPT*LYAYITHL YIYLTLCIYAYVYNYICTHI/NHII HVITYYIVIASIYYSMSAWYNIKVSKD RQTYENIALITYY
12743	26644	A	12872	439	256	SYFMRRGDRTKSLYQFTLSRRRWQSTC PSMDENINKMH/ITIMEYISAK*RNBY SYMRHE
12744	26645	A	12873	356	43	OTPERHSHSHSQSPFLGAPMGIRASPV YSLLSCVLLMLSPQRVLFFPSAFFQQQS /WSGKVAQAYNSNTYKAGSIT*QGFK TILGNLAPCFYKKKFLRNS
12745	26646	A	12874	341	205	RETEKVLRLKKFFSQFLKRRKNNRFF LEKKKKVKKAPVQF*VRIE/CSF*KK KVGQFFSPKIFIFTFTEBTSV TQRFNGTILAHCNLQCSSSSPASAP* VAVSQDCALBLGURGLCLKKKKKKK KKNFGKKKSKNLLFKKKMGT
12746	26647	A	12875	474	206	PIRANGPVFSPPPPPFAGTICPHPLVIM LSRHLRQSHPTTVQPTWSGLLPSPPA* LSLETQHFKAHFIFP*H*SSGLGPGWG SPVGEFGP/HPKLCIQAAAAEAWPRE GTKARRHEGLPPAPCANGPAPRD/SGRL EFPTLPTIPVSQSPGR*HGAGGRPSCLR AFVPSRGGQASAAAGCRQSFQDLALLP LGSPILGQQNFSARGR
12747	26648	A	12876	257	467	YRVFTLLPRLEYIMACNLDLGSDF/P QVAGTTLK*LSRASRVAGTGVHHHSWL IFK/YFL*RRWRFSLL
12748	26649	A	12877	867	1409	GPTVLVGGQDWSVLAQPAHRSFTPRGG AGLAKCVLHKFPSPQLLGAFPQCK QYRVPPPLELQALLQARSPTTY*ANVL CQAGQSPSPSCSPWSPFPPSGRAHDLGA APQSGQKALASTSPDAPV/SVG*WCP SNPALQGGQNGARPAVITSGLSLYD CFLDGNWGRSLGP
12749	26650	A	12878	1416	740	IRNPRNVQLDFAAAPWRSSPLFLLLF SFLKTVLRGSMIPSTVPS/FHKGPAQL YSLSLRS*SQAPSPAPSSLPSPHPG LTQPGRRRKADIS/CSHSAFYVP/SL PHLPWACPLSLQPVLSILFCFVLF*D GVLLCHPG/WSAMARSWAHNHLPLGFK

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						QFSCCLSPSSW\DYACKPF\GLG*FLF *VEDGGFTLLVRLWNS*FQVHLFPQP KVLGIQA
12750	26651	A	12879	961	31	PSPVKDCVAVAGERGRPTGGSGVWRSH ARQPLMRLGLASEPAPCVLGSRPCFHV AFETPMWSPASCHFERCPLWRPALVAA GLDPFLLSSTLTLAVCRDLLRSWKKG DVCDSRNCWSTHSRPACRDAILAPILAG KGECIGLWG/AAANCTGRV/TPVSGLT STVFSSARG/V*GGLPDSGGRPVWG PQGP/PLPGLPAGVALAFLERQPPAP ALSHSLTGLSLFLGAWLQCTRHGRAPVL LEVSIVACGQLCEAAQPTFTQPLGLQLP TPSATSPAYLWVWLLTLPVSIKQXRV SFLTKZ
12751	26652	A	12880	232	28	PALWVPVVARFDSMRRTGQNMSSKKA PGVAHTCNPNLTGG*GGH/W*GGQFF TSLAMMAKPRIPP
12752	26653	A	12881	331	1	KNGPFFKNPPEFFPPPKGVPEPNPTPYF PWPEPIF*LTGPGLKKQKLPFQ/KGEL GMGQGMNPLPFWKGGPPRESKSPRF YKTPPPP1FKKKKKGGSSRSTSPRV
12753	26654	A	12882	370	287	VSLAGCGVAMINDV/VLHKVKILAK *IIKK*CI**FRGHSK/RNFSG*AMWLM FVIQHGKPR*GSLKARSLPAMATQD PHLYEK
12754	26655	A	12883	656	1168	EPSPVNPHEHDARINSGKKKSKDEKAK REDEBTQLD/IVQIV*TVINPOISGTI AIVDEGTYIHALNNGLFTLQAPHK/ER IALKPGYGYLSTNSDELVV/GRSLAIG PREQWEPVQNGEVNRNGPAMGREKRN GTQWREDTHTSFPLFPSTGGQPKAHNN WRKVCH
12755	26656	A	12884	205	452	ASGSAHRFRITFSFETGRVLKPSQTDHT NRIRGGPNVK*SFL/WLGAALHACNPNT LGGRRRTA*ACFRFSLGNTVRPCLY
12756	26657	A	12885	112	290	KYNIQYNTVFSCHDPLVSNLEFFFFF KGKGFPLSPRLKARGRVWGYLNPPLPGK RNFNAPPQGFELKGLPPP*SPPPGGVG QAKNLGGPGQPPAPMGKTPFF*KNQNN PNNGGQPLAFKTLGGGPKISF/PPGGG GLNNRPSPGPGSTWGGGNPLSQKKKKK KD
12757	26658	A	12886	406	190	TSLLAGQGFRLP/LKPPVLEQSPIMARK \YBQPCPWTDKWNKQMSLITVG*YAA MKRRDVLTCATTCR
12758	26659	A	12887	440	160	RVCVCVCVCVCVGVFVCPALNLSLILYN *VYLIFVFNHGRVSPSYFLNL*FFEH VNHV/HNYVCMQNTKLYLSYLETFR/ CPC*FPPIILLH
12759	26660	A	12888	201	411	HINDVILIRHALGNFLTSTCYIVKTIWL DAVAHTCNPNLTGGQGG/WIT*SQEFKI ILGNIGDPLSTKGNK
12760	26661	A	12889	138	464	SCYMPNSEMKAPPPHNRHS*APSTH KMNRNMVSEQMGLPSTKKAEPPTWAQLK KLTEL/TKKSLNTRGTQTSKNMLFA ATMIVSTGCAGVPSSSKETATIEDKP
12761	26662	A	12890	146	366	FSVSMKYFV*TH*FYHL/KLLMLNYL*Y

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/155,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						GFLAINTSQNISCSQKIMKLHL*GRGVV AHACNPGTLGG*GEWMA*AQEFNTGLSN TAKPYLDF
12762	26663	A	12891	358	50	EGRQSGVSSFPVGVTVINYINLVAHNNRY LFPHSFGQVTSSEVKVLA\GCSILKASRG EGFFPLPGSGGSKCPLAYGCITPISASS CDLLLWCVFSSYLAY*DTCHMI
12763	26664	A	12892	227	456	KLTLTLKLFKE\IEDRTLSKSYEVSIT *IPSSSSSSSP/ISLINTDAKKINKIP RNRIOQCCKILIFHKFSTGIYS
12764	26665	A	12893	461	89	LYQMLSERPDMKICW*\RCTELQTLHC WQCKIMQLMKLWQFL*/ELNTEVPY DSIPLDWY/PKITEC/YTSTQTLTYCM NPLEYYSALKRDKVLHATTWNLNI/ LSKRRSQKSTYCNIPIL
12765	26666	A	12894	222	185	RIVMQVILHLNAGCVCVCPVCD/CVCL CV*MCVHIHIVISTHTYIHIYVCM*ICR LS*CEFY
12766	26667	A	12895	186	166	IFFFFPEMGSHSVTQARVQWHNHSKOR PPP\GASDPPTSAY*VAKINIFFFF
12767	26668	A	12896	55	485	TCWDCRDEPPRPALESVPLTSLFDEFS IEIADLVPHPTPCSHLPQPP*VIIFYC S\KPLVTGSSSPPRKPPPSLHEPKSASL *PPSSTIQVRRSSPKG*PSPPLA*VQFP KGMTITPLCLSPVLVPSTIPLPNVSKP LPFY
12768	26669	A	12897	923	312	VDVIRKQIEITLRCHLIEVRIAIIKKT RANKCW*GGCEGALVHC*\WC/NYILV QPLMKVWRFLSELKLELPDPAIPLIG ISPKONEII/CTPKFLAOPFTIVKIQT QPRCSMGWKIKKL/W/HIERSTR*LE YYLAFKKKAVLSFAKTWIDLEDIMLNEI SQTKQEKYCVISLTCGLKKKKVKYIEIE NKTVITKVRIRNRK
12769	26670	A	12898	320	3	ESNRWGRIVRPHSPQRTWLCVPVPGPP NAPDGSFPLAICPVPPSCRL/CP/DD CLASAGV*GGFPLPRTASPHHSACPO EQPWPPQCKLVGAPNSTALSEGS
12770	26671	A	12899	138	447	IPVPHYKQNIYNEDTLVITINLMCYP GSYIKSTGRLRPEVERGLPTTMC*FS SIKNIIFY*KLKSYRKL/WLQTVAHAYN PSTLGG*GRWIT*GQKFRD
12771	26672	A	12900	279	1	INQSIHONIKSTYISQCKLIQ*WKIIN RFIR/NKILLYVPATPPVGV*LKELK SAC*RDNCIT/N/FTALFCIGYGSNLG NSTALIGSRVLP
12772	26673	A	12901	235	183	IINYGSGPPPKKKGGKKLPLIFYKKIK KFLMPKKKLPGARDIV*JHIFITV* IDVITRADPTSATILIALITGVKVFS* LATLHGSNMK*SAAVL*ALGFI
12773	26674	A	12902	180	19	LFITYLTYLFCIRKCHPVVQAGLQ\L IIASCSFALIGSSDPPTSAS*VKGI
12774	26675	A	12903	406	949	APVGHGFCVSV/CGENGVSLYCPGS* TPGLKLCSCI\CLPESWDYR/R*APVGV LGFVFLHLL*KPFFFDYMKSLPQLK YILQG*CTLV*GVRYSSFFIFFFFLRR SLA/SVTQAGVQWRDLGSLQSPPGFTF FSRLSLSSWDYRPPPCPNFANFLV



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
12792	26693	A	12921	438	127	FPKOLFPSRGWVGPMIVLL RVVNERIVPRPHIKSMVMVSTLLGSG DALNDLFLYCMKESDPYKERPVRERER ERERERERDRCEWK*APGWRERPVQSLR ACHPPWHRFALAGPVPSAQ
12793	26694	A	12922	158	460	EARVELLLSSRCCKPRAVITARTQPAVYR LQLEIRNFPGLSPRLCSGATTACHSLD LLG*SDPPNSANR\AGTTGCHCAQTUNS CKADWLVLSSSRLTTHR
12794	26695	A	12923	33	484	GQAACIPGLRLSPPADAHCHRHIPSPSP PSSTA PRDDVGMQITPDNFFPDQPLA TPPSQSLPLPRAP* PQSSVDLPGLLFK LQNPQTGPBEVDTCVQIKTSKARE VQNRKTPQAKSGRHRHRIAGLGHAP QSRRLRHTVG
12795	26696	A	12924	335	332	RIKVVYVRGHAKK*LRGP/VARTCNQYK LGGQGNRITQAQEFETSLGDIGRPHLYK KKKKKGPF
12796	26697	A	12925	302	407	AQWLNAITPAPMRAAGLLEPRK*AW VTV
12797	26698	A	12926	766	244	RVPLPPPAL*LEFSFSGRLRLARSHSTQ LRSSPPPVSPST/FPSPHRSPPSLSL LSVPS/PPLHHSFSGRAHILPPLPLI FPSSPPAPPPPPSSSSSSSSSSSSPPPP /PPINMGTPRRFFPPPPFNKPPPEINFG PKKKKIFSPRA*KFVFLGPPPPPPPP FFFFLGINLL
12798	26699	A	12927	127	720	WGLLESTETQLQSLPLGLVSVIFGKIF YISGLGICCTKIFPSALPSAQPAASLPL PARSALGLVFEHFC*IS/CNKKLP HHI*LIKTSYGLT*LEFFFFTKSLIF SPRLNCRGPFLVN*HLCRLG*GNSPA*P FGAGIEGAPHGAGLFGGGG3AFLKKT G\LRHVAPGAGANSGETGNIHPPPLNPPK GAGE
12799	26700	A	12928	308	49	KEHM*AVGHENICVGTGP*GERKKGTER VFKEIITPNFNLQITIKPTQBTQHTP SRNRNKI/TPRYIIKFLKTSNKKLLT TAR
12800	26701	A	12929	375	2	GNLSLKTINTILEVLARLQKKIKRRK LND\BQADTFTTI*FCVRQRTKSTDKL VKLI/ERYFKVATYMINFLKKSNSFHTP ATINC*KQIPFINATKTIKYLINPRKK CVRFVGKLTTPER
12801	26702	A	12930	202	379	SSBNFSGRKTVMCCIGLRHMSNLWLT AHACNPIT\GWIT*GQSFETSLADMVKP CLY
12802	26703	A	12931	209	376	TVGEMYLKVKRI\WLGVAHASNPNTL GQGGMIT*PQSFETSLGNWAKPHLYK
12803	26704	A	12932	280	31	LSCKVFKVLEELKTYNKKTYTVEVS IVOTTEDACACEYTSNVTGPGAVAHCSN PST/RGRNLT*GRELKTSPANLAKPRLY
12804	26705	A	12933	1	189	QMYTESEP*CKWTLGDYVW*W*FIS*/ IQCTIQAGNNWNR/RLCMCSGGEYMRN LCAFLSILL
12805	26706	A	12934	108	409	HHSHLKLKPNVNFSPCHFTVIVPISL*R VFFVFP*IFLSSSHFLSFCECPIMFIM PPFKFLSCNIVFI*NIIFLFL/VHV*G

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						*STLVSLVFVFFFLQF
12806	26707	A	12935	225	11	TLLCMPSFLFWGFCFCVKTGSHYIAQ VEVLWFLSGMIKWHCSL/KLLHSSNPPT SAS*VAGNTGSSYCTW
12807	26708	A	12936	74	12	GTTHASAGVINILVFLLVFFVTHSLCI HISKYMFVYICVCICTRTDFYTEFKSFC TFCFFGSSFFFLKKFPLVAGLEEQGKD LG* LKPPPPRLKKFSLTLG/ANR*RT NG
12808	26709	A	12937	166	311	PHS*WEOQMVRAPALEMQFLTKEIRGL PL\DAALPLIM/CHRRGCTQLFI TALLI VARKCNHNL\ANENINX*YIHTDY PLAKONELLLEATTWNVVL
12809	26710	A	12938	51	296	LQVYTHFLTHWTCCTAYICVYCKYLR Y/LHT*IPEDANSVKKXTHTHIVVHL VYPHTTYLACS YIYSKVCVCVYIYT
12810	26711	A	12939	426	28	KGPNLVNPRVFPSPRP*TPAPVFVFGSP IKKIFFFKAGGVKFDLSLGRPLCFFFLK TGSCFVP\RVECNGLITAHNCLLPRSN DPPPSDLQVGVKPP\AKLFFFFLM*X GMHLLDYQGETCLSQLGWK
12811	26712	A	12940	11	213	ATAPGLFSFFETGFCSDQAGVQ*HDHG SLQP*7P\GSSDPPALASQARITGVSH CKGPEHTSLIT
12812	26713	A	12941	416	38	WINNHRLGFFPNCNDYICKLPRIGPDVA SLLIHNS\GTWYGATLCSNNYFSP IKYDHQK*FAPTWGQYTFVTLPQDYS SAL*HMTVHRDLHLNQNITLVHYSD ITMLDLMSRKYQAL
12813	26714	A	12942	361	74	LTHPSFSVSPNTHENAPALGGYSVY GVALLPFFETNKLAPTHLQGLA/INSE LR*IOEPPLQSGSGFFSCNVFLAPTE TVQKEDPMATG
12814	26715	A	12943	125	401	SSPEFRGIFLNPFAVQKQKSNVLLSPR SQBLESRIKIKVLDTLQDEL*GQAQ* LTPIIPS\IWEKAGGLEPRSLRLRSC HCTPANVTE
12815	26716	A	12944	92	306	KRTTNSPWGCSAY/GVAILLFL*IL/KL LAPTLHLGLPSNFLRKIQSPSLG\SGS GPIDGNKLVAFGGLNIVS
12816	26717	A	12945	322	24	NFKRNTNINPPLRGYPLPLRGSGFLTK KVGEPLKKKKKLNQGSYFLSTYTVK* NN*/WLGAVARTYNPSTLGGRGGNIT*G QEGFTSLANMVKILAK
12817	26718	A	12946	2	448	GGAPMKRHSGLDRNYVDTPRPSQLFLF QLYHNYLKPAYEATKEYMERKETLCIPC PAIQSFPPKSNCTYGYLQMETCAHTQM *MYRYIYTYVMHIYICH/YRAICTYVT FE*KYLLQKCLLCIFLFFLQYLYKYSY LNRHIFLA
12818	26719	A	12947	155	415	LLFTGQRGQCSSHHHLLGKTLIRYGHGS RPTSLMAG*\GPPNLRVAGLGRAPATL GLRYGPDGYGHQGN\BYCTMGASLQRR RVRD
12819	26720	A	12948	247	250	KYVYKIHIYVYKCVYFTHYGYTYLYT DVYKYTYLYTDV*ICICIKYKILYNYI YIHLINMYIYIHLINMYIHIHV*YIYI HIYI\IVYIPIYIPLTYTK*HIYEVG

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12820	26721	A	12949	25	407	EYITTLWKL EALSELLLVWGLLGLTARKMYQQWNL VQYCLLVLP*P*NL*BQRFRFVEGLDHR EP*FHVLCGTHSEKSPFRFW*EL*IRX LTLVA\GOVATYNPNTLGHRRRIT*G QEFETSLGNVVRFLFI
12821	26722	A	12950	370	106	ILYLETLIKSFISIRSPSAVDSDHFKSS TVGKMLPNSITCTDPI\FNKKKSLMWQ SLLLPFSQKLPSQPPVPSQSPSPRQGS I PATR*QLA*GSVQVNLFGSILPTVELF SKWESTAKLLLLINDPSKVSRYKIVV DQFSGKGLTF*VSH*KKKQWV/PQVY AINRFLGGRGWIT*GQGFETSLANAG KPCFY
12822	26723	A	12951	280	319	IOLALSLGICGPRDIATFCS\SDCTQ NFLSVLIMVAKR*KQPKYLOIDEWINON OCIHMSYLVSKGRKYLCKL
12823	26724	A	12952	337	113	DPTVCCLODHTFTYKTNKLVWGWTKY /CHANGNOKRAGVYQIEYP*SKSLSE IVON
12824	26725	A	12953	9	186	NENTYSYKKNQNFIALLPVVTNNKQP TCPS/SGEWINKLL\YHLMVYYSVAKTN /ILVYVATSVNLRILILGQDPKRVILT V*PHLYRKYKLSSDRKQIHGRLEVENK GK
12825	26726	A	12954	46	381	CSDMVLACIKKLMSYSNGHIOAMDYY TAL/NKEL/LMYATI*ANLEIDMLSKIR OTQKDNCLMVDCIYIRYAEQSSL
12826	26727	A	12955	19	250	GARHSASGTGWRKDFTRFGAVAHACNP STLAC*GWISRSFETSITNWVL/CL YKSIOCTKCLACFPNLSAID
12827	26728	A	12956	173	163	EKDNLFLTFRGNVLAIKSSBNHRIIT ELKVTLRFDVAHITCNPTLGGRSQ/WI A*GQFELISLAKKVKPCLY
12828	26729	A	12957	301	79	KHHHPKKHNFVLCVQVCVVCYVGHF YLFLSLFSQ*P/CICCP*CVCCSFLLOCF *SATYLKII
12829	26730	A	12958	314	126	VPFMGRHSNFFPSFRLKRYLALLPLRLG VQWQ*SAHACNLR*PG\SSNSEASASRV AGITGACHHGWLFPVLPVETWPHVQ\G AGIKTP*QV\SACFSLPKCCDRCEPL CPATSSILNL*TMDRL/POBPKNQ*PLL VSMCAVYFREGQGVYFQRLNCKREF IVRSPWAINLEKGLRMGAV*IRIMLNL TLT*GCTEDEKTVSNRVNQLTPT*LG DE*DVKREKNINDEIKLITCNSEYTKSY RLGH*IKLGAFCFPM\VMWQCGNNGQL KVQV*GVVAINCHESLGG*DRITRY QEFETMLDSSSSSLQIKLILAGGAR L*SLSL*VSMVRCSPFWP\SNFCLPK RDGVSPYNPKA/NS*TPDLQSAIFSLP KVLG
12830	26731	A	12959	529	1697	GTRFRILSEKFKKEIDFFFFFKQSSP PPGKQKQTL/C*QKTFPTKQKTNLGPX KPGGQPKKPKISHPQIGPFKKKTYNP* QQFVMNPFEGKKEGTPPFKFKDPGANLK VMGLKGGVKKRGGKTFPQRA
12831	26732	A	12960	1	395	LWRLTSPKSAGWAGNLTOESMQLPKS
12832	26733	A	12961	90	436	

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						BCHR / PAESPLA*SVLLFS LSTDWMPFI LI / MEGDILLYSKPIHFNVKISSONTYRN IWNVWPHV*TL*PSQSD / CLK*TIPTI VLLTCTH
12833	26734	A	12962	415	463	LRARDQVLPRKILVLC*TLFFPCAQIKKKK K / WPGAVAHAYNPSTLEGGGWNIT*GQE FKTS LGNMVXPSGL PPHMI
12834	26735	A	12963	774	316	SISPTCSGKIGGGLNHRHPSKEDKTG / RY MNKCFISLVISSECYLKP*EDTH*TP / LR MAKIKRADH / DKC*QRYKGTGTLIQC*H ERNVMVQPLWKTIV*QFLKRLNIHLPEDSI PLLG / IY*RRKACVINTIIMPLIASL LVKAK / AKKQPKCPST
12835	26736	A	12964	44	395	MYFTLVNKSLEKFLGSRQLPQQQPFL HFLKAL**FPFPQTQNGNGVTPPAKTTP PFPPTLSSSSPCPSPAEGGSRPPLSTP / SCLHLVIGGAASNPSPPLPPPPQCSG LGYPVC
12836	26737	A	12965	424	50	MAFPFLLCAPDAINNNKKCOREINNEE PPNEFLKNNHIMIFFFEARSHS FAR / LE CSDALSAHCKLCLPGSRHSPASAYRCPP RHLANFSAFLVQTGPVRVSDGQKDLQTS *SALLMPPLDPAIP
12837	26738	A	12966	245	44	QSKELGNYPLEPSPSPSPSPAPHGLPPP SSPSPAPZHGLPLLP / SNTVQPQ*RLTAT SLWDP PASPRPG
12838	26739	A	12967	205	30	QBGASISRIKRGPGVGAMLGMAHACNP STLGGQG / SWIT*QGEFTSLGNPHLYQ KXRN
12839	26740	A	12968	114	465	DVSNSPETHKREPPKKTES*E / EPKSL LMLPS / P*NSS*CANREQQPSPQPHLP HPLPTSLQVHRLP**SLPPNLFETLYD / SPEPSLLFVIQFPA*TSPP*PPVYSSP PSPCTCLH
12840	26741	A	12969	1618	1038	VHMVDKIDINLNNFSLSGTMMLPFKETS HR*DRGDPGF*SCLYSAPIPTQLPFL*Y LPQNFIEG*PS*NSRIKGTSLKTYISRV PSFFPSFL*DVGS / TVPQAGVQWHDGSL LQPPPPGPKRPSCLISLSSVDYRHPLC PANFLDF**RRGPTMLARLVNSIS*PCDL PASASQLAGITRMSHTLPHVFFLVN
12841	26742	A	12970	197	411	EQALESTVCYCLNPLPAPLRPRQDC / G PCRFRNMPGGRTRWLPVITL*FAEAQ VWLEARSLEQAWATW
12842	26743	A	12971	616	777	NGHGVRRHQAQINFFVFFEDGGEWQLTC TGAGDSSSVVIGEP*VFAC / PDSVLFYLH P / LRG*TIYOLKTP*NYGHW / FV / F RFLPPTSLSLQGLCSSTITHTCCLL VGSINSSISAS*LDGNT / GVRHQAQINP VFPEVDGGEWQLTCTGAGDSSSVVIGLSP RYKXKRLIKNYL
12843	26744	A	12972	222	389	VITKALGSDLELGRQLNN*IKIHQVQW ILPVIPIAL / LEAKAGGLEAKTSRPAAE T
12844	26745	A	12973	425	145	QIIFFLFQKIQNPINKASFFKKNLTQW TSQRKNSAQISVPKKNKSWITDINVT *TIQLTKN / NIGKNLQDGLGKEILNL TLKQSTKG



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12845	26746	A	12974	322	411	NNKKI PMSTK* KFFYCFIVQLIFETILS VRVLESLILINVI* YCIICIFPPL* L* T * EIRKVKFTSPFQIEK* KRRR/ WLGT VAHTYNPSTLGG* GGRILA* AHEFETSIG NTGRLPSVQKIL
12846	26747	A	12975	428	1	SRKSSSQFRLSFFPSHFLDLGAKGAVSQ DRAIALQPPCIPRSR* S* RPPSRPCFRR PRPSRSRKNKERAGEKKRPRSLQPRPP HLAGP/ VPRRQGPSAGFEAFATDEPP PQRSGLRGGSANIRSKQTSLSLRPRVRG RVG
12847	26748	A	12976	60	294	NHCTETVLEQ* LKCVQVCVCVCVCVCVT ERI/ CFFKFLIGKGYGCIYLPKTKF/ L IPIYI LYPGRBSLKKKFFFLT
12848	26749	A	12977	6	341	DSLTLPLGLTCSGALSAHCSLCSG/ FK QFSCFSLPSSWGFTG/ VPPRMPQLIFPY FSVKIGH* RVG* AGLKLLIPASASP CWDYREPPFRPGDLWNF* FTGFKLRFPQ FPL
12849	26750	A	12978	296	42	SQPASLGKFSVDLPLLAVCPIKGIK/ TL WDFSFIIYIKQ* WPRAGIFMPY/ NPST LGGROGRIS* AQEFKTSGLNIVKPHYL V K
12850	26751	A	12979	20	373	KLYGGINGWFFFFRGKLSATQAEMQGH LG* LKSPPPG* RNPFPASASGEPITGS HHKPGIVFYIHKKPLKTFITLGRPTPP SFRHMQPAPMGVYSILGEKSLTNQWD PQTKKG
12851	26752	A	12980	380	96	FVFPFPPWRAQKGSIGREIRPPRGNQK POPP* KKKKNYPQGGGPPSPFPPEG* PKKGNPFGGTPP* TEPFPPWSTRGK KPPSKKKKKK
12852	26753	A	12981	331	71	ELLIVSWVMCTPVVPATW* GRELVGRI T\KSRRLRLQ* AKIVPLHSLGDRVRPC PPPTTKKLANLCPWTEGSLSFVYLEQ FHSC
12853	26754	A	12982	383	189	RRLKSCMSMTPAQPNKJLSQAQMLTP VIPTL* EARGGSLELRSPRL* AMIEP / CTANVTE
12854	26755	A	12983	144	6	ILAQ* KTWLSVVAHTL* S/ TLGGQDRI TGAQF KTSIGNTRRCLYK
12855	26756	A	12984	341	509	ETLYTNR* YTAIEKNRIMSAGTWLELE A\ VIL\ SNLV* EQRTKMLPCSLPMGMEL K
12856	26757	A	12985	387	125	DLFPPTPKLPRPTCSVAQVEVWCL/ GSL QPPQPPG\ SDPPA* AS* LAGTGTGRHHA * EWFPP* VIFVQTSEHILGINFPGRHTK VAHGV
12857	26758	A	12986	151	350	GRGGF* FLF* LFPFGQRPPTTPPKAPP PLGFFFP/ RFFPFLRSLALSFRKWRD LGQLQPPPPPTTGY
12858	26759	A	12987	251	1	RMSLLEKRESIN* EARV/ CGRVIVVATE VIKIMIGISMVAHAYNPSTLGGQGRRIA SAQEFETSLGNMTNPLCYKKTTHKSR
12859	26760	A	12988	320	3	TPAGVKDFSPPPPPGGVFFGRATPPR* KFFGNFWKKGFPPNVRGVLFKFWG/ KNF FPPNLPKSLGLRFPKPPGP* KADPPFPL FFFFFEMEFLRLCCGWSRVQAS

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12860	26761	A	12989	353	183	EVGTHILTAIAIFISIAKRNHNR*GSLTDE WVRKNSSLSQSMETYSALKKNVLLHAA P
12861	26762	A	12990	377	2	LSITILINPPRPSLQRGKYGPPPPKKNF PQKTPPRAPKKKKPFFFFFSPFKNF PFFFGKQSGGGFGPP*PLIFRFK\NPP PPPPKIGFKANVFSTPPPPINGFFFFF FTRWSLALLPRLEC
12862	26763	A	12991	134	298	PPNSYCDGSIITLIKSDRNITREKMY/ P/IYIANTIDAKVPNKVLPNRIQQ*IKRI I
12863	26764	A	12992	892	171	QT*SH/SLSRLEYSDTITAKCSLKLMS SDPPASASQVAKPTGCHCTTQPHITSGF GLKWPVGLLLEKCHFAVFPPLTGLS KIPISILFFKLL/LNPKTVAHTCNST LGGGGWTT*QGEFGLKCHNPSKPHHG QHGT
12865	26766	A	12994	324	4	SLYPLLFAQSIYFLVITRSMESCTYF FVVVPLDSLVQIHVKI/HKIGIML*V N*QNCFKINISE*L*YINPSTVADTLCG QGEITRAQGFKTSNMKPHLY
12866	26767	A	12995	106	531	WLLNLFAPLNDKGFVLPNRSRIFSQOK VKRSPFGCSFSDNDVGSCTVQAGEQML FTGVIGTL*PGTGP\SSDPASASQAAG TTGS*EHITQNLNLLYSST*QTI*L*TT DSHILIFASLYAKEQLITFYVQATSLQP CT
12867	26768	A	12996	1	367	NTEPFLNIPFKDKVS/CSTIAQAQGNRL YSRCSLKLGGSSNSPTSASLVAGSKGRH HTRL*LFYFVSRRQDYLWPSVVFSSP FLSFFFWKGFPLPPSWARAPINWGS LPBRVKPIFLA
12868	26769	A	12997	3	379	YRPSSTKAVLVVFFSFFFLGTGG KGPPKAGPNPTITWRGKNPFI*KKKKP /RLI*KKGPPIKMGFKRRRFWLKPCKP QFGKREG/SPNYPHRQDPKAPSLANK PQFGGGGGGAPKAS
12869	26770	A	12998	230	409	SCRPKELLALFLSSTISQRWEQPIIT/ PSTDE*INRMHIHTMETYSALKRKTVL IHATT
12870	26771	A	12999	310	343	DPVCTII*ITCDIINL*TECSKVN*SLKF YKILILPHVNCVWPSVGNCHKMLCDCVV* KQN/LNPGMVAITCNSTVRGGGRIV* QGEFETSLGNIVRPSLYNKSICI
12871	26772	A	13000	390	289	IKLCQPRGVKLDSPKAPPPFFFTFES CFVS*AGVQWCH/LGSLQFQTSGPNPNA TSA*LSLIFMCSNSYVCIVK
12872	26773	A	13001	1	289	GLIRQISVNYLPGVRSIAQAGVQRCDIG SI*PLPPKVKQPSVAGVTIRGCHAWLIF FISRSB*GHPVKGASSDSTPGFSGAG ITRLSPhALACT
12873	26774	A	13002	359	105	KQKKNPSPPGGGGGGGKPS/PKPPFPN SRD*PPKNSQSPFFLKKKFTNFT*KKK NP*KPNPPLKGGKPKGFPSPPPPLKPK PNV
12874	26775	A	13003	243	293	MNSOFLKRLIRIESPYGVSISLGTYST EK*KACPCKTCTQMFTSALYIAKKN\N KCPSTVRN/IKLWHINTNEFFCQ*KKFII

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12875	26776	A	13004	465	307	CIDMPQFVHLTVRGLHSLPLFCYYI SRACPIILKLFMFG*CLLFVC/SILLVF YFVFCFVILFCFAAYMOFFNQCLFG
12876	26777	A	13005	207	3	DGSLTMI,PKLEC/RWLEFGVIMACHLE /RLGSNDPPASASRVAGTTGVCHHA*LI FIFVFKMRSHYTPRP
12877	26778	A	13006	2	56	DLALLFRL*CNMGITAHCNLK/RPG*LL GSRDPPTMVS*STGITGMSHEAHRPSPS CDF*RSCSVQAVQWMDYSSL
12878	26779	A	13007	402	74	FQASLKRHGLFFFLSKPLVYNKKIPRPL VFLKKA*PPPGRATPFYICCFPHKGGP GRVKKKG*PKG/SPPPKQSGSTPPFL GAFKKPKVTTPF/KKNDPKTLKGPPFF
12879	26780	A	13008	356	145	RPPFFFFFEFTVSHFVAHAGVQWHDHS LQI*TP*SSREPPASAS*VAGTTGVHYL PGSQLPILEHSPPR
12880	26781	A	13009	227	353	GMSLT*/SN*AQLHTPVILAL*EABAG GSSEPSRLSAWATW
12881	26782	A	13010	249	32	NPDSHSAWAKASVVFQIARVGGGLE SRSLRLR*AMIV\CTPANVAQERLSLK KPPTIETLFPSPQPSQ
12882	26783	A	13011	247	403	TPGGGGKYFFFGPKIKNGGGFKNGGG GKTRGP*KKQASSSPFAPPFFFGAGP FSPPPRF/KPPPVFPLGP/KKKLFFPP PGGLFFFLGGPPSPFFFLGGGL FFPGLGAMGPMAGFSLAPGNLSKKK KSEGLGEGNSVLRVLISSQLPGRN R
12883	26784	A	13012	206	386	TREAQTFNFPPLYS*KAL/NLGTVAHT*N PSTLGGQRRITSSQSESTSLANMVKPH LLEI
12884	26785	A	13013	354	31	YKQNTNDIHH*HT/YIPVVPKGRKR KYLEVL/QDDMTKNFLNLMGNNIYFQ EVQQTPSRINSQTSTPHIIILKSKYKT GREQWILSVMLNWEAVVGPPEVRS
12885	26786	A	13014	1	419	EETSEFKARCLGYPFGFPRRLRSRPL LG*MLSLHPQGSQPPAGSMSSSPATT STCSCSPPAAGCTRGRTGRPFNTASGP AELDNAGSSV/EALTSGLPARGLWQQY AGLVDPRLGLGPMTSCCSLPPFPSPARF
12886	26787	A	13015	109	426	TSIGNIARPH*QTHMATRSVPPFSKND ST*LRLLPPPPHMC/PD*SLKSN*Y*H YLVNP\IWPMLTLVLCLVCFRDRVSL CCPGWSAVVPSRLTAASLWVQVILPP\ RLAN*IFFLRWGLMLPLRV*NSNAGDI LPP*PPKVLGLQA
12887	26788	A	13016	149	422	LKRIFFLKVPFHTIDAPGDNDNCPISC FNGILKGLFFFKKHL/NLGBGAIPC NPTLLGGQGRIT*FQEFETTPANAKP LLYKKYK
12888	26789	A	13018	162	377	QSGFYFERVSKLPTIQGMMHMQSFV CTSL*HV*TGWAQNLTPVIPA*2D/AL AGGLEVENLRPAWST
12889	26790	A	13019	205	427	IQTGGPPARFPLNFWAGKK*RVPPBGG PPKKKKKTPPPHGGGERGGS/PFSKKKK KKTPKKRAGVFFDGGPRKGGDGNPPR LDSKPVGAPPRPGRLNGGPKIFFDGP FFPLQPKGRP*PGGEGSFFFLGVDP

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,151,26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
12890	26791	A	13020	248	358	LGEPSTFCLLDPENA SRGGEAQWLLPV/I/PAF*EAEAGGSF EPKSLRPAWAT
12891	26792	A	13021	2	434	ITRAGSDTQEHEITLYTHLCVYNRFETK KAQVKKKVVWHM*PQLLRLEMGSSLEP RSLRLQGAWTLPTVSTTQAWAT
12892	26793	A	13022	162	410	LTQRTAASQITLSPSSTSLKIPISSES GGGGSVSVTQAAQWRVHSLQP*TPGD KRSSHGLGPHIPSSNDVRSKDNVMPV
12893	26794	A	13023	250	40	LKLNIFSCSLATWSSCHTSLFKYFAH FSFF*IDFYSSYLLDNPFFRN/GITN ILSSSVTCSFYLLVV
12894	26795	A	13025	264	1	VSTKHGRLLEPEY*CFIHH*BEKVPE SIFEY/PCQTFPLRKSTVRGAAYACNP STLGGQRWII*EQSFETSLTCAALRL VTLR
12895	26796	A	13026	110	523	CTDSSSWTQDRCKEDRLCPGTGTCAAP GLLFLSAPPLGPT*PSQHPSPFHVSLSG PSPGRLRPOLDPLKHPSTSLAPRLPGPA S/LPRLPEHPHLSPTSGACTPLPFCIGE QRHNPPLPTSLLLNLGLDGHCLATPSVS
12896	26797	A	13027	52	53	CPITLLQLTLC/LPFPQASAMVDAP*ARP LPFSSILACCTSGEQGSVVGLAEPVXG YNLLVCRLLRPLEKQGIWAVSRFSLYS LSNPLARKG/NPLTACASWR
12897	26798	A	13028	262	381	HPGRRLQVRLSPGVRLSLCNKVKP*QI IYTP*PSVSLSVINTYLGKPSVVAHTYN PSTSGG*GKWLIA*AEPE/STLCNKVKP CLY
12898	26799	A	13030	1	846	FRPTQAGRAPWALTLPNGFTGSGPALL SHSSRCDIQMGCNTHAVDDSTGEGPHK GRMRSCWLTFRGLTKYGGQPMEG RERRSRRRQMPGRGHSTMASWSLQOC MRLKLQWASDLLSQLEMQIPSLPPQESG SLGLTGPRSLH/CBQITGLSPTPGESWS EELG/GGIVGGGRGTVAGRGHREAGNK PSGIWGRQCCASGDKAMS*I*LTSLY/AR RGEPPGRPVRIKWLRESSQNRIGGEGGR WE*GQRRSRREGRECPVNGGRKKPLRNG LMWS
12899	26800	A	13032	308	1	KYHDFWCWITLALSDAQSLDHTCV/CV CVCVCVCVCVLRDQGSHECL*CEG*LVP HPVPGPVLCLLSPVIYVCFICSLTKVKE SLSNFFKKLNKALLRECI
12900	26801	A	13033	763	244	FLGPRIITGLRHEISVETQDEKSAVRGN THDNYENVEAGPPKAGKTDKELYNTG QSNFERHIYGNRTSSDYINPQKPRPSEV PQDEDIYILPDSY*L/CQNDICYMMIN IHKMSTAKRNQTKC*STVDNIRKRWY TTTTETVAANK/DTKLIWSQKIYHIF SLKSGS
12901	26802	A	13034	326	58	EHYKCNVQKIFQKL/IHL*SKKHVAYE DKYYKYKGVVPLLVQIHLIYTFYTGK P*SSCSNVPQNIYIYGKSCCKNKPKN TFKKKP
12902	26803	A	13035	199	3	RFIYNHVKCITTFPLPHYF*KLVL/NLG TVAHANNTSLGG*GGRT*GQELSTGL DNITARPHLTV

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
12903	26804	A	13036	94	448	GS CATSMAFKDTRKTAVEFGVVGILRI KPLEKVCADLITGGKPFQNL/KVKGPFVCM PTKTLKITTRKTPCGESSKA\WDGPFQMR IQK*LITNLHSPSKIVKQIISISGA*PGID SEVNTNADG
12904	26805	A	13038	964	1717	HKLSGVKDLKDFMRQAGE\VFFA\DAHR PK\LANEGVVEFASYGDLKNAIEKLSGK\ EINGKNINLIKSGK\RPSPRSRSRSDPG TQSPPLGSPRSRSPSPVVRK*PQVQEAR SRSPQARSQVVFVK*CPGPCEKPCPK \KQSIQSKITLSPSILWIRPEVSGPRSK VPRSVDSGN
12905	26806	A	13039	2	725	SLLPSVPLPLFLFLPLFLAYLLQNLKPLQF SPDLKSKHLLIFPCNA*POYKLDERSK* PENGTLNFSILQDLNNSCRKIGKMSVVP EVQAFF\SHQSLPSLCAQNS/CPNLPSP FPP\PVPSVPTPSVTEF*SSISTDPSD LSLPPQALLIARPS*VPILPQPLIKPI ILLSPPILLTPRPAYSFIP*L/CPPPPQAQ OPTLKKVAGANGIVKNAPFSLQIR*H LGSPPSNTIKIPSSWLVQQ?
12906	26807	A	13040	1131	2	DGVSLSPRLSCSGTTSIHCNLEHLLCLIN DSPASAS*VAGITGPATITPPLIFVYFFF LVETGPHFHVGSGLRLPTD\SDRPPASD SQSVRTITGVSH\AYLACSG/CTRC*FP IT*EGCVMMNINSK*ITLISLYLRNM NKDPI/VIIRLLVNMPSGQSHAW*KK TNKQT*ILELVLSVTSQCVSVRNLSP *VFPSTK*EGWRCVNPSTLT*FIPQVA *TCQRHGLMKIQT*NPGLDPSIVSDHOT Q*BPSVKVQLDISHDKLPMSEELYHCR HTLASGKQISGVPTIFLHIFHGPFYFIY /CIFEMESCSV/SQAG/VQWRDLSSLQA RS/PGSR/RFSCLSLPVOHPPPGPANF \CIPSGDGVSPC*PGMSQSDLVIR
12907	26808	A	13041	97	626	ICPTQVKVLNESQVQCMPPVATNENG AGGVLEPGS*EL*/CPVNSHCPANAT
12908	26809	A	13042	2	431	HDPTDSQIKVKTIMGSEFCWGUAN\LT PVI PALWEAR/AGGSPVRS
12909	26810	A	13043	405	1319	RYRKKIQNKPLMLH/CLILLFNSATR*T LQK*SF*ISPLESSA**KEPPFLSVLSV TSVKT/SAIPMPHWNVRNQVPVQLIP LBNQTHINEVAMLRFPKMDRNLKRIQ RTONLDLWPFCKKQALKKKGGTQIN EQMLFHKTSRKFVRAICHHNFWRINGI HGAVFGKGTYYFARDAAYSSRFCKDDIKH GNTPQIHGVSLQORHLFRITYKSMFLARV LIGDYINGDSKYMPPSKDGSVYNLYDS CVDDTWNPKIFVVFDPANQIYPEYLDPH *PHFQISVVKKALFIFAGRFALQSSH
12910	26811	A	13044	23	450	RSRAAAILQGLRLPLPGPDSPRLTGRQL KPGTGRGSRKRGKPCSI*FRFRRET*PQR EGGRALGATSRQAPPCPPRQWELDAS AKAAAVAPPKVGFKAVSRDPRAEALGG KOSP\GGKSLKGVHR*GGLGPL*GAP EAT
12911	26812	A	13045	172	16	AHVSPEVDKTKFW/LGPVAHICNSSTIG GRGGQIT/R/GQFETNLINMKEPHLY

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US951,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Y Tyrosine, X=Unknown, * = Stop codon, / = possible nucleotide deletion, = possible nucleotide insertion)
12912	26813	A	13046	181	9	YKGGPAMLPRKLCRAITGSSMAHCRLLD LPGSSDPSSASQVAGTGTGCHLQARGG NV
12913	26814	A	13048	2	3507	YVRVSLPPPPPAAGRFGAAVADAREEE FEAAPPPPPPPPLRAAARPPGQPRPP AAGEAQAADNMHQOQQOQKAGEQQLS EPEDMMEAGDTPDPRITQKPVINGIV ALSDGHNTAEEDMEDTSHRSSEATFQFT VERFSRLSESVLSPPCFVRNLPMKIMVM PRFTYDPRHQK(SVGFLLQ)CNASDSGT SWCHQAVLLIINFRDENSFSRRISH LFFHKENDWGPSNFMWBSVTDDEKGT DDDKVTEFVVFQADAPGVANDSKITGT VYGLQNGQATCYNSSLQTLFTFNLAK AVYMMPTBSDDSSKSVPLALORVFELO HSDKPVGTKKLTKSGWETLDSFMQHDV QELCKVLLDNVENKMGKTCVEGTIPKLF RGMVSVYQCKEVDYSDRRERYDYIQL SIRGKNNIFPSFVDYVAVESQLDSNKKYD AGEHGLQEAEGVKFLLPLPVILQLMLR FMXDPTQDQNLKINDRFEFPEQLPLDE LQKTDPKDPANYILHVALVHSGDNHGGH YVYVLYNPKGDGKCKCFDDVVSRCTEE AIEHNYGGHDDDLVSRCTNAYMLVYIR ESKLSVYLQAVTHHDPQQLVRELGEEK RIEAKRKRERGAHLYMQOIVAEQQFC GHQGNMWDERKVKTKYKVLKNSSLAE FVQSLSTMGFPDQDQIRLWPMQARSNGT KRPAMLDNEADGNKTMIELSDNENFTI FLETVDPELAJSGATLPKFDKHDVMLF LRMYDPKTRSLNYCGHIYTPISCKIRDL LPVMCDRAGFIQDTSLLYEVSVKPNLTE RIQDYDVLSDKALDELMDGDLIVFQKDD PENDINGELPTAKYFRDLYHRVDVIFCD KTI FNDPGFVVTLSNRNNTYQVAKTVAQ RLNTDPMLLQFFKSGQYRDGPGNPLREN YRGTLRLDLQFFKPRQPKKLYYQQLJKK ITDFENRRSEFKCWLNSQFREBBITLYP DRHGCVRDLLECKKAVELGEKASGKLR LELTVSYKLGVBHQDELLCELSPATSR TFRLRSIPLQYVDLDEKSNMLTVVAHIF KRVGTGTGIPPLRLRHQCRNFRVWKRRI QSLDLQKEFEKPKFAIVNNGRHQYIN EDEYEVNLDKFEQPGNMSHPRPPLGLD HFNKAPKRSRYTYLSEKAIKIH
12914	26815	A	13049	30	477	VRAKHCAVWERNFRFTVNTSVKFLDTS PEIASLSWGMQKVKGSNTTYKDCCKVAPG GSRTWDWRETGTHSGVQPAACDVKE VVEKGVTQLVIGRGMSEALKVPSSSTVEY LKKHGIDMRVLQTEQAVKEYNALVAQGV RVGGVFHSTC
12915	26816	A	13050	179	389	NIETIOSMFPI/DNEKMLEINLKKAIRG IHKYASQVLMFMPFPTLWEAKVGEPLF PRSRSVNWTWRDPI
12916	26817	A	13052	466	1489	PGKGBMTRSPSPFLAIVPRPORASRPLL CAVSPMASAGATAKHQILVLDPPIDL KFKGPFIDVTTINILKRNPSDRKVCFKV KTVFPRICVRNPSGIIIDGSGTVTVGVH

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						LQPFYDFNSKSKHKEFW/QIFAPLNTS DMBAVINEAKPHELMDSKNR/CPNENDK LNDMEPSKAVPLINASIQDGFPTQPHSAS LHDITETRLTECKRLQSGEMKLSSENQ HLRDEGLLEKLVAYSDKPGSTSTASPD VTSLPSSLLVIAIETPGLFFFWRRSL TLVAQAGVQRDLQSLQPFSPGFKQFSH LSLPSNDYRRPPHAPPCIFPSREGVS PCMPGMS
12917	26818	A	13053	892	189	SYDFGALGCRFAFSGRKGSGATRMH PMSRERAKFVKSGL/YCKITRELMHAR CCLNQKGTILGLDLQNCLEDPGNFHQ AHTTVIIDLQANFLKGLANTPRGFTQL QTLTLQPHVNCPPGINANTITSYIDNQ ICQGKNLCNITGDPENCPENGSCVPDG PGLLQCVCADGFH/GIQVYAPGLVLTAY VLRDSGSHSIRLSALGDPAKPKSQDFM NYIGLITDLRSI
12918	26819	A	13054	423	12	SPNQKIFLQKCSLRPTFASQSALTWP GQSTRFWEQALFWALMDPQSKRAS/MQL EPFHARTWTHARTCGHTGA/PCSARTEV YVHLHSPFAHARTHARTSPVETCCRL HARTH/YCTPSPFOLSLLAVARQPS
12919	26820	A	13055	16	349	RSSKQIDFWTQSPRAXNSHTRCPHPRV AAAPMFKRKTEGDAGDKCAKVKDESQK S/ARMSKSAASKAYAKPIKADAMNGEN VPNGIQRLKAFYDLQACRHLTLIDFA
12920	26821	C	13056	716	594	MMQTTGTGVMPPQARQCLEFPAGTGRKD SPLYFSEQSWPL*
12921	26822	A	13057	353	2	IGNFGKTTFNKPPFPKFFLSKFFMFLF FLVKTRSCYVAQAGLQTPG/SSDSPASA NQSAGITGVSHHTQSEILKYTVFCLTFQ TPYTTIPSTWSIPCCSHPSCYLCFLPAC FLRQSF
12922	26823	A	13058	864	529	EVSSTKTAGRCGALVISMLCIIFFQGL FTRALLRTECSALLHADPEISFVVVVVF FKTESCSVAQDGVQWCDLRLSKFPPT/G SSDSPASASPVAKITGWHHARHGLKS
12923	26824	A	13059	2714	1376	GRYDGLVEQLGGEATPAVGFANGLERLV LLVQAVNPEFKAADPVVILVLSADTQ SAPMALASRLDELPOVLMDNHGGNFF KKQFARADKQGARVAVLGESEVANGTA VVKDLRSALAVGVILGWGALIGRWYNS HQVDSARASALAYQNAVAVSBDKPDSEI PAASKFAENKNTYGALASLELAQQFVD KNELEKAAQQLQGLADTSDENLKAVIN LRLARVQVQLQADAALKTLD/TPYKGE GWAALVADLRGELALSKGDKGLISVTL LSGCSLFNSSEEDVVKMSPLPTVSNQFTF TTAWSTSDSGSIGNTFYNLHFPALADNVV YAADRAGLVKALNADDGKEIWSVSLTEK DGWFSKEPALLSCRTSVSNPNQTEKEN KQRTGEPVAEPEQAGVRRHLYLPFAG YRRRAACQARPAKACATEGSEHGN
12924	26825	A	13060	99	254	RHHHLVAFKLSALGVKVRVDKAFMLMPV IPAF/LEAKVGRSLSPKSSRAKAT
12925	26826	A	13062	127	386	FSYIYFFFLFFFLCVFTDGEPLMKML GKPKTIMKKKGGSESYSELPETDQNE

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12926	26827	A	13063	1	209	WL/TPVITPLWEAEVGSSEHRSR GRYITLLRVPCFLRQQLCHLACSLEL PGSSDSRASASQVAG/ISITGVHHHARL NEVFCFFFLVCFCE
12927	26828	A	13064	132	1	SHAMCCNYLKRFGHARGLMFW/ITALWE ABAGRSPEVRSRSAL
12928	26829	A	13065	269	134	TLWSVFASS/NAWMLTPVILAPWEAKAG GSFEVRSRLRICKQKVL
12929	26830	A	13066	853	461	RLWRSVSQPLCACVHMCVSVVCGLAH AGTYAVSTCVH/MCVCMCARITLAKI CSETGNLIFKAKIISLLDLFLNFSIKY KQVLKLSRLAWKRIKILTLRPFSD VNTFERINYLINDISIR
12930	26831	A	13067	57	2066	AQPTGRGTSTVAFTFATARSKGGVWFLP PCPHAPPTLLSTSRVITPASPAASMKAL RLSASALPCLLLINGLGAAPFORPEAQF PFLSSHEKPEVAGDAVGFKDGSAFEVR GARNSSEFQDEGLFQGVDPALAJAVLLQ ALDRPASPPAPSGSQQPEEEAAEALIT ETVRSQTHSLPANGEP/EPAPFPRQTP ENGPRASDPSEELALASLLQELRDFSP SSAKRQQTAAAEETETHTLTLEVNLES PGFERVNRASWGEFQARVERAELEPPA PSQFQARNEDSGLEFETHKFGQGVSSPK THLGEALAPLSKATQGVAAFPKARRE SALLGSGEAGERLLQQLAQVEAGRRQA EATQAAQGERLAIASILLQYLQGLQ GARQRLQGRQLQAAEEREAREEHEA EQERNGGERVGEEDHEAAEAAEADE AERARQNALPASEEDGEAGEDKRSGE ETPKHRRKRAKGTBEGGEREDDEMDPQ TIDSLIELSTKLHLPADDVVSIIEVEE KRNKRRKQAPPEVPVPRAAPAPTHVRSF QPFPEAPAPADELEIXNEVLPFDURE DEVYFPGYHPPFNYIRPTLQPPSALR RRHYTHALPFSRHYGREAQARHAQBE AAAEERLQCELENYIEHVLRRP
12931	26832	A	13068	282	53	PGFPQKGFRRKKILPDYVPQGAENSK ARPPQGVPGTIPA/LMRVKGGPLRSGG PGPPGAKGTFPLPINTKKS
12932	26833	A	13069	177	2	VSLCRPGWECSSGVISAIGNLPLFGSSN S/PALASRVAGITGARHIALLSLFPKVL SRA
12933	26834	A	13070	789	302	PHPEFYYSQVFTYPPISPHPTHTHTVH YPTSSHTISCHLASSSSSSSSSSSS SSPAPFYSPHPIISFILAIHYHPYIS THLPHLSSPHSISPRDRLLYCPQNSV PPIHAPFYSPHI/VHMSRHTPLRQTS IAQAGIQWRDLCSLOPEVSSRSA
12934	26835	A	13071	193	2	PPYLKSHSVDLSFGVDDPQEURTPS /LTN/TKVSVKWCPTVIPARVEVVR ESLEPRCSTRA
12935	26836	A	13072	122	1495	LLSDFFPFETE/SRSIAQACMWCYLLSS LQSLPQGFGRFPCSLSPSSNDRCPPEC LANVCIFSRDRVLPCWFGWSKTPDLR
12936	26837	A	13073	178	347	CCLCNDSVLCMYLLVCMHACHALY IKTNK/MQIGAVSHACNPSTLGGQGEWI T



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12937	26838	A	13074	165	34	FILSPFFFTVSYFVAQAGVQM/LIIAHCSLDLPRSSDSPTSAP
12938	26839	A	13075	205	105	GGWQVQFMSTIP/ATWEAKAGGLLEPRN SREVWAT
12939	26840	A	13076	3	357	HERETQAERKRFIAFFFFKMGSCSVIQ ARVQRHDLSSLOPP/RVAGTTGTHYHTW LIPVFSRTDSRLPSSPSRPLTSVISLII PLSLIPTTYLTTPSRSPSTSPPSHPSPR APLTSDP
12940	26841	A	13077	3	477	STPALCAKLSGGSRASVAARVHLESEBQ FLATLRLPQKRTSGSYVITLKKYDGR TKIPKKGTVEGFEPADNKKLLRATDGR KKLSTVVSSEKVNKQMYNSNLRANMD GLKKRDKKNTKKTKAGSNSS/ATTAAP AATAATAATAATAATAAQ
12941	26842	A	13078	1077	1566	RQVTSLDPLKTPFTSLFTSPPTGQLDS GATAPTVVMWSPGAPTPRGRESAAHQN/ YPVGQRS\RMAGLSPRSFCWVEVSFSR/ SHSC/ICWVQLGSAVLQSQSGFGAHE GSRRRGSSPPCPPLQTLQVFSPOELSM SAPHRLSVTLQGCISTGGAPSRCLRA
12942	26843	A	13079	3	396	HERGRKNSVT/RLTQLRKNWASGHDLQ GKILQRLYQBSIKRTQPTKLPEGPSHKL FNNYY/CTRIGRRRSVPPFIIMSSHKAL VSRMPAYSPALAAKKAIVTAPSIYRG EGSSEHPLRHCTLTIVRL
12943	26844	A	13080	467	109	SLVPPVVSRLKPSCRYLLENVHMLVPEB QEFHSGKRAAGSLSPSPVPVYQWTPSIVTS SSFFFLERCVCVFFFFFPCFFFFFL/LLF FGTIKKALYLLRARGCKQYNOQKLIWYLT FLSLIVK
12944	26845	A	13081	458	51	VSLFCTVAPILLPLEGIIFFSCSLEWKA PMRDVSGVFLTLFLYSLVFFFLGVFFFL FFFLILPPEKIFFFFVFCVAFVFFSPAF GAVFLF/SLNWSVLPGVGFPTACFFFFF FFFFFFFLRQSPALVAQARMQR
12945	26846	A	13082	23	327	RSDSEGGRRGHYFIPIYITHHTYIPI YTIYIICLHYACLS/LICHTIPISTIYI HTYIYISYAHYIYIHTHYIYIHTYIHT YIYIYLIHIHYSWVCKGS
12946	26847	A	13083	352	153	KRLVEYYGAIKKNSVLH/VSTMRLKN ITLSLKTQSORHLYIIIPSVRNQVRQV HKYRSRLVDSB
12947	26848	A	13084	121	417	DIDYCYCYTPFKYLTKLLPYVGNYYI THLVRRVLCSTHWVYTHIHTYICII YIYWKSTWLFSGLSKTYRTHDLATTY LVFCLHTVTHVSST
12948	26849	A	13085	242	12	LSSRLPWLLTKRITSKLILPSRL/LPY GWCFKFKITWVSQIRNLAQMLTTVI POLNEA/SGLLKPSRRRPAMTW
12949	26850	A	13086	274	340	GGEKKTPEGFLSKSFSGGIFGPPP/P TKRGVFPSPKKFFFPKTKNFRGGGP KIPPPKKDFPSKNPPGVFFSP/YKSKK IIFPPPVKLGPPKDFLKGPPPPFFFTF FFFFFFFSQEVNKLKLSSTSELIIFYLV
12950	26851	A	13087	241	405	PPPSKIHIGNPRIOSDVNRATGWAWLT PVIAPRWAEAG/VSLRPNSRPNAAW
12951	26852	A	13088	537	375	KSLTSLRLKRGOTLHACS/L/CTSL

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						LGSSDLSLQPPQLAGTGA CHHTLEKI F
12952	26853	A	13089	448	186	GALVFPSSQADPPCPKMEQSFFFFFLL ETGSRSVSKAGVQLHHQS LQPPPPGFER SSHFS VTTI / TLYIYHRLALHVFELHIN GIMHR
12953	26854	A	13090	365	191	GQEREKERERERKKRQKKREVS / RSEES RVRDLSSSNRALSERSALVDRAPLSR PG
12954	26855	A	13091	148	316	DRMESCSLAQTGVQWHD\LG\YLQSPFL GFKRPFCLSLSSNDYRWETS TEPPQQA V
12955	26856	A	13092	712	229	FVAVVMAEYTLASIPOTREKDKVNCSPFF KIGVCRKGDRCRLNNKPTPSQVVFTEL QEKYGELESMNVCDNLGDHLVGNVYVVF RREEDGERAVAELENRWTFNQAVH/GEC TRGGFCNFMHLRPI SQNLQRLYGRGPR RSPPRFHTGHHPRERNEVF
12956	26857	A	13093	835	405	ELIERLGPNQKPFILMKNMPSPSNMKA SAALLCLLLTAAAFSPQGLAQPVGINTS TTCCYRFINKKIPKRLSEYRTTSSHC PREAVIFKTLDK\EICADPTQKVVQDF MKHLDKKTQ\TPKLLNHDWNLNQAMT LRKPN
12957	26858	A	13094	1137	424	LCPSHFAPTLTLQPGAHNMCCIKSRPK RLGLGRLCTLVNKNMPTSSILGKSHHSL VSIHQNDALWKAQVLSWAGYCAQG FSPGDSLKYSWDEKDLTVPOPTDNG SVLRWISKRGKPLAVBIBGRATGLPOLA PWOTS\CLGYKTPIV\HLFNSBMO\ENR PYGGEARHVCSNAALLFPPLRCLGGEK HKSGLRAHPVIVLSLELYDIDSFAHMF FADLLLLITLLSCYIPFC
12958	26859	A	13095	1	324	ARGERERERERERERERERERERERERE RERERERERERERERERERERERERE RERERP/RPRVLFFVGRGESHPEKCBEN KKERAPFSRALRKISISTRGVSITTEA CVFVIGAHRCVRSVYIYI
12959	26860	A	13096	508	840	DGVSLCRPORTADCSGAISAHCKLRFFG SRQSPGLSLPSSWDYRLKMPRPANFFF CIIFF\VKTGPHLVSQ/AMGLDLINS/SI FPKLGLPKCW\DYRREATAPGQSELLNR TGM
12960	26861	A	13097	53	254	WPTKSCIVAGQVQWMSHSSLQKQTPG VSSHPPASQVARIITGMHCNWLHLII LLRAHGSPLC
12961	26862	A	13098	329	67	GGGAPILLKGRKLLPKGPPPIPSIVSAF FAWGPYPGYCFLLKKGQPFV\VFPPSPFG KKKNSPPPHINQGAKTTPNPPLIFSSF FFF
12962	26863	A	13099	253	444	EGAFSLGTTFYFIFFLVLNFTLLISNQ QIWNKTVW\PSPFLLTLALTTLLLP SPFILL
12963	26864	A	13100	341	590	PMASQICIGRIPFPLYLKNYFNPQRVU HTCNPKTIGRGALITQQQKFENSLAN\ MAKPHLY
12964	26865	A	13101	55	184	RLREPTPIYSE/HAPTKYYRMAHNYPH SPPIQPRHRYVFL

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12965	26866	A	13102	433	762	RNLLNCKRGLERKGRASVPAVPLFLQR RVWPRPTAELEACMLAQHCNCQNVKME YFQLSFTKQBI/WLGVVAHACNPSTLG G\QQGGIACQBFKTPSSKVRPCPYLK
12966	26867	A	13103	349	250	DLFFSTKPPPPPPPKNLGPP\GPFPP FQBG
12967	26868	A	13104	3	236	YPOHYTSCPTFYQTLTKRNHNFLLIFFBV GSCSVQARVQVCHHGSQPP/NSSDPP ASAPQVAGTGVSHRAPPGNQNF
12968	26869	A	13106	154	4	KVKNTVHYNGKYFLKSNQGSTFLKBIL /WLGGVAHTCNPSTLGRSGRIT
12969	26870	A	13107	391	150	RPFKPKMKYSQITSGIKSVYTRKYL TKKXKNSQALW/V/NAVATQBAEVSQ SCEPSSRPKCTMHPWTECAPAWT
12970	26871	A	13108	90	252	KVGRGRCLVCFYFKGGSTVAQKXVQ W\ATIAHCSLKLKSSDPQNYEDSGT
12971	26872	A	13109	197	414	LYEFTIKTVLLGLCPLGRVGCSSNQFF SLEMRPHTVANARVQHMLDLSLQPLPR PNRFSCLR/VQOSSWDR
12972	26873	A	13110	2	317	GRVGARVHKHGQRRTGVSIVPHILPLHV LKKTPSLRDFHFSVLK\NLVLCTLHL FL/GVRTPRNDPFSVMMLLFTAPLDRPS TILGTGLLYTEGLTVALRLAYLR
12973	26874	A	13111	413	162	LILLQPAECLQLQASATLDCCLPRC RDCRSLVHSLVNLGAQGVOWRDLSGLQ PPPPS\TCLGLPKYRDCSLCPAATPSGK
12974	26875	A	13112	40	296	ESRLSALYIYHICVQYNRHLLYGTIN /SIHTYTHHTHTHTIYIIMRAPALEDK I CSLCSQDNAPILVSVKLQRNYFLT RR
12975	26876	A	13113	2	288	FEPRCKNSARGKVPRGFSNLPVTVET PBGSKTGFELSS/RRHRQIHSSAQPL TAVPQAGDAIPEDASGHTWLPFLHAQNC FLIYIQAPEQPPA
12976	26877	A	13114	685	340	LSFPFAGGARFTYTFPTDARGQSTWTCG ALKPRPRALRDNAENLPQELQEHQALT ATLNLRMEEGMNRIEDLK\NVNIDL\NV QAGIENSIKEQMLKTVTNMSPVGDGAS YRSH
12977	26878	A	13115	65	3021	GVLTMGDEKDSWKVKTLDSTLQEKRR KQBEKAEIKRLKNSDDRGRKDSLSEB ELRDHCEITIRNSPYREDSDMEDRGE DDSLAIKPPQQMSWKEKVKHRRDKERKH KCRHHSHSARGKHARVKEREHERRKH REEQDKARREWERQKRRERKREHRRER DRLEQLERKPERERKMRBQKQREBQES RERRABERRKEREAREVSAHHTTRED YSDVKASHMSRSPPFPRRRFELGDRG KPVKREWEEDLLSLDLOLSDERKTS SARESSARESSGSSSEESSESESEBOS TSEESSESESESESESESTGNSSEASE QSAEKVSESESESESESESESESESESE LPGRVPVPESRFDPSGSESESESESEV EGTPQ\SSAITEGTVPSDPLSPLELK QELPKYLPALQGRSVDEFQCLNRIERG TYGVVYRAKDIDKTEIVALGRLEMEKEK EGFPITSLREINTILKAQHNIVTVREI VVGSNMDKIYIMVYVEHDKLSLEMTK

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						OPFLPQGVKTTMTQLLKGKELHDNWTLLHRDLKTSNILLSHAGILKVDQFLAREYGSPLKAYTPVVVTQWYKAPELLGAKEYSTAVDMMSVGCIFGELLTQKPLFPQNSEIDQINKVFKELGTPSEKIWPQYSELVVKKMTFSEHPYNMLKRFPGALLSDQSPDL MNKFLTYPFGRRISADGLKHXYFRETFPLPIDSPMFPTWPAKSEQQRV/KRGTSFRPF\EGGLGYSQLGDDDLKETG\FHLTTTNGOGLLRPGQPSLRVAEVELBPVIGRNSAGDHKRGYLPANNCIDPTNNSSYVFLPCFVVFVVLCKLSRIKPSLLWRKELCFPLRDLPAERAVGIFRGARVQGHKHHHPLPLSTRTGLGMAVIMKGTGGRVDCIFGAGDGLCWDIERCPLAPTHSSRPALSTTS PRPPTTQOLLPAGLEQVFFYKVGVLKCIKIFFEE
12978	26879	A	13116	469	202	MTITVGLCEYTKSAVLVQHSDDLPAFPAQVFVFLAVLDVVDIKIVHVPVCLFVCLYEMESCPVAGAGVQWRDLGSLQPPP\PGSS TSCF
12979	26880	A	13117	193	383	AARMASTFFVFWFNFSTF\SLYSICVVCVCVCVCVRMHTVQLYFFQVGQCSLLNPLFFMN
12980	26881	A	13118	146	350	HYLVKFLLLAHPGSKAPPLNTLQPPPLATREQPLTVTFKYPPTS YKMAP\PYLPSLTLFGLSPPAFR
12981	26882	A	13119	124	254	HALQTLLRLDSQAMHALVIPATW\EAERAGGLEPSSRPAAWAT
12982	26883	A	13120	150	45	SLERLECSFTVLAN/C/NHLHGSSDSPASASQVVOGI
12983	26884	A	13121	336	446	IPLKTSMAQNLTPV/IMPVMAEAGGSELEVRSSGA
12984	26885	A	13122	181	39	QNLTAQDGVQWCDLGLSLOPP\LPSSWDYRRESLCPSSFFIFWKGWFT
12985	26886	A	13123	463	2	GPAVPSGLYLEKGPMPRLCASHSPESHSDHKGGQTLPRI PQ/PLIGRGGSR/PLAN GAVAGLPSNRPRIVPLAPTRSGTRVRPHTGHQPGMSPGCGCESKVPESAAWPEAYPHFFLLPPTQGCCEVLGPLYTADPWVICVSLLPSCPNSTAVDUD
12986	26887	A	13124	429	263	DHFSPLCVTCSQSAQVGVQW/LYIAHCSLKLLASSDGPASVFGSTRITGPPLSF
12987	26888	A	13125	310	486	NKKTTRGESSKQRPVSHPGWGTVAPSGFTAASAS\RARVILLPRPPE
12988	26889	A	13126	124	461	GSPIQLLPSPLAALTTRD\SEAMGSSCVSAQDGVQWRDLGSLQRLPPGPEFPSCSLSPTRAP\PSGNDYR
12989	26890	A	13127	2	337	RGAPRMAVTLAARTMLGVVGVRTWQARGTSDQSDENVDRGASITRAGGAFGRREOAEERYFRAQSRBOLAALK\HIDEIIVHHKKRIERLQKEIERLUQKIKMLKP
12990	26891	A	13128	681	422	CRSDRWAKERHKGKRGQSSQDVMKALMEAPKQTAQYFFIFYFFETKSYSTVQAGVQWLDGLSLQRLPPPG\SSDSPASASCAWPQTAH
12991	26892	A	13129	299	579	LVMFCVKVTKIERLNLMRFGTVAHVLWSQHFRGPRWAVHVGWGVDRP/RLTQHGETP

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						SLLE\NRNISQAWCHPVVPATREABAR ESLEPGGOORLQ
12992	26893	A	13130	268	438	KVDESKMKRKNRPYNARNKXKASFP NDCNSSPARVQ/SWTENEFDKLTVEGFR KW
12993	26894	A	13132	1108	1529	KIHSSFVLLNAKLVAVAARTPKFYKKKT DLPQTYHSAQTAVPEIPSAHSTFIRSF IHSFIFETESYSVAQAQIQKHDLPSP GS\SDSP\ASVSRAVTIGVCQQAWLF V\FLVET\GSFPHLSPLTIMRNKKQLFK KSH
12994	26895	A	13133	497	370	RFSPTSPLECSGLILARCS\LDPPASA SGTARTYVGHSH
12995	26896	A	13134	217	373	QNHTEITTVAKKHGPGIVAH/SLYNPS TLGGQGLITQAEFTCSLGNMTLS
12996	26897	A	13135	257	507	PVSFGFFPL\CPVPHTPHLCPFCRYPES PQQAQAQHCAGAPQCPNPRACSSRGLF RCFPACHHAPSCLLCVCPPPLQCRCVQG
12997	26898	A	13136	137	309	PSPPTHDPQFCFLCFLEVFETE/SSIVA QAEVQWCOLGSPDGSSASPSSASLPL SIW
12998	26899	A	13137	297	419	GGSAVYIWEITVOVLNMPVIPT\WEAY AGGLEPRSSRPA
12999	26900	A	13138	213	492	QVGINYPPTVVVPGLDAKQRAVCML NTTATTEAWGLPGAISAKCALVHW\YV GBQMAVGFESEAREDLALEDYETCGPW NPVTEAERR
13000	26901	A	13139	246	534	DRVLPLLPLECSAILGHCF/APASQV TGTGTGHHITQLIFLLYCWLCPPPLASE ASASSPPLLPGFPLCFSSSTTSITAI TTDYVDVSRSS
13001	26902	A	13140	1	206	SLNPFPSFSTNSHSFQRIVQNCNH SSL\SPTSASQIAGTGVNHAQL/VFV FCFAFMSPOLSNSC
13002	26903	A	13141	164	582	GLVLVNLVYRSYLVMPVYIYNSRLQVTD ASRERRENESSMFCRSVCRM/PPVPGP SCVHPSPRSGISPCPTHPLCKTQABA \PPRPLPRVGGPHLDQSCVAAARPLYD PILVAHSSWPAPSPVPVPQEDTEHGA G
13003	26904	A	13142	235	367	LALNTPCWLGVVAHACNPS TLGGQGEW TRGQ\QANMAKTCLY
13004	26905	A	13143	91	403	GALQPATAPWEPLSG\AEAGATSPCTG G/SGRGASENRGCTRGRVPGGRRLN PRANSSWPAPPGSERPSAINCPRARE CGRRVDNQALFAAPAMVEV
13005	26906	A	13144	558	147	GHSFQNWLLGCPQLQRHLLHPPDAEE CGSPWPTLRPHIHPSAGPHGSTHK\HA GGCLFPLRPSPTHPCGPPVPLPWQ\QA PLCHPPTHSPTHMWCDFGSKALTPPPA AQSPSLIKHANSFPCSPNRRPGIP
13006	26907	A	13145	321	421	GCAGWLTIV/TPALWEAKGESLIFRSL EPANAY
13007	26908	A	13146	3	398	TELLQSHDKTLTDKILLDBQRTWPLE MESTPGEDVANNVELTKOLEYHINDLD\ KAGPERIDSNFERVSAVG/KMLSNS IAC YREIFHERSVKANFTVAIPQPHKLSV TINLIYQDPSTLRQDILLAKR

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13008	26909	A	13147	228	261	SKTQSRSEYYSLSCVCCVCVCVCIYIYI FFFFETETPL/APAQGVQRCDSLRLRP PP/GSSDSPSTSSQAWDYRRPQRTS LHYFVQLKINLHRVKRDLRNTTR
13009	26910	A	13148	3	275	KHLSDLQILRLGLSSKTRKTRYSHPAQG RSIFILLRPSVDWIKPACMDGNLLFSKF TNLNVNI\TKKHPRHNVRVWPNVWAP WPKEVDT
13010	26911	A	13149	218	382	AWDHIKLSEFYTAKETT/RMKRQPTENE KIFANYPSPDEGLVTRMYKELQLYRKKI
13011	26912	A	13150	391	29	GCFLPLFMFLPFFEMQGVQVWCNLSPO PPPCGLSSHSPASASQVVEABGCLNFGQ GCGSLADRARLPQKQKREPEREKRRK ERASCAPCGAHTTVPWMOQKHTCNLHP WLTVFETNKL
13012	26913	A	13151	351	157	FOYSEFLCVYINFTRLSTLNYTICTYEN LYL\NIHTYITLTYITTYHTHTHIFYEY IGILTGIT
13013	26914	A	13152	402	111	TFPGGEEKPPFTLEPGPPRRBGGGPGPG REGGFFRVPLGAFGSPRPK/RPEKSGPV WAPQIFLWGGKSRALKEGKGFFFSRIT LLVFATEKKKKKTTLF
13014	26915	A	13153	310	141	REHEKQKPLSQVRNCTPLVQMAQEAAG GELEPRSSRLQCSMT\TPVNSHRPPARV T
13015	26916	A	13154	153	21	LNKCVISWLGVAHACN/PSTLEGRWIT QGSEFKTSLSGLAKPHLY
13016	26917	A	13155	429	275	SVDTPLKTLINRQVFKSA/PFKCVS/R QARVKFKRYKPKVKTQWFFQKLN F
13017	26918	A	13156	303	42	YIEKAFVPTIITNARGPHKQ\TRATH THTTDMHATHSPALIPAPADNGLGT FHHKRTTNDKVKPRLSCEAAIPSHLKS REFR
13018	26919	A	13157	198	13	SHGVAILLPHFLHNRKRAFT\YSPAMSS LCEIQRPSLG\SGSGPLSGNRMSQKHR KYFAKI
13019	26920	A	13158	192	2	ISNSHRKDIKDPVLLTQKTYLLSGQM WLTPVIPAL/V\KAEAGSLEFRSLRPA WATDRDSVSK
13020	26921	A	13159	40	190	RVDPRVRSRSVAQAGMQWDLSSLOAP P\PGSRHSPASASQVALFLNRK
13021	26922	A	13160	1	178	PTWLSFPADKTNRVA/MKGVGHAAGEY GAELERMFLSPFTTKTYFPHFDLSHGV SSYL
13022	26923	A	13161	411	41	ESLQICVGLIAKPSWDACRPWLQGWFR YFLLTFLGLVLLVFWFSKIFYLYHLK NPSLSCTNLD\FNTQYLYCKKKRRLG AVATACNPSLSSQGGRTTRGQSFETRL GEMAKPDWVD9
13023	26924	A	13162	372	218	FWKRSMTSKKGLFKRGSLSLSLS/CDT HTHTHTHTHHAAGCLVLAQVX QGLVLSFWLKCAGGTATKCHLSSSHT TSA\QVAGTTGTQIHIAQLKFFLLILL
13024	26925	A	13163	247	89	PPSTAIASHG/CSSPGGCSYGVATRLP LRSSNKLAIA\LYGLAL/NSPFCNFPQPS \LGLSGPLSDNKNALCCFKPSSNLP ATAVLGNYSLNTVSRGRDPGTPNACS
13025	26926	A	13164	122	409	PSVSLFFPPHNTIVIMGLLKINSIFGE
13026	26927	A	13165	69	313	

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						GLALSSRMKCSVITIVHCGLLDLSGGP PSAAS/RVAVTAGTCHHSWLMFLSFV
13027	26928	A	13166	310	26	IKSMTPLPALNVLSTYLPRLPCRERG MVQDRFFCFLPCCOCTIFSETGSHSAAQ AVSQNKKTGWAWLTPVLPATHEAEAG BSLERGRQLQ
13028	26929	A	13167	296	68	KNGPLNLATKSLILITMKCLGVVLGGKP NCSKLKKNKIKTKKGGWAPWLTPLPA/ LLEAEGRSLLEARNLRPVWT
13029	26930	A	13168	2	235	GAIPCPREPSLFFPLAGWAPLSKNAEPFH CTGCTTFFPLGWTGAPALITIGNARSP PWFLPLSGTRALSACCTF
13030	26931	A	13169	248	406	TERCGFDLLSLGQVQWITSVIPALE/EA EAGELLESRSWRPAMWATQNLISLCK
13031	26932	A	13170	33	308	NSLQGAEMAAQSLSTFSASEGYRGRER GRGRGRPRGR/RSEGRGRGRGRPRGRGR RKVLLLRICVWRVRLRWNRGRIGVGRG VTYLMESBI
13032	26933	A	13171	294	56	ICKRNVLPFFIYFLREGILTLPRLCSGA ITAQCSL/GSSDPPSTASTVSGTTGACQ CALSSRDALISLCYPGWSQAPGLK
13033	26934	A	13172	71	476	DSLNDYHNTYQMPLYINMGLAVTISLL GILVYRSHLISLLCLBGITILSLPTLIA TLITLNTHTLSLNTVPTALLVFAACEAA VGWEECGPRSRPTALILEGPLRSQCPRT CVRRPACTRRGPAPVGRNHSIGG
13034	26935	A	13173	86	318	NNCNVCVCVCVCVCVCVCICIIYIYV YICITYYKIIICITYYKIIICICVCIHIVYM YMCVYVYICICMCVYICIDSKR
13035	26936	A	13174	466	726	NCKFGAVTRIG/DLFWENGLSCLL REKDPPTTSQPTDQPKHLLNFKSGKR PLFTLPSNLPHYPSTSPSPQSWRHTSIS PFS
13036	26937	A	13175	128	325	FLRVILCKHNVGVCVCVM/VACTGNM CIYMCVCVKSWKLKPELKCICISDEVGW VLTQWAGREEN
13037	26938	A	13176	134	311	INSNSEKMGSHYVAQDGE/WQGLPFGH GIAHCNLLKLGSSNFSASISQAGTGTI VANG
13038	26939	A	13177	577	1052	SPTSTRIGSGVAMNLSQPMORT/CRSKV ASKSRLHGLPLINAEPPIVRCPLRHRY/ KAQNGRGLSLEE/LRVAGIYKVAQTIG IS/EDARRRNGST/QALQAKVQRLK/ED RSSLILFPKK/PLAPKGDSSAELEBLD TQLTGPEMPIGNVYKKEARVIAD
13039	26940	A	13178	496	678	TINFVWAQLKTRPRKNAVPFPVIR/R LRNRNLLTLKGEICSDPKWYCLPFPWKT KKNLV
13040	26941	A	13179	192	421	GIYVTLPLRFLPLRQSLTLSPRAGVQVC NLCLPGSSDPASASRVTC/ATGT/CHH GSANFLYPLUGDVFVGVGVR
13041	26942	A	13180	144	5	LQIATKLKMLZJVAATCNPS/TLQGW G/GRSQGQEFETSANIVKP
13042	26943	A	13181	351	51	KKKKKIFPGTKGRFFFLKGVGPPPPK VSPPPPKISPNPNKINPLKA/IKSPQ NNLFFPGPPSCKFFPPFLNPNKSPWEN PPSGGFSPPKKKKKSAI
13043	26944	A	13182	2	218	IHFQCFVPLFFETEFCSCHPGCRAGVQW

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						RD\LAHNSLLPFLG\SSDPPTSASQSA EITGMSHACPIFKHIS
13044	26945	A	13183	33	304	ERHGI FRAVKILCMLQRTWYATHLSRP TGYTAPRVNPKLWTLGDNVSM/SGSLI VINTALGWGLLIRSSACMGQDGNLC TFLSLL
13045	26946	A	13184	277	13	FSFFLIVHWGSCYLAQGLLELGSSNPP SSASQAGITGMSHHPAMIALTKRAFVS D\NSLSPFSSSENAHLSILAQHFCMLGPF FFQ
13046	26947	A	13185	140	361	ITCCCVCIYTHLHTYVYCVYIYTHTYI RYCV/YIYHHTHYIHYIYHVFYIYIYT FMHTYIYPIYVWGLLOGL
13047	26948	A	13186	64	759	CLSAESAFTSTWNLQYNDIRGLAAAL RLILSYTDSYVEKKYITGDADPDYDRSQ WLNEKPKLGLDFPNLPYLIDGAHKITOS NAILRYIARHNLGEBEERKIRVDILIE NQVMNDNIMELVRLCYDPDFBKLPKYLE ELPEKLIKALTS\BFSGGKRPW/SGDCK ITFVDFLAYDVLDMKRIFEPKCLDAFLN LKD FISRFEGLKKISAYMKSSQFLRGLL FGKSAWNNSK
13048	26949	A	13187	41	426	LFFFFPESGQFWITQAGRR/WDHGSGL QPGFPOLKSGPCLTLRRSWNYRPMGRCH TQLVFAPFFFPREKKFLGAPGTGPKTRG LRGDSRFQFGQGNKGQEDPPRAKGLIF LEPERGQAFPGVFFPGTQ
13049	26950	A	13188	39	197	FFFFLRTKSCSFLQAGVQWCHSSLSQPO TPOSSAPSPASCKGTTBAALK
13050	26951	A	13189	221	396	QIQLOQABOLMDVTSTPFCWLYDKQIV YHECRMWNSHCP\PPKGLLRDITPRCW AP
13051	26952	A	13190	2	826	PGSTISSRRRGKSGRGHFFSPRGSG VASIERAESWSTEPAKALKPIDRKSVMQ ICSQGVVLSLSTAVKIVENS LDAGATN IDLKLDYGMDLIEVSGNGGVSEENFK GL\TLSALKHHTSKIQEFADLIRVETFG FRGEALSLSLCAUSDVTISTCHVSAKVG RLVFDHDGKI IQCTPYPHPRGTIVSVKO LPSTLPVRIKEFQRNKKKRACTPPAFPC RDCQFLEGS PAMLPVQP\AKLTPRSTPP HPCSLDNVTIVFSSVKG DGSSR
13052	26953	A	13191	235	1	SPCARQCCPNNPAGQEPRRRLERPGKKN WPRSIKFFLPFAV/RARFPLPSAPLRQL VSGRVGVRGPRGKAVVSGGLN
13053	26954	A	13192	2	386	VYIYLLGFVETRESCCAQARQGVSPCMWG WFOFPA\SSSLPAAPK/VAGITVSHIR TRPDVRGFKC/GLQLRSHLALL/TS SHREWFYVLLFSFVSKGFFIFFFLFFF FFLGKGFVFFFPFGGGGQOI
13054	26955	A	13193	749	506	GOTKAPVLSYQASPSIKQ/PCPOAKDH PLEPSMHPGTQLOSCSTMLGPRQLSS KOPILLPPRSHLSSPMLRACKGLTS
13055	26956	A	13194	73	297	RMPGFGATGSPFSCQRIKPCFAGAGSC TYAFCKCKSYKCTSCKKSQGAFFNQ GAGQSORREPRACQAGAQ
13056	26957	A	13195	670	390	PRETYIKPFARSTGQFPKTIHPTSRRP STRPDARPHARPPVHT/APSVHMSDRP



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						STCPSPSIHVRPPTDVSRRPQYSLSPSTSLALPGQSCIGR
13057	26958	A	13196	2	438	LSFTSTIEFCHLLFLNQLICNYVIFTKSS TISCRAIGRLLVVYPWQRFFESFGDLS TPDAVMGNPKVIAHGKKVIGAFSDGLAH LPLPKPTFATVSRILHCAKLHVDPENPT LLGNVLVCV/KMHNFGK
13058	26959	A	13197	57	499	SPSWPRSSARPSCGICLLPLGLNDHGKAP CLRAARHSQGHGFRKGRKEGCGLWAAGW TKNPVPTWRAG/SRRPGVTSPPPVPSV QNPFP/PPQRHGGQATRPVLTTPPKH MSPAPILLGDQRI TAPPPELLYRPPRA ATCDALRGG
13059	26960	A	13198	34	465	GILPYSFCVLRAPISSKKVRKQCTTPRIH L/CXATRKQCTTPRAPIINSTRKQCTT PRHLSROLGNAGALPRHLSNTRKQCTT TPRAPLNATRKQCGCTPRHLSROLGNAG ALPRGHFLKETRKQCGATTADAFYETK IGGG
13060	26961	A	13200	177	1075	PTSSSHAFPPKKKLQGLVAATITPMTENG EINFSVIGQYVDLVKRGQVILFVNGT TGBGLSTSVSRRRQVAREHVT/KGKDID QVILHVGALSLKESQSLAQHAARIGADG IAVIAFPFLKPWTKDILINFLKEVAAAA PALPFPYYHIALTVGKIRARELDGIL DKLPTFGGLKFSUTDILLDFQCVCQNRQ QQPFLFGVDEQLLSALMMATGAVGST YNILGKKTGQV/EAFEGKQFSLMNTYQ FCIGRFINFWKLGPSVSGTCAIMTLVS GDSNGPTPASTCRKPPGEFT
13061	26962	A	13201	35	464	VQEFKTLGNVAKPCLYKKKKKPSPLGG GVPPPPKKTWVGGTLPSPQIRPAGPLIF PPPLPRGQGGEPSPKIGGGGGGSS/YP PPPPCLTGRA/PPSPISAKSSPPSP CQYVHPPLPLPFFFLHALRRATAPLFL FLVRA
13062	26963	A	13202	1153	259	AGVLRLLGVVTSRRMSSDNGQTLCTL EFAVQMTQSCVDVVRKSLQGVAGVDV EVHLEDQMWLVHTTLPQQRVQALL/BGT GRQPVILKMG/TGQPSSEGGQPVAILPGG GLGTQGVVRFLLT/PERCLIGTT/PG LEPGLHGLHVHQYGDLTNNCNCGNHN PDGAS/HGGQDSDRH/RDGLQ/VNAGN AAGGRFFMRDQCKVWVIGRSLIID EQEDDPGAKRQSGSLYKTRISLPSGL SCG/LAKSAGLFPSPQSKICSCDGT/ IWEERGRPIAGHG/RKESAGPPAIL
13063	26964	A	13203	281	420	VDGSKKYNEPMVITPAWKAAGSLLEP RKSRTAWATREDSVSTKN
13064	26965	A	13204	3	1125	SDSPOTPRMRVAPRTILLLSGALALT ETWACSHSMRYFYTAVSRRGRGEPRFIA VGYYDDTQFVRFDSDAASPRGEPRAP/N VEQBGPETYWDRETQYKRAQCTDRVSLR NLRGYTNQSEAGSHTLQNMVGCGLGPDG RLLRGYDQSAYDGKDYIALNEHLRSCJA ADTAAGITQRKWEAARAARQWPAVLEGT CVSWLRVYLENGKETLQRAEHPKTHVTH HPVSDHEATLRCAWLGFTPAEITLTWOR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location corresponding to last amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
						DGEDQTDTELVTETPAGDITFORWAAV VVPSSGEEQRYTCHVQHEGLPEPLTLRW PSSQPTIPVIGVAGLAVLAVLAVLAV MAVVMCRKRSSGGKGGSCSQASNSAQ GSDESLLACKA
13065	26966	A	13205	417	13	GHPRVMLQCHMGASASLINTPPPIESYQ PALTRSSATKPA/TSAPSITPMTPTVTAN IS/VHPTANTTTTKLSNPTSS/STLSTP IWIHPSILPAPPSTPAPLTTVTNSATTST ICFHVQLQAHICHCICLAALLEYTS
13066	26967	A	13206	1139	559	QLSLSLTHPSVARVQSGHATPSSIPW PQKPKRSGKRTGLRWGGGSHLSGGT KKGKAKKRDHCAKGPDLAQGPFPFRT QLLSFCHGCSWAKDQPP/GPPHACTATW EKTVTGSGCRPVTKPSDPDPFGVQAGPT KGNPAPMGDGCAGFRISCHPVPITKPLS NTGICVLLCYEFGFLIIVGCGNGFK
13067	26968	A	13207	306	332	ENGEIRITYTYICLVLEKRWNEBAGCSH HL*SQHLKRLKWDYLRPGVPDQPGQHR ETPSQKLMK*INNDF
13068	26969	A	13208	48	233	GKQHLKCLWCRILFLSAVISIRNVYL T*LSLSLSQCVCVCVCVCVCVCVCVAIL ENYPR
13069	26970	A	13209	250	2	YCBODLGSSRPGVSKCRFPSPDRDKRM PWPGAVTYANPSTLOGRDGWAIA*AP ETSLGMIVKPHLYTHTHTHTHTHTH
13070	26971	A	13210	615	120	SVFWPLGGVSNHSGYTEVRGPLEKAVCP LSFLRYCAGRSAAIFRAIRLPKDALSLG KLCPQPPFLGAPLS*EALVCVPLHV STCLG*ACPTCPDPERSNWLPFBNTPR VCPDGLLPPVPLRGPGVCVPLHVSACL LSLFSNLLRLRTGCVNFSVPLVLC
13071	26972	A	13211	239	429	FILLRNKLQPTVACQCPSTLSSQGN IA*ACGFETSLDNMVKPCFYLQKIKKK KIKMLGV
13072	26973	A	13212	954	503	VQLPLQORDLYLFAFNLPYRCNQHFL SKPRAPILAGGSDRWPCPCPFWL*PNC HVSAAHAPQPPCAKPEAPLVGCPCSFA PSLEAALLILRAGLVVLRAPCFSAHLL SCHSQCCQPCSEKRSCLGORDRHAASN PLSAVWPPE
13073	26974	A	13213	1844	1147	LHSQIYSTARAKASLMKSGSDKTRLASS RPVPSVLGVPWNSTLHQPNQNMGPAPQ QQQGPSGRQAWCTPGEAPGAEAAPQ*QP HFEEDHSGGQASAAALGPPSPSQRDV QEDHGWQORSAPRSASSACRCHSHL PCVQLQHHPLGLRVSAHSRPGPSP SSSGSLVPGYLPQGLAGLGNLAVLCP PGLLRVHAGAGYGPSAQHLHALLSSSL RGKRLRF
13074	26975	A	13214	413	60	LCSKSGHGFAMDCSTLTTPRLFYIL HMPITVPGQALPVHTPFL*KLPLPLP SCHSPLFLD*AGESPPPGGLFHPHGG VLCLNPHSLKHPVLSGSSVSTPGSASPS RSRAL
13075	26976	A	13215	67	196	GLSLSSPKVTHNATMGICFQNP*KA VYHSMKQKILLFNCA*P*YPLDFGEQNP LHGSHAYSTIL*LDLCKKEE*DEIPY

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, N=Methionine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=-possible nucleotide deletion, /-possible nucleotide insertion)
13076	26977	A	13216	161	2	V*CFMLLWKSTTM*KRIITLLENMA SVFFLLIDRRLLYTKSVWVAYNSSTLGQ RGRRI*AEFFKTLGNKARPRVYQ
13077	26978	A	13217	57	184	CLTVCKDKVSLCYPGWSPV*SYLTAAS NSWSKALLPPQPE
13078	26979	A	13218	292	400	LKRVQGRGHLDLNGQGLD*L*SNLSLSH TPSHRRTV
13079	26980	A	13219	186	394	YLVLSF*FYFLFI*FLSRVSLPFIPTI* *LGIVAYTCNPSTLGSQGRRIA*AEFD TSLGNIIVRPSLI
13080	26981	A	13220	315	448	KTDLGVVDRVYHNPST*GG*GGRIT*GQ KFTSLDNKRARSCLYK
13081	26982	A	13221	3	13	LRLPESFVSVERLWASCCGSELVDRK KKKKRRLSEBHKRIKAF*FTD* EVIDYHKLKVMALGFDVKGADVNLIL KDYDR*VIGKISFGHSIRIVTDQL*R
13082	26983	A	13222	1	715	VDMSHSGPELTHASTHSGKMAA*WAS LRLVAPMNGRIR*THRIGAAVAPEGNQ KKKRTILQFLTNYFYDVARELDYLLRO MYKVHEENRSTYTWLEKHGPGAGAPFI LKQGGAVKFRDKEMIRPKYGHFSQETW NFCFVVP*EAVDAGDCDINYEGLDNLLRL KELQSLSLQRCHVDWCLSRILYPLADF VAGAFRWAGCPRI*FRGAKHG*FHLQ*D LSSGWATCPGTSPT
13083	26984	A	13223	1019	1238	LTGAERYKSDGLTESVTANLEPEAPRVF SRLDDEAPVTVLPAKPLPAP*HTARP PPQRRRSMQLAPARPFL
13084	26985	A	13224	1534	1181	EMNSEPYTSAGGPRAGRGARLLPVPKSP GGGAVAGPOTPLPABETAVRLISS* NSSTAADPGAGAPPLHPQAPBAGTWSA FLRVIFCPFSLGFGCKEKKIAFVPPPT DEKCL
13085	26986	A	13225	328	22	CLESFDRDRFQGPAPPKHPPPLAPLSQ PGKVQYF*PESNCKLSGQETKSSRSVPT SPAPSPPPPPFLYFSLTAEQGEV*KET LDSRAPPSREAPICQV
13086	26987	A	13226	180	5	NSIDYKINVRNRRPGVAHTCNPNSTLG SQGRRI*AKEFETSLGNIVLLIYTIY YI
13087	26988	A	13227	237	528	VGLQDPLLATLDSFCSVLWGGSHLAF HKNLYVHIDLNVYFRRISFYFTLSNAI CLSLYLGSHTLSPFL*LFYCAVTTLYLC LITTLFFLIPKV
13088	26989	A	13228	140	366	NATCLAHMPSPYAPTY*C*LSGLLRWV LAITPTVLMILISSYHNSISYGGTFRS NFFLDQILITFLIYELHIV
13089	26990	A	13229	257	25	LPAHSIGRDLISAQPYSPRPGGELRAEG QSSLSVARSLS*LHVVCVVCVCVART CNYFACVLSKTVLHLE
13090	26991	A	13230	561	52	WPSCSSSGSHLLPPFPGSLG**SSSP LPAALAPAPCAAPAPAPLRPGPATPT AAAPAPAPAAASLSAARAAGSPGGR PSARGARRRPSGCPAPPRILGPAPFSS APRTTPT*GRARSGSAGNAPSARRTP QGPPAACSLARSINWAGRGSGCRAL GA
13091	26992	A	13231	335	103	CQKYSTSYCNKHLATVFIICSRKI*DGL



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						GALVRLPKSARQASRLTKVTVVIRSLKAVC
13110	27011	A	13250	299	1	ATARLRFHLGAMWYASVVPPTQBAEARG FLDPRSRME*AMILPCTPASVTDKIP SLASQIHRPSRVACVILLSSHAPTEAPS RMPPPSPLCPAGSRA
13111	27012	A	13251	106	146	LCVLRQVROATWTRYSSQIFAILDCMT TLSSHPAKLYCNYVLISNQSPNHLRL* SGMISAHNCNLCLFG*SNSPASASRVAVC FKASQASYLD
13112	27013	A	13252	217	158	LEPEFCIPFFFFFFFPPETRSHSVSAQA GVQNCQGSGLQE*IPINFFGKEGVLDK LLISTYQNAQPKVAVTVCCTALQGR QSETLASQRN
13113	27014	A	13253	150	56	THLHLLLYETESQVAGQGVQNCBLS IQSPPRSSCHSPA*AGVNNLRQENGWSF EAEIVLSPDRITALHGLQIETLSHIYI IILLSTISFIOLLI
13114	27015	A	13254	174	145	PCLRMITYDFKSALEIAFFCTAILRYK LLIKVTHFKMLVAADCNENTLGSQGG RITWHEFKISLANMA*PTTRSYSQRV IMGITIPDEWRSRQPSHISGSPKUYF
13115	27016	A	13255	179	273	GQMLTPVTISAL*EVEVGGLLETSLSQA WAT
13116	27017	A	13256	264	382	GLKIGRGCSNMFTFVPIPL*EVKARGLL EPRSLKSAWAK
13117	27018	A	13257	1199	1563	YLAVGPAVPEPLDLPEQAGATCGPVSHY KIFAKLWAVGSLDIMPGE*GSFLSVF TSLCFTYGVTPPHSEQPHRSPASAGL LLAKGRAMLVSTLCIGSPAPMLGTIPP HKVYNGLFI
13118	27019	A	13258	194	242	ILYVETGSHYVAGQGLLELGSNPPAST SELAGIERA*ADEFTYGVGWSODECIKM KQVAHASIPALSEVEAGGLEPEPRSSRA
13119	27020	A	13259	322	120	GPITVLDAFQMLCLSTSGQQADGITYPA FPIRKGGTQWPKVPIPTLNEAKGRFL *PSPRPAWAT
13120	27021	A	13260	237	1	TSKKISLGNWQKQIGPTWBG*AKRFFE PGKPRVQNTQVPALDFSGGKARLCLEK KKKKOKKTKLGLCTHSRITYSRA
13121	27022	A	13261	52	318	SAVGIIHRCDDGSH*P*TEPHQLSFLSL PSSWDYRGITRELFQFPWIFLQLITAV ISSESTVLKNLELAVRGSHVRVDMAV PINPF
13122	27023	A	13262	274	1	KKKKNSPWWMTPTVIRGSEPG*AGELLE WRQKVLQACVPLAKVVDCTKVVGQCL ALQPGHQGIFVSGKKKINPKTRKYWAL FCSLFC
13123	27024	A	13263	717	877	NSTKEMAHWPGVWARTCHRESTFGG*GGW IT*AREFETSLPNVKKPLFKYTKK
13124	27025	A	13264	288	131	SLYIWHSESLNTINKISGVNWCGLPVV SSTWEVEAGGSLEPR*RSWAK
13125	27026	A	13265	80	287	PMNGEAS*KTSILQAWCAPIVDAQ* NEAGELLEPRSEWLVWATRALRISRGL RFRFLRRFTSTR
13126	27027	A	13266	3	241	VGLFLFFFTESCSTVQAGVQNCGLS*L *PPPGGIRDSPASASQVAGTTGTHHTW LFLFYF**SSGFHYVGLGRSSHS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion
						GV*PFFCLEGGFFSPHKKFFFTTTSNLC SPKKSFFLKFPFPALEFFNLPLKKNIPSP PFLKKAFF*EIFFCGPPFFFTFQNTLF FFPPPPPPPPPPPPPPPPFLDKFVY
13160	27061	A	13301	233	406	VTVRGMEVVLGGSSDGVSRPT*V*FL KYLIGAVAHAKKPSITGGRRGRIT*ACE LKTSLCNKVRRLRYKINK
13161	27062	A	13302	92	429	GSHFNSELIBKFFYIKRNPITILNCFY LKHQHPHYTKPLVSVINKEP*LATVAH AYNLNLGGQORSA*THEFTSLGNTV RSLYLKLNKSNVWVCTAIEWVGLPL LQKRVHSVQSQAMWHPPTVFWELAGTGL LKDPSLSL*CPMTVHNSHCTPAMAT
13163	27064	A	13304	115	312	LRSPSVLSPLKCGGTITWTSCTFDLLG *RNPALPSKVVTETGLIHHALIRLLTF FF*KNVLF
13164	27065	A	13305	90	246	PGVVAECNPSITGLGRGRIT*QBPKS SLCKIAPPPEKREGRKBOGKKERG DSSPSPTMPCKSGSVNKTGLMLGKKKKK KKKKGGPP*KKPLGGNPLPGGKKKFFP *RGAKNPNPGDFWKKTLFLGGKLGPPPP PQR*NPFFGGGKIGTFFPPKIKPFGEKK KF
13166	27067	A	13307	179	56	WVLVYKQSLT*QMVMSVISALWEAE AGGLSVTSLRLA
13167	27068	A	13308	425	290	KKNITLAPPGYFNPDPQRFLLSPPPPNV VIFFFFLFFFFFLFFFFFLIYABGIG VMRGRGEGKMR*W*KFFGRRVLNIRSI LANFKHVVPIW
13168	27069	A	13309	214	371	TYF**RNTSQMWLKPVPKLMREAGG *LEPMSLPQGVNTPSL
13169	27070	A	13310	975	572	AKGVVGVGRHSLVSLGTEECQASTALS LDKSGMWEAARRDELVCEDRCLLCHV PAGVRSGLKPELGSRKIKGNQSGSKPS VPSLGPFPQGGNDALSKGTRDN*AI LQCTPADHSAKQAPHTLPIR
13170	27071	A	13311	270	10	TPNKSIL*RLQFSNTKLANGLGVAHS CNLNTLGGQGARITSGEFTKGLGNDIP IPIESKVIKTLGAMVSPDAWDAIKRTG TSG
13171	27072	A	13312	103	290	LTEUVSGVIL*NCIYLLPOYTSTRWHAY IHTYIHTHTSTGLSSTSVGSINIKSKI FGGKKG
13172	27073	A	13313	136	1	SNTSSSLVTIAGGQNCLEGL*PLPKP KRFSCLSLPSSWDYRL
13173	27074	A	13314	88	183	RVSTLLKSCFFFFFFFFFFF FFFFPSQKKKMLKKNKKB*KKSCFFFF FFFFFFFFFFF
13174	27075	A	13315	481	517	LISP*RPKGPGRKKRPNLKKKKIGEA RGKGRQRKTPORTGQKKRRRYRRIGR RNYR
13175	27076	A	13316	307	196	GMYLPLRPT*WVAVITPSRETETVHAPL EPGQRLLVAMITPMHSLNDNNGKSPFT QPPKTSKQTKNDPKPHILA
13176	27077	A	13317	2	209	PARALDLKSGSPYMESCSDAAGVQDSIV GDHL*LRAPAV**GQTVFVASPSKVGGI TGASHHPGLFFL
13177	27078	A	13318	3	178	SFCFSVLRETIQGLIMKTL*ITHTHT



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						HTHTHTHTTQREIRERDRERGE SQVLGC
13178	27079	A	13319	40	382	DSVPSLLKLLMETGPHHVQASTITTS *FFILEGFHHVHAGLKPSSSRPHILA SQSAGIYGCEPLRSARLLINYIGSRLMG LRNICLSQDHECLLCFLQALISMYR FCLG
13179	27080	A	13320	107	1	PPLINANSQWAO/LTPVVP/LNEAKRGG *SEVRSS
13180	27081	A	13321	111	382	ASSQLLELAIQVFPGINIPPTTKQGVF SKCTLVTSKILAGLAMPKDSRSRPRTVA HTYNSSTLRGQDRRIT*AQEFKTSLGKI GRPLCF
13181	27082	A	13322	49	108	CGLY*FFF*ATRSNHWAOGLFPLGLSS FPASASSVAGTGMCHHTQIHTY*F*V
13182	27083	A	13323	1	257	ARQERERERERERERERERERERERE RERERERERERERERERERERERE REVARERE*CV*EGT/VSDREDFERA PPRVLGAVAIIVSVVCLASLIQ
13183	27084	A	13324	1	248	EFQYILCSALIPORSKILK*ATKEVKKS KHIPRISQDTRKYNMSAKAKRRNTIGI GRMRHLKIVYRRFRHGLEENFLPKH
13184	27085	A	13326	375	1	PPKRRGKTHCSPPKVFPPQNN*TTTTP QLIICYL*RGVFPSELPII*APAPFFF FQFFFFFFFFFFFPLQGXWQFDRD DABGHLASSRSPGAVFPQGMHTTGSTR RWGQCVFPFPTRP
13185	27086	A	13327	382	15	NWPGHCP/LHFQNMFLRKTQPIFFCLKNF FFFPKKVFPPEKPFLEKPPVPLN*K KPPPPFFQWQGGPQYCPFKKAPLPI RQKERFPLWKGQDFQICPPGPLKXXX RAAADLGTS
13186	27087	A	13328	2	220	GRVGSSRAVALVFFFFFFFCCFFFFF QNP/PLKRGKKKNTPLPKKKRPLRGQFK KQKEC*EKKKLSGPK
13187	27088	A	13329	427	289	IQLWSSL*K*LHTHTHTHTHTTTCFL TYMKELSTHPGNK
13188	27089	A	13330	203	269	INFGPPREPFGGNQKQFPSPAGFEPWN PPQGPKP*KKKKRKPFPVWAPGGSKV QNPGLRETGVFG
13189	27090	A	13331	216	418	DVPVHYCRLYKPC/LRLHSIVKQYLLW PGAVAHACNPTTLGGRLWIT*GQFEA SLANVVKPHLY
13190	27091	A	13332	160	325	WERQLFKIAQSGRLANLTPVIALWAE EGGLFEYTSIR*LWATQDPISTKMFK
13191	27092	A	13333	339	62	GMLPLFVPPQKRGSPPYCTGVYNSPPL KKQKFPSSIGLIVLPVITPPPPAPFF FFFCFFFTTTTTTTTT*RLMRMR FSCFLCP
13192	27093	A	13334	45	384	DSVRIWTLALLLIRIT*LPQWNGYI RKSTVYQCFDPISPARVPSIKFTLGA ITFLFDLEIALLLPL*ALQTTNLLPI GMASLLLIILALSLAYE*LQGLH*AE
13193	27094	A	13335	270	660	AGSRRLPRLVPGPSLWNSPLCRPVVA QCIRVSPLLTVGAVLRPGQCLDWPCLV YARLSGWTGVPCRYGKGCCDYGCCR FBSGCCRCDDRCRCGCGCCRCDDGCCR YDRG*CRCDGCGCHYGR

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13194	27095	A	13336	298	349	KTTFFPYGLRGSKTGT/L*CSGVITAIH*/SL KLLGSSDPLSLVAQAARTTGCACHDQLT NAFFFFFLERVPTPLKNNPFLWVGKVK WULD
13195	27096	A	13337	865	518	KSATRRRVSDTHKMPAWGGYSGLQQR GELSSLP*PESPPPLILFLKLP SNPL PCSPLPCTQGGQAPYVS IHTSLKFPN AKLSVCLSRATIFS
13196	27097	A	13338	154	354	FNLQVQPDGYFVLFTICHLPTDSKSGKA PGAPCHSRNPHIKRTLQWVQWLTIPVILA LWET*/FSHQENSGLGVAHCTCNPSLTGN QGGWLA
13197	27098	A	13339	262	11	QEHFSKLLTP*/KN*LSASSNSTHAYVA FPKAKHGPOLNSKTAP/LGTAEAHCPNPI LGGQGGQITRGQAFKTSLSANMAKPRLY
13198	27099	A	13340	358	164	TKKGKPRFFLKTSKYSRQWMAVPIBSG WBGEGGAFF*/TGRPKIWLTEVGPLP/NL GKKKENPF
13199	27100	A	13341	147	2	FRPQKVSVRVGLAHACNPITLGAQGH II*/GQEF*/ASMANVVKPSSC
13200	27101	A	13342	367	17	TSRSNWLPHVLVRFP/TALEDIRETGSFT KKRSLIDLTPYAWASFTLMEGKKQV TSSINGSRQKRSQS GELLST/PSDPSW AIIWLMPVFPALW*/SETGSLFEVRP/SRPA WPTW
13201	27102	A	13343	166	492	BGTGTLGGCITCLVRGALNLFHLKCS WVGWRGAICCMELRETAQKLSVWKLYP FEIVFSPSSNNPREGAVAHICNPNTLGG */GGRIARAQEFETNLQTVRPHLFR
13202	27103	A	13344	804	1124	TFFCFPFL*/DRVNDVAPWSSSDMIMG LQALTSWGSSTPPPTLQCSOLDLQDTW PPYPTSPFYFFLQGRGLTMLPRLVLNSC TQALLPQPOQRSKTPISLKTN
13203	27104	A	13345	280	448	GGGGRKKKT*/PPPLENNFSPFP*/PFP KKQIKPFPFP*/GGGGRKKKT*/PPPLENN NFSPPFPKPRKGIFFLFPPLSVVKKKG PPGGTRPLAPL
13204	27105	A	13346	232	400	AELRYCSCGHFL*/SMARYKTKPGVRNL TPVIPVFWAEAR*/LHEPRSSRPASATQ
13205	27106	A	13347	138	332	RAVVKSPSEIFYPFF*/RAHTF*/SCVCL GCVCVCVCVC*/THTHTHH/THETHDY
13206	27107	A	13348	314	395	WLGIVAHAYNPSTLGT*/GGWIT*/GPEV
13207	27108	A	13349	388	371	IMNGWQDKLVSRTVQTIKK*/KPRNRP EPRAPP*/WHERNGRKRERMEGRKERER KKGKGRKRRKKKACIYKVKIEISNNLA NLTINVER*/DERRDPDLSWVLSRRVSS VFIALVTCLTSQFFLSLHNLQILPLG KNL
13208	27109	A	13350	412	40	LVFRFWNCLFSRELFGCPSHLLTKSMSQ MNVVARGDIMYTFPDLFPKTKNNCKLW QCKRGSLHWCRRCKLVQPL*/RPT/R SLKGLGMLPYDPATSILETTPKRSKV Y*/RNICTSRGV
13209	27110	A	13351	372	148	FFFFFFFFFFFFFFFFHAGGCSRA*/D GVMLISGT/VPLLISTGVLTCSISD/GQ PVHTSLGNLVVPYSQRLPY
13210	27111	A	13352	209	206	KKKKNNFSPHGNKNGGPPFGGPPPP F*/TFFKGGGLPKGPPPGGFFWNPQNG



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13228	27129	A	13370	43	412	RPTRPKRONYGDSEINSGCQGLGKKGMN GKSTEDFEGSETTLYDAITVGTCHNK7I RSHIVYNTKSGP*HKLWTGGHDSV*V PQLRKTYHPGERCL*GRLSMYRGREYI GNLCIFCSLLL
13229	27130	A	13371	136	1	KSPTWFGAMAHTCNLTLEGGQGWIT*G QGFEFSLANMVKPSDAW
13230	27131	A	13372	228	385	GLLIHKLKFRKFWLGFVARTCNPSITLGG QGRHIT*QGFEFSLANMARPCLY
13231	27132	A	13373	277	429	LETITKAGLETTITSSGQMSIWFQNK PWDSKKLFNLLSTISSP*SSKNY*PWQS TVARTCNPSITLGGQGRWIT*QGBPEISL ADHWKPARVGRHVRGLQVS
13232	27133	A	13374	194	3	NQENYTYTHTHTYTHTYLL*LLQ WVYLAYFLCLSYPSLFAQPTHTTYTHT HMHTLL
13233	27134	A	13375	377	228	DRVLLLLPRLECRGITHMAHCRLEPLVSN S*APALSFQSAESTGVNPFVS
13234	27135	A	13376	255	465	NAWKCFPTTKTTPVTPLTHVSCCKPFRN RQREWKLPTRVRLPS*ALIFPVTCYIT SRWFETKDFQKK
13235	27136	A	13377	336	38	VWCTFPVPVATQBAEAVGGSLESORLRIQ *AVITLVNHEHESALASRRGPEETISVK PPLPTLIATHCPSLPRTQDITSRFLAQ RNTENNRLQMEARA
13236	27137	A	13378	376	293	FFFFFFFFFFFFFK*KLTKKKLLSSQ YI
13237	27138	A	13379	215	16	HLTNSFTTATEBSRTVTQHSVYRKALIG LGAVHTCNFSTLGGLRWIT*QGBYKG IPPHGLEDVQ
13238	27139	A	13380	184	64	VDESLEGWMDDEWMSQWRGGINRYMHA WMD*QDQWIGG
13239	27140	A	13381	233	417	LKPITWGRKPKGFPFLDPFKQKKYFNGP KKKKKKKKKKKKKKKASRAPE*KKG PQKTP
13240	27141	A	13382	34	360	RNNTTNADHLDKNTILSPQINLYLRON SSRLFCRH*QMSKSPVKIPAGFVLYI* IYRYTHTHTHTHTHDSLYMETHTIRMA NTIVRQNSLEHSYLLMLRMTIKLP
13241	27142	A	13383	214	71	QTLNDSGPGVVIHACNESNLGGHGGKI I*QGFEFSLANMVKRCLY
13242	27143	A	13384	352	312	DKQLTHRTDSLYIFTY*PQSCSEFIS YNNFPCLSQVLYLCPSLWTHTHTHTHTH THTHTHTHTHTHVSGRSLFSGSPHTE APRSRVSVYT
13243	27144	A	13385	393	271	IEGQIQYTSITGNKFRDFYLILCKEGIM SRKISFPSSCHLRQQ*RVRLRERDRRK RQRERQRE*GRSVLHPHT
13244	27145	A	13386	180	440	PVRRTLCEDILCFPSVLICQFHLLI QHACPKYKPNNSRFGSWGAVAHICNPS TLGGGGRWIT*NQSPFARLSNNVKKPLRY KNI
13245	27146	A	13387	190	47	EGRKVPSTLLQHTLLQTVAYPCHPST LGGQGRGASAGQE*DHLE
13246	27147	A	13388	188	470	ADFFCKGRDSSAGFPGFPSMSLGC WTRPEPPGRGFIQAVVRRESAQDWARP ELIKSNWNPGLVAHTCNPSITLGGRGNT A*A*EFENSQ

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13247	27148	A	13389	454	367	NKKKPPPPRPF*PPPPPLGRTPPFFKRNPN NPPRGGGNSPGSPSGFGGKGKDPFPGGF FPPPPYPRGGGNPF*FKKKKKKRRASLD P*NSSQPCPAYEKELNFPAPLATVTLPP GHSS
13248	27149	A	13390	34	354	HTLLALLLIITTF*LPQLNGYTERSTPY EOGDPISPARVPFSLKFFLVAITPLLF ELEIALLLPLP*ALQTTNPLPLVMSSLL LIILALSLAYE*LQGLD*TEY
13249	27150	A	13391	1089	792	THSPQVQVSPDLKQPKQKAMPFSPSLQ NPPPGQQSHSGAGGF*VPPGFRQPVMA SRNCLGLALPRTTHFSPGGTRDKPRTQ DRSCWRDPNGPOV
13250	27151	A	13392	299	428	WTRCRGRGRSCLPVPFSPAPALLSLDWD GTRRR*AGGGTQGGSGCMGAHWGLGG EGSGCRSQUALPREAAERREPKHGSIPIR H*L*TESLVSVEFRIA
13251	27152	A	13393	382	413	HGKTHLYKKFKPKFKFATMPA*WLTFTVT PTLQEAEEASLKFKSSRPAAVWTDPS LQKI
13252	27153	A	13394	64	401	GGIPKEDSQAGAFGTGERQQGLVPLL KNGQLSTDACVPPMGRVGVRRAGPPNQ AGEGGGGQGCBSLGLLPEANRCHFNPS TLGGRSQGLA*GQEPFSLGNTVRSQPY
13253	27154	A	13395	146	18	FSPGVVAHCNFTSLGGGGGTT*GQAF KTSLANTVKKRPQ
13254	27155	A	13396	1056	679	DIQVPERFL*NVPEPEARQEPFDRANGE HIDRDCRSDPAQKKRIPTNKCBRAGCR QRHMWLTCSRCSNFTCAHRHPLDHD CSGCHTFSRAGLALSRAQAVASTSTVP SPSQTPSCTSPSR
13255	27156	A	13397	440	423	THSPFTQRRV*QRRERERERERERERH ALAEHRNTRGISTGTTGERGNLMLVOH LGLPLSSRRLGFCPDGPGQGHCLAQGDQ VRL
13256	27157	A	13398	2	256	IRTLGSAVEFI*YENYTYQTLKKGNRNS HMQSQPNRKHIRKYIAANA*WLTFTVI PALWEARAGRSLESRSRNPVSTKKKTQK
13257	27158	A	13399	102	922	LSFFPLFSETGSCSVAQPEVOWCNHSLQ P*TPGQPSMQPOLPQBQOQRTAVNHGR A
13258	27159	A	13400	198	55	KDYSAVVHTCNFTSLGGGGWIT*GQRL KTSQANMVKPHLYGNPKIEF
13259	27160	A	13401	19	447	ESALNLPAGLIGVSHRTQPIFCILNAL ALGVLLILERSPLQSPQVPPSHSHYKPS LPSVTGRRGPRPRAARPTAQRRYRNS PVLLISPGSVHVASPALPAEP*TGAPST FPFCVLRPLLLGNMOLLCTKLSRRLPP VET
13260	27161	A	13402	93	410	DGNLNYSLFTHGRADLQINQVLTIPSTT AMFYHYCQPP*IVHGTINT*PPVYHON PIHITPSCIRASTAINLLSHLNCYS *ATPHLGYQOYTLPLTVHST
13261	27162	A	13403	55	387	SNSTHYSLKKSAGITKFNHNLVNCICI CQVVPLEMVRNRTVLCQYVVKPRILLY QHFTALLVLTTLFTLRPGVVSEACNPST LGGQGGRII*AOEFKISLGNIVRCLY
13262	27163	A	13404	39	365	SGDRRVRLKKLTTP*LSQNGYTERST



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						GWC
13280	27181	A	13422	604	1121	LQSGDLF*EINFLSSCSLLREKDFPTTIS GPQTDQPKKHLINFKSAPYKTIIDARLR VTILTVRAHLHPGRINSHVAHTKPVWWSL HTDAHEIWCRRSDSLKLVPTPLPLEAA LRNITHSLSTPPPKNFRFRMTSTLFCVI FLINIRRQEQASBPKPSHRIICDLHVY AQMA
13281	27182	A	13424	214	22	IRESSSTPSSPTLPESCNSIPFPF*KFI WSGVVAHAYNLANTLGG*GRKLARQRF NSTRAGLM
13282	27183	A	13424	397	330	SEYNSCS*VOMHTLVSAQAEAEAGS LEARSRLCALIIPVMCHCTPAMAFPM
13283	27184	A	13425	729	885	AKCYFVRNLSLAFGVAHACNPSITLGGQ GGRT*GQRFRTSLANNVKEPLY
13284	27185	A	13426	231	2	ASVFFKATLVDLHM*YIYTYIYTYTHI YTHTYTHIYIYTHIYIYLVNMQYICLV HINANQQQYIYIGRTICPF
13285	27186	A	13427	184	171	LS*YIYTYTHIYTHIYTHIYIYTYE QPSSQSS
13286	27187	A	13428	372	166	CRFRPRKINTTFSHICGS*RVDTLIEAA* HMLGTVAHACNPSITLGGQGRNTI*VWEF KASLANLLTPLLQ
	27188	A	13429	391	437	MYSLGVGFFHSTI*LLKDFWGSVVVHT CNPSTL*GQDGRIT*GRKLETRPGNRAK LYLYKKN
13288	27189	A	13430	39	254	EFIPRAQDLSTSQGNRVPRLYRKFKN *VWNCASVVPAMWEAEAGGLSEPGRLRL HSNMDKGRSCLKK
13289	27190	A	13431	336	488	DIWFGVVAHACNPSITLGGQGRIA*A*E FETSLSNWARPMLKKLARESGA
13290	27191	A	13432	154	481	FFFFFQKQKGF*KIYFFFKLGR GAIYV*PAILLPG*QKSPASPL*KGGK GCAPPD*LIFFFLKXKLPLLGQGLKL RALGKPPPPPSQGGINGVKTFFGL
13291	27192	A	13433	388	280	KSKLNGCCVALCLGLT*SVLLA*PKT *LFCVSLMDYIDTCSLSISIYLSIYLS IYLSIYLSIV*SVS
13292	27193	A	13434	187	48	SISSTKQPGVAHAYNPTWGGGGGRIT *GQRFETSLANNVKNPS
13293	27194	A	13435	71	309	DSVSESESEBEVLAHPIAAERYHCERA ET*VKALLMLELDCDERVSSRSUTREDC TRELDFLHARDHCVHKLFSNLK
13294	27195	A	13436	18	375	RPVAFGRPTRPINTLIGLLIIT*LP QLSGYIBKSTPYEGDFDISPARVPVFSI KFCILLAMTFLLEDLSIALLLPLP*ALQT TNLPLIVMASLLLIILALSLAYE*LQK GLD*AK
13295	27196	A	13437	373	27	THPTYSHQEQSP*PLTGALSAIMTSG LAW*FHFSTILLIGLLINTLITYQ*W RDVTRSTYQGHPTPVQGRISYGLLF ITSVFFVAGFF*AFDSSSLAPTQLGG HNPPTGITPLNPLVPLNNTSVLLASGV SIT*AHDP
13296	27197	A	13438	575	699	LGTVAHTCNSSSLGGRGWIT*GQRFET SLANNVKTCPKK
13297	27198	A	13439	247	168	LENGIYTRVLRHREKAKHFFFSNYSYS DKRTDTFLVLEKHI*HHHTHTHTHTHT





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13319	27220	A	13462	577	766	AQWHTSIVLAA*EAAAAGLLEPRSSRLKCTMIIPINSHCTPANQMRPCLLKRF SINSFISK
13320	27221	A	13463	206	387	VTVGPTFAEAGRGHLLTCCVTKQKWL GTVAHAYNPSTLGG*GGRT*DGSEFETS FLGS
13321	27222	A	13464	167	41	DFNLGAVTHACNPNSVGG*GGGIT*QGE FETSLANMVKPNWS
13322	27223	A	13465	480	79	SRVTSPLLLNSVTSKSLLPVSGQGS KGVVSTQERERLSFGVHGFTFGPCPLC VSGQPSLCPSPPTSPWNSLSQAPGSI RYLL*EPAATSAAPPALGLDPTAFPP PLLSRDQWNAAGRGQDRDKGLP
13323	27224	A	13466	3	373	DANVAEASAHASVCHITDFLLALLLITL TP*LPQLNGYIRESTPYRCGLRPSPAR VPLVYKFFLVATITFLLLDLERALLPLP *ALLTINLPLIVMSSILLITILALSLGY E*LRKGLD*AE
13324	27225	A	13467	214	55	TRQKIFNLFS*KKFLIPPARAKDFLEF IFFFFFFFFVFVFVFVFVFVFVFVFVFVF
13325	27226	A	13468	111	358	VMKVFTY*IGELVTQAYLFVKSHQLAHI LFHSMYVLP*IKMFWGIVAY*YNPSTL GGHSRRIS*AGRFETSLGNVSPHLY
13326	27227	A	13469	199	607	RIRGTSQKLLLLKLSLIPKQPTRGTP P*TTTPPNTTNPPPPVAATADDPSPA HFVSSPYMDLGSF*PCGSPGRQREI EQCKDKIQNFPPTTSRCSNDLSLKG SARRRGHLFCRPPVNGFRSPKPK
13327	27228	A	13470	128	256	EDNWAHLLFTITPQSVVSGSLRPSR SLO*AVIVPCTPSE
13328	27229	A	13471	94	388	KRGKTEELNSNRHRTHLCLLADLSA LPLHYYYYYYVWQRNSLPDQPGQGET PCLPKIQLINRAYNVPVVPDQREAR *LPEPHRQRSORPE
13329	27230	A	13472	359	73	ATEPGOLF*ESESINVTQGVQMLDH GSLQPTPTGLKPSFLIHTGITAASHYT WLNQLLMFNVSLLTFYESPOLIQRSHI LCNSIHIFLE
13330	27231	A	13473	332	10	ILSKRGFPKPGRYCEVNFLCQVQAK*V RP*EDTSLCHBIYHTHTHTHTHTN LKP*TSKRLIPQKTSLSLFLCLIKSLL RFQTFPDAGSTGNSVGCACFISK
13331	27232	A	13474	355	385	IMVCIKQSCVH*KIN*FWGTVAVCNPT RTLGQDRQTA*AGELKTSLDNMKPC L YKKFF
13332	27233	A	13475	297	425	RKSAWNTMPVVSPI*RAAGGFTLPGST RKAWNTAGDPILYKK
13333	27234	A	13476	160	1	KSTGRLMVAHICIPSTLGSQGGWIA*A QEFETSLGKLSLPHIQKASLIW
13334	27235	A	13477	334	79	QKSGCINLTKRGKIKRGKQASVLLI HN*KLNSNFK*LDATSI*YFQWYL NRPCWVAHACNPSTLGGKGLIT*QGEF L
13335	27236	A	13478	234	385	YAKPHVSINEKKPDVAHCNPOTLGGQ KMIT*QGEFKTSLANMTKPIY
13336	27237	A	13479	408	129	KRSINRKKGGELSSSIFLPLPDEE PPSPPFCPLPPPPPCPLPQSG*GAC GRLEPC*MDLGPCPCPAKVFVSHSCSL



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13355	27256	A	13498	164	22	GTRKRLTKSGVVAHAKNSSSLAGRGWGLT*QGQEFETSLAKMMIEPSV
13356	27257	A	13499	277	363	TYLCYIPNLCIFVGRIEQR*LI*PHRS TLNGHILYVRPSPNPSQAVASVPTCTY MPTWEVVESSQKK
13357	27258	A	13500	1	270	YTCSVLLLVTVNLLCLLYKLNFIIGML RKICTVYIIYRIEQYYLKQASTCCLGVY PTV*ZYMYTTYMYMYNYIIYIIYIYI, CLCLDG
13358	27259	A	13501	170	383	ILYSSKLTYPSPQIVIPFCQKST*GWVN WLMVPVPAI*EAEVGGSLSTSLGQANA TORKAPFFVYKEYKN
13359	27260	A	13502	31	402	GDYILYLRGQWGFARRKQACNLFPNT FTHILICLTNTRFSLAKSCERANET TDQNCVTKDLALDKVRLPFS*GQCKVI KGVVAVACNPSLTGGQGNITRGERPK TSLINMAKPYLY
13360	27261	A	13503	232	446	RNRFGAVAHACNPFSTFRGGRGRIMLGD *RS
13361	27262	A	13504	196	390	VNKARKKHLYPVARKILRPGVVVHTCN PSTLGGRGQWII*QGQFETSLPLPKTKK LACGRGCL
13362	27263	A	13505	146	7	LKYVLYWLGAMAYTGNISTLGGQGWIS *QGQFETSLANMVKPLCF
13363	27264	A	13506	177	18	SNFGRPRQQDHFLDRHSFETSLQEK VKCLTRHGQACVQQLERLERLDRDLGP GGGGCV*SVNII
13364	27265	A	13507	117	338	NKILKKKGGRGFKESKPTSPGLQNSF FMGPFKINSBAGV*QRREGKNLGVPLK PFEANPLFARGPWTKNF
13365	27266	A	13508	306	443	LARYEPAVKTTAC*ACQLIAVIVPL*EA EAGGPLAEANLIRPAMAT
13366	27267	A	13509	146	390	KMKKHHQSAHKKKKYKGRGPKSKPTS ACLQNTIFLPFKPLNSBAGV*CRDWK NPGVQFNRPFEENPLFARGPWTKCP
13367	27268	A	13510	119	356	NEDNLEGGCGXR*LLRTGVCSNFAGN SGIRNCESGGLPMRVVGTESVLSGL FVCCVFAQEKAKATGRAEVSICP
13368	27269	A	13511	221	21	EDLQDKPLGSCYSTCGWAKQWYLQHG GAGSKCRINWLGAVAHYNPSTLGGQGRN IT*GQRFSL
13369	27270	A	13512	163	418	TFPDDQCLMLQDHACVKSIIQSA*YLP AVLAHWEAKAGGLLEPTSLPAMAT
13370	27271	A	13513	239	21	FGNLGGPGGTACTQPSLGNIVRYPYTK TKPKPKPNQNTKIS*ANNMCPIVPATR KARVGSLEPRRSRLQ
13371	27272	A	13514	135	11	KFFFWPQVLAIAHYNPSLGAQGGRI*G QRYETSLANMVS
13372	27273	A	13515	162	57	BGLTSSRRPPLGGWVT*QGQFETSPANM VKKCLY
13373	27274	A	13516	424	54	PKGKFFPTPIWVVPVPLVPPFKPKPFR IFFLGPPKKKFTSPPLKLIFFF*KGPP FFFFFFFFPPFFKKKKXLLGGFFFF FNAKPSFLSLFFFKKILPLYNNIMHK DSKAVILHHH
13374	27275	A	13517	310	349	GGPLKXGLFFSROGERFFFF*GAPPPF FFFFL*SSKIWFPLKSPFFFFFFPFC FFFFSQILLFFISSPCVFFFLNYSRT

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13375	27276	A	13518	273	393	CSYVCAILFLKFGNTYSRKARHILW IKLSYRKATTLGGQQRWIT*SQBFET SLSNM*KPOLY
13376	27277	A	13519	450	139	IPP TALVSPFAKHTNQQQGLVRRSSKG NNMSKGWELIHPSRI*FCSNHTLRLIALW LGAVVHTCNPSILVGRGGWIT*GWBFKP SKTSMERFCILSRHKTRGOS
13377	27278	A	13520	47	427	KMKOLFEMLAVQNTITFLSHSIFRTIR* LITLEPLMFRYYFEQ*RTLLPPKF*DRVW LCHAGGCL*CSGTVSAHCNLRLLGSSDP STSSAS*VAGTVQAGHIMLILNNRELPL QKFFIWSRNLFFP
13378	27279	A	13521	199	98	SLFSVKLSY*CEEFPEDIVSKDPIPVVLE VVKRESCLCALPNLLK*EKNIQVP* VFSTIKAKAQIGKVAHACNPSTLGRG GWIT*GLR
13379	27280	A	13522	314	18	QTLNFYILKTYNLSLWVC*IFEARFOI LV*V*NYPF*SLICPTFSWHTQNT** KNLIIWAGAVAHTCNCTLGDQGRILAL AQEIEPSLGNLALQ
13380	27281	A	13523	18	231	CPFAVFGTSLRQYQLRYDLD*KIGQAW WCAPVIPQTQAEVGGSLRISRL*CAM STSMNRHCVANAT
13381	A	13524	239	463		RVOVSECLLHREKCLYFQIGLS*LIPQT GWLKQKLPQTVAHTCNPTLARGRKRI T*GOEFETSLANI*VKPRLY
13382	27283	A	13525	388	468	SLRLGTVAHTCNPTLGG*GGWITRSG
13383	27284	A	13526	342	369	CTLNLTLLYSISDPGVSAFLATGGDITR NKVRKT*LRIGTVAHTYNPTLGGQGR LT*AOSEFKNSLNGRPHLYKTKTKTKT
13384	27285	A	13527	241	231	EYVCINSHSSLYFSSSLYIHM*VCVCVY IYVHTNSHIYTHMYIHTHTHTHICIYKL BEKYKL
13385	27286	A	13528	241	231	EYVCINSHSSLYFSSSLYIHM*VCVCVY IYVHTNSHIYTHMYIHTHTHTHICIYKL BEKYKL
13386	27287	A	13529	34	299	SAPASASPWIGVLYRPLACPDARFSPG PEANCGEIEITSLRVTLSRLECSGTIT APCSLDLQGSRDPPPSAS*VSETTGASH HAQL
13387	27288	A	13530	158	45	SGHRSRARNL*PVISALNEASAGGSPFI KSLRNRRLPG
13388	27289	A	13531	342	1	CPFLKGAPPPPPPPPPPPPPPPFLVGTD KLILKVTNKNKGPKIDKAV*KNKNQARG LP*PDIKI*FYKWLGAVANAYPNLNGG *GGWIA*E*EFETSLANMTKPYKYYK LA
13389	27290	A	13532	589	742	RIMKMLRKKICGTGGMVAHAVNPSSLG DGWIT*DOSEKASTANMIKPHLY
13390	27291	A	13533	74	446	HVGLPSRLTSSVSHPRHCKHPRTESEHVY KILARHFOCKVSRPSDAGSSEGRPRDM TQTFVADTPPHLSSITATRTMTATIGV GVVAHAYNPNTLGGQGRRIA*AOSEFKTS LGNLAKPCLYKH
13391	27292	A	13534	1941	1040	APHLLPYLSSGGFYCSLGPCLGLSSHNA AMHKEPLHNA*SDRPSAPIDQIGLSPS ATHDTHRTLHICKSIFKSRLEHIEKER ETDS*RG*NTQR*VERSEANENYKPTIEI



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13406	27307	A	13549	321	2	QSVSTASWYTLQNGSRH GLWVVTHEGYDRNLGYFD SQASVLSFYT TA*MVQ*LQLPDKVQIYPARFLFINDMP P*WLLKLP SFPGPTVAHPYNNVTLGGRG RRTTRDRFETS LANVVKPHLH
13407	27308	A	13550	216	13	GYS GKETV FSKMRKG QSGFCIQGPSIFM GKAGINQI I PKPTT LGGRGW IA*GQEFK TSIANTVVKPCLY
13408	27309	A	13551	199	391	KDPSIF IACFKRP FTTGSGGQEWLIFP HAYNPST LAGRGRIIT*QGEFLTARIG NMVKPCLY
13409	27310	A	13552	70	239	ATCVKN*RTSNAWVCVTPVATHERAAG GLLEPSSRLKCSVLAVERHTSVWTT GQKQNLFPVITFALWZAKGSGFAPSLR LA*ATVPGNWFKAHSLLANLFLP
13410	27311	A	13553	105	257	Y*HESHPVTCGLQWCSLGSIQAPPEV GGWLELGRQLPKWKPLAP IWTPESG
13411	27312	A	13554	499	165	YTDKIRSTSLLEVKGSTHSMCPVKFTQ LQKAGGIHMAKLSGQVRDREMLGTVAH TCNRSHLBKGGQIT*AVVFTSLGNMA KSCLCCKYQKLSWVQH
13412	27313	A	13555	415	719	DKVSLCHFGWECGWVSQLTTASISQG* TILFPQSPE
13413	27314	A	13556	224	523	QVSLQLPFCVLFQPHYVNRQAALLGRCY VSATNLLINAIWQVYNSLKMCEENQVNS LQNMPP*HRNYFGRAGHGGSCI*SQLIG RLRH*NCINLGGGCGSELRLRHCTPANA TKASPS
13414	27315	A	13558	355	1	KYVPHKGKISERRLCSVAQAGVQWCDHG SRSLFVLGSDNLLASAS*VAGITGCMGS SDPHTT
13415	27316	A	13559	73	259	VVKISLDFLLGDAKKAQYQSDIKRLRLG RGAVSHTCNPSTWGRGGWIT*DGFEFT SLPKC
13416	27317	A	13560	205	21	LMALLPGSSVDVLS EYGMHFNFNVLIS KEYPILFLFF*DGVSHELLPRLCSQMSIA YCHLCQGSSDRDFLKQO
13417	27318	A	13561	254	481	TFFSPSMFVRPGPYTDAQGVRLFTGA IIVHCSLKLALLSDSPAS*VTATGM PPHLAFTVK
13418	27319	A	13562	174	369	LFSKAGRCYLQNLQCMWSGKCMWPMRGI DVTREYPTFLAHRVLTAAATSGSDFLQ AQWLMPIVPAI*ENAGGESLEPKSLRLA *ATVPGPRSLSQTLHRSLEGL
13419	27320	A	13563	371	109	RQLAAVHLVPLPDRVTWAVVTSLEL LGSSENGVMNDNTHFGLLLRDYK*GNV *WLPVPI PALWEAKVGRIARGQLENSL GSKARPRV
13420	27321	A	13564	206	486	SRVRCGFPFNLKPKSSCI*BOGQAVAH CNPSTLGGSGGQIA*AQEFKTSQGNVAK PHLYKI
13421	27322	A	13565	212	398	YSPVHDKCSGVKLGLEFFFFFEKGFH FSPAWKARAKIGLNCITLQCKGNFAP KPKKAGKGRAPQPKLLNFKKKGKGS NGAKVNPFGPKGNPPP*PPKGAGKKG TPRPGPFFF*F
13422	27323	A	13566	26	395	ATRVSLAPTKNKINWGWKPTVPPQGE GEAGEFL*PQKMRVRLNKVLPSPRPD
13423	27324	A	13567	400	195	

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13424	27325	A	13568	316	154	KTRLCPKKKKKN SQPPFGLRWEDRLSFGVQNPQKQ*LMNV IPAFSGARVGGSLPRSSKPA*ATNNLK SKVIGGGICDCKASKVSVESNMGWGC
13425	27326	A	13569	297	475	FDFYFTY*ETKSHSAQAQGV*CKHSSL QP*PPGLRQSLLMPPPKSAGLTGVS YGT WPI
13426	27327	A	13570	116	332	NRVLLLPKGEYRGTTISARCSLKLLGSR PPTSAA*GDETTTGVCHRTTPV*FLKTFP IELRPGTVPRVGHWRP
13427	27328	A	13571	233	405	TVPELRASCKLKKKKKKKGEKNLKKIK GFFPGGPRV*GPEAKNPGGGGPGIPKPG G
13428	27329	A	13572	408	3	TFCDYFKTPPPKGFPPFINGPSPFLMRG PSFFFFPGFPFPPFLKNFFPPIVVRKGG GYKRGVFPKKKGGPPQLFPFFFFFLI* KKTRPGTVAHPCNPSTLGGQGRWIT*QG EFLSLAKMAGRVVRPGNCESV
13429	27330	A	13573	273	406	IKFELAEKRGHS*NTSTFGQGRVLA*S QEFETSLLNMVVKPHLY
13430	27331	A	13574	385	38	KRNSPPPPGKRNFFFF*GPPSPFFFF FFFFFLLGKKKT*FFPPPSRFFFLKP FPPKNQGPINFP*PKKKLGD*ARPPPLT GGARGAPL*FKKKKKKKLIVRPGAVART CNS
13431	27332	A	13575	230	53	HWVLKKNKQIKPTKISFMDNAIKDSVGG AQWLMPVIPAL*EPDMGGPVPEKSLRPA WAT
13432	27333	A	13576	406	33	VNSIVNVSPFPRVSTTIFPPELKSQSVT QAGV*WHDLSLLQLOTPGLKRPAPSRG LSFTYLLSIFYPHSSQTELFPVGTIAASFP TNSRLLYLSLLCGKHPLVPSLPLSTI WYFSLRVSHHFP
13433	27334	A	13577	426	294	GGFSPPPVFKPPQPPFFFGDLKKISPP PPGKKIFF*KAPPP
13434	27335	A	13578	268	3	LQAKGPAMGEARGCSSEVNGIPKRGFD L*VSR*PSFDVSHVIGRVQRLMPVVPVL WETEDAISFPCSSRPANASNKTYIQK PQRI
13435	27336	A	13579	395	49	EKKKFFVCFPGFGNPNFTSTQFF*KGL ISPSGLSTRGFFP*RVFFFLKQFP LSPRVENCNGLIPDP*PPGGEVTSFQVA GAIGPPPPPRVNFYFVKGGFLNVGDMF FFF
13436	27337	A	13580	68	466	GASPAQGSTLHLVLPRYFKPIPTVTRTE SFSSGLVNTSPPELHFLPLINKERGPGIP LPCQLLVIGSTSLPFFSLPDSQDK WPLKGVPCHLVGS*PLCEQWPPSPHW IPLMPTSKSLQAPPMNSA
13437	27338	A	13581	67	249	ATAPGLLCSYKIFSGQLQWCVPTQLAN ETRAGGSLKARSRL*TMITPVNRCI LAWAT
13438	27339	A	13582	359	3	QDSQNVAAAPASVAVSTCNRGPLPWS GGQNRGKSLPLQVHRGA*GTENKQGG TPRPGGGPGPSAPRGSSLGARHKLPHH TTLSSSRSLPPTNIPAPSFPCTEEF HRTREI
13439	27340	A	13583	174	1	FFFFFVETESHSAQARVLEYSGAIFAQ

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						CNLDNLSSSELPAAS*AS*VAAXTCT*KR
13440	27341	A	13584	192	206	LPFLVSGSCYVAQAGPEFPGSGHPLSA S*VVGSTGVPHETQLV*SFSSLYNLERN C
13441	27342	A	13585	244	28	KKPENQENIYFYHLNVEHQIRISLGP GAVAYNCNPSTLRD*GGRIT*AQEFKTN LGNMARPRTRGSTRTF
13442	27343	A	13586	312	701	RGPEET*PTRKSSPPTFRSCESVS KLA RPPRCSSAAQVPRLSLRSPKPPPRV SGAEKCAPLPLPSCSETOALPRNSFLC QNASPLLSLGLPSPPTQALQPRALHQ HLGSTNKEDAHVAPAKKK
13443	27344	A	13587	410	292	GYMIKQQTIVYHECRN*ANSHLHLPPEGL LRAVTLWRRAP
13444	27345	A	13588	428	36	TPPPPPFFMAQKKKKIIPPPGSGKIFPFL KGPPPLFFFFFFFFFFFLLKKFFGLK GPFFFPQD*QLENLKBSGLGWEKLFGR ALLPQORSFVPGLGPTRLFGLVFWFFG FFFLPGLGCEFFALLFNC
13445	27346	A	13589	3	364	TAPDDQRPVQAGEPAHVRAADSTHOLG A*RRVAGHLPPRVGADPHFGASSREGAP PLHPPNLI*HRRPNSGCRFLPQPAAPPQ GAEGRGRDRRGTHSVAQTGGPGFGSG VTPSWRSS
13446	27347	A	13590	778	910	DRIRSGAVAHTCNPSTLGGGERTA*G QEFKTSLGDMVRFCLY
13447	27348	A	13591	230	3	KLVNILVERSLVANKSTVSEGRNVI RSP ASLGMVANTHSFSTLGGQGRQIA*AQEF ETTLQNRADCLYKKHSVY
13448	27349	A	13592	223	340	LFPITIPFWESVVGSL*LTGPQAVTHA YNPRTLGIRSGRIT*GHEPTTILSHMTK TRLYHELL
13449	27350	A	13593	35	220	DRABLSPRLCESTMTVAIKS INLGSSED PLTPAS*GDGTTDTCHHARLIFTGADFC IDASS
13450	27351	A	13594	87	369	NVOKTECEISGKNQIQKGSVTRKCSNG LNFNPFISKKIASCKIKGLTRE*KYKSQ ARWCTPVIPATEAEVRGQLEPRSLRPAN ATYQPHFKS
13451	27352	A	13595	261	489	SWVNERNVVG*KHETSQAQWLMTIPA LCBAEVOGSLARSWETS LCNIVRLHLS KKKRGKORKRGONQIAPSR
13452	27353	A	13596	238	2	NDCLWNLFRIPANVSTFGLHMSLKANT PGNNRFXSELGTGRLHTCNPS ILGGQG GWIT*QGEFVTS MQKGSVAVNQ
13453	27354	A	13597	36	687	RDVHSTYQAGS KQDWGPGAEARLS SSR RGAYS CPVPITTAEGKTRGRDMLLIL GLSWGSPSLTLLPITNAIRPPEM*EPAL PONS TS*SGARFPQGGKK*EDGSEWSE CZCSHSPSSSGPNPSPSPSAVCLPGLS GLQR*PKQLSPPALSLPVSSLLVLSLSP WPPTSSHLLPQALPQSLHQQGSHRAVD SFSM*GMVLSRRNRDCTRA
13454	27355	A	13598	367	468	KKQRRGEPWLTPAIPALWKAQAGSP* VQSSRP
13455	27356	A	13599	183	380	IT*SMIAVINSVVEKTCQPMIRISRPQAV ARTCNPSILGGQGGLIA*VOEYETNLGS



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13456	27357	A	13600	161	657	MAETHLYKN LIQGCWCSLFFSTRVFLAIGMKSQWCR PVAMD LGVYQLRHFISPLSLSLGTENA SVRLDNSSGASVVAIDNKIEQMDLVK SHLMYAV*EEVEVLKBOIKELTEKNSQL EQENNLLKTLASPEQLAQFQAQLQTGSP PATTQPGTGTTPPAQPASQSGGPTA
13457	27358	A	13602	121	423	MIRVNSFGLVLYSQVYIYIMRYTYTAY LKDFFKDGVLTRHPRMNTVTTCQSLBI LGSTDPFASAS*ANGTTNTSIEHGQLYSY FKIKRPTYAEMEQYKIKK
13458	27359	A	13603	1889	1717	VFRIRPLSWTPPSSI*RPKPPSPSTSHF GKPSMGPPGLNRCVPVQALLPGWYQHCG R
13459	27360	A	13604	81	267	ETCCTIGDTLTK*YTSQMLWCKPIVPAW QAEVQGSIDPRSSSL*CMMTISVNNHCT PAWAR
13460	27361	A	13605	267	418	THASGMVTHTCNPGTLRVASGRIT*QGE FKTSLGNIRPHLYKIIINKYI
13461	27362	A	13606	428	24	CPRSNPRKREPTLKSEPIITLPIITGLIL DDGNSPTAAAGSVFASTLQPCCSLCC* VKSSPNWPTASLQPPFGSAQTLPVRYAL TPGPSLVSTSLGPRLAPGLPGSPSPSP QVTLDSERYPSPTCTPAFALED
13462	27363	A	13607	267	442	RPPPTLKVPWLGVVHACNPTLGLGQGG SIS*AQKLENSLSNIIIRPHLYKQKQKQ KK
13463	27364	A	13608	3	280	YRLSVICEDPMREREQTCFPFPSPFPN RYCSTRLDGMEGSQGD FRKGFFA*APCR SGGWRGCCSPAGAPGSLGSGSGGPGV SPWQKRS
13464	27365	A	13609	291	248	EKAHGSQPMKGRRENSMCKSSSEFRVVA HSLAGVKDGGK*GSGAGGSPKLG*AV* LDPEHAGQAVFCGEAGARTQIGGKGR RDOAPLPLSPNLCGSGCLPTKHSARM P LRVKSYSQAQLGRTTCTRPSPTTTFDS S
13465	27366	A	13610	267	3	HTDLLYNTPTHTISPRCDPRHTATPCKQ SLLFFFMESCSVARAGVVRWHDRLSLR FLPPRF*KFFCCSLPSLVCGRGRGSSQT YTS

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13470	27371	A	13615	197	428	KTMVGLKTSASFHQDPFIQLPLNNHLSVP *TMLGSGRFLFPPTVSHI CNPSTLGG RGGWIT*QQEFETS LATWKP
13471	27372	A	13616	445	550	YSTTRGRARMLTPVLLVWEAEAGGSP* GRSSRLP
13472	27373	A	13617	3	435	TWVLSPADKTNVKAAMRVRGAHAGEYGA EALERMPLSFPTTKTYPPHFDLSHQAQ VKGHKKKADALTNAAVHDDMPNALS LSDLIHAKHLRVPVNFKLLSHCLLVTL RHLPAEFTPAVHASLDKFLSVSTVLTS KGR
13473	27374	A	13618	719	918	CEGRREKWKIGRERKGRGRKGEQMORE GKGRCEGRKKPCTSRPSSSRDRSNII ISKHASAVEA
13474	27375	A	13619	847	938	HLKPAVPALLEAEVQISLEAQSRRPWA TQ
13475	27376	A	13620	349	409	NLWSHPGAAVHVCNPSITLG
13476	27377	B	13621	25	189	MVLSPADKTNVKAAMRVRGAHAGEYGA ALERMLCFPTTMTYPPDFDLIHGSAQ*
13477	27378	A	13622	142	356	RIVENEKINAEKSGKQVLDLSIPRAY LDQTVVPIILQLGLAVLAKERPNNIEFL ASYLLKNKAQFEDRN
13478	27379	A	13623	18	1353	AGAAQCEVVSAGEAGARTMSEADQLRQR RPLRPQVVITDDQQAPEAKDGS SFSGRV FRVTFMLAVSLTVPLIGANMLLESPID PQPLRQISGIALFCSFKPEPLLLGLVLP NTKLQAERLFENQLVGPESTIAHIGDVM FTOTADORVVKLENGE IETIARFGSOPC KTRDDEPVCGRPLGIRAGPNTLFEVADA YKGLFEVNPWKREVKLLLSSETPIEGRN MSFVMDLTVTQGRKLYTFDSSSKQR DYLLVMESTDDGRLLLEVDTVTREVKVL LDQLRFPNGVOLS PAEDFVLVAETTNAR IRRVVVSOLMKGGADLFEVNPMPGFNDI RPSSSGGYWGMS TTRPNPGFMSLDPLS ERPWIKRMIFKLSQETVMKFVPRYSLV LELSDSGAFRRSLHDPDLVATYISSEVH EHDGHLVLSFRSPFLCRLSLQAV
13479	27380	A	13624	18	1353	AGAAQCEVVSAGEAGARTMSEADQLRQR RPLRPQVVITDDQQAPEAKDGS SFSGRV FRVTFMLAVSLTVPLIGANMLLESPID PQPLRQISGIALFCSFKPEPLLLGLVLP NTKLQAERLFENQLVGPESTIAHIGDVM FTOTADORVVKLENGE IETIARFGSOPC KTRDDEPVCGRPLGIRAGPNTLFEVADA YKGLFEVNPWKREVKLLLSSETPIEGRN MSFVMDLTVTQGRKLYTFDSSSKQR DYLLVMESTDDGRLLLEVDTVTREVKVL LDQLRFPNGVOLS PAEDFVLVAETTNAR IRRVVVSOLMKGGADLFEVNPMPGFNDI RPSSSGGYWGMS TTRPNPGFMSLDPLS ERPWIKRMIFKLSQETVMKFVPRYSLV LELSDSGAFRRSLHDPDLVATYISSEVH EHDGHLVLSFRSPFLCRLSLQAV
13480	27381	A	13625	1	384	QSFROTGRKREKREKMSLSDHMLLAKL ADQPLTPKS ILRLPETELGEYSLSGYSI SFLKQLIAGKLQESVDPDELIDLYCYGR KLLDQDTLDVYGIQPGSTVRLKSNPE

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13481	27382	A	13626	980	1089	PDQKPEPVDEKAMRD KRIRIQLTGGLYVPPHPIPPQSPPIPP RPTSPTRT
13482	27383	A	13627	116	587	VGCELRADSWPVPSQPBQNSGFQKQAFI WPEAPSR SARLPITYTDYDSRLQTOES QMLGSMARKKPRNTSRLPLALNPLKSKD VLAVLAERNEALVPVGA/VPEPASPGSSE IPATTSAYLIERELKPKLRKKQELAKHF QKQVKYRVNQITLRKQ
13483	27384	A	13628	150	484	VAPQASRGVRKTEVGBQQQGTACGGC GHQCTPPTWHLQRAHCVPSTCGAGGHL QQRASCRAPSPQSQVQYQTVGRQDHPH GVGRSSRGELAKWSFTHGLLVYCNPL
13484	27385	A	13629	330	397	ARCBWLPVTLAWARAGKSH
13485	27386	A	13630	10	137	SPTGAVLLTLARGTLSSLLFLANSNYE RTHNLLFTLNDFFPS
13486	27387	A	13631	380	98	FQWLVSPFTATLWFERDRKKNKTEREKR AKGERGDRKEERREEGERGRRGERS DKREPKKKSKEENHPKVVKFSFICSFC FLTPTFPVVF
13487	27388	A	13632	56	827	PLFEAPTACGPNVDCGLLHPPEETGLQ PISSDYIELLQSGELKRCPSGDMKQWI VPCLSCSDNRTCDWREITWQHNCQYGV LTKPOLQQLCGRKLIFIGDSTNRGIMY YLIERLNRTLQRWQVHGTFYHNVNGG KTLISYSYYPQFWISPSLRPTFENALEH LLQRSRPLENTGQTVLVGVQWLNNSNH LQIHKVLKSPFTTLNQPVTKSCLQAIY FPFLSPTLHNSNCLDLVYSFTYSFNIYFV VGFN
13488	27389	A	13634	3	2718	SGPGRITVAPLLERAPVHECVALLPFD STMKKPDKKDESGGOSNPQGLEKSA VLQEARVNIETP INPRAKAILTKLILYL INQGEHLGTTTEATEFPANTKLPQSNPD TLRMCYLTIKRMSCLAEEDVLIIVTSSLT KDMTGKEDNYRGPAVRAQCITDSTMLO AIERYMKQAIWDKVPVSSSALVSSLHL LKCSFDVVKRWVNEQEAASSDNIMVQY HALGLLVHVRKNDRLAVNMKISKVTRHG LKSFPAYCMMIRVASKQLEEDGSRDSP LFDFFIESCLRNKHEMVVERASAINVLP GCSAKELAPAVSVLQFCSSPKAALRYA AVRTLANKVAMKHPSAVTCMLDLENLVT DSNRSIATLAIITLLKTGSSESIDRLMK QISSPMSIISDEFKVVVVQALCALCQKY PRKAVLMMFLPTMLREGGFPEYKRAIV DCILSILLENSSSKETGLSELCEIEDC EPTVLATRIHLALQKQKPTINPSKYIR FIYNRVVLEHKEVRGAVSALAKPQAQN ESMLPSILVLKRCVMDNDRVDRATF YINVLEQKQKAINAGYILNGLTVSIPGL ERALLQYTTLEPSEKPFDLKSVPLATAPX ABORTTESTPITAVKQPKVAATROEIFQ EQLAAPVEFRGLGPLFKSSPEPVATES ETEVYIRCTKHTFINHMVFQFDCNTLN DQLENVTVQMKPTRAYVLCYVPAECL PYNQPGTCYTLVALPKEDPTAVACTPS CMMKFTVKDCDPTTGETDEGYEDYVLR

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13489	27390	A	13635	118	629	DLEVTVADHIQKVNKLNFPAANDEVGDE FEKEETFTLSTIKTLEEAVGNIVKFLGM HPCTESDKVPDNQNTHTLLAGVFRGGH DILVRSRLILLDTVTMQVTRSLRELPLV DIIILASVG LWALQLHPPELPSPRRGTGAAGVVTGVA MIRFILIQNRAGKTRLAKVNYMQPDDDEK QKLEIEVHVAVTVRDAKNTNPFVFRNPK IIVRRYAGLYPCICVVDNDMLAYLEAI HMFVEVLNEYFHHVCLDLVFNPKVYVT VVDNFVLAGEITRETSQTIVLKLQLMLQS LE
13490	27391	A	13636	57	221	LHHCPTPMAEVEETLKRQSQKGVQGTI VVNTEGQNEPLHGCGDRSPRPAQGPC
13491	27392	A	13639	344	544	LSQGHAGALSSLVHVLCLLSQQLLN VLVTVLAIHFGKEPTPEVQASWQKMTVG VCSALCFRYH
13492	27393	A	13640	319	623	DNEEASEGGGNDVRNLQSEVGVKNTM TONVERILARGENLEHNRKTEDLEATS EHFKTTSQKVARKFWKKNVNMIVLCVI VFILILFIVLFATGAPS
13493	27394	A	13641	2099	769	TRLAGRVSVASRCPRAVGGLLVERSK ARRPLLESRVMAAVPELLQQEEDRSK LRSVSVDLNVDPDSLQIDIPDALSERCKV KFTVHTKTLTFTQSPFSVTRQHEDFV WLHDTLIETDYAGLIIPPAFTKPDFDG PREHQLGRRGSMTEEFAMKQSELE ASTYLAFFKTVSSSHVPLQELSSPVL KDRNFHVLFYDODLSVRKNTKEMFGG FFKSVVKSADENVLTGVKEVDVDFPEQEK NFLINYNRKEDSCVKADEMTRSHQNV DDYHTAACLSLALBEPTVIKKYLLKV AELFEKLRFVGRVSSDEDLKLTLLRY YMLNIEAAKDLLYRRTKALIDYENSKA LDKARLKSQDVLAABHQEQCKFSQ SESAAKELINFKRKRVAAPRNLIEMSE LEIKHARNNVLSQSCIDLFPKN
13494	27395	A	13642	210	772	SVMVRYSLDPENPTSCRSRGSNDRVH FIGNRETAQAIKGWHIRKATYLLKDVTL QKQCVPFRRYGGVGRCAQAKMGWTOG RWPKSABFLLHMLKNAESNAELKGLDV DSLVISHQVNAQPIRRRTTYAHRGRIN FMSGCHENLTESQIVPKPESSEVA QKKIKSQKLLKQKLR
13495	27396	A	13643	168	2172	SPLCRVSVPSFCFRVCKKKKKHKSQKH LYHEVVRKPKLVKLVGNGEVTELSQGS SGHDSLSFEDKNDHDKDRKRRKRYG EKQIPGEEKRRRRRVKSDKKRRDRRV ENEAEDLQCHAPVRDLDPPEKPLTSSL AKQEEVEQTPLQALNQLMRQLQRKDP AFPSFPVTFDIAFGYSNLIKPMDFSTY KEKIKNDYQSIIEELKDNFLKCTNAMI YMKPETIYYKAARKLLHSGNKLISQERI QSLKQSIDFMADLQKTRKQKDGTDTSQS GEDGGCWQREDSGDAEAFKPSKPSKE NKKDKNDLEDKFKNINLEREQQLDRI VKESGKLTRRLVNSQCEFERRKPDGTT TLGLLHPVDPIVGEPSYCPVRLGNTGR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,915,126	Predicted beginning nucleotide location corresponding to last amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						LQSGVNTLQGFKEKGRNKVTPVLYLYNG PYSSYAPHYDSTFANISKDDSDLIYSITY GRDSDLPDSFISIEKATQDQYPYVMAD SLLDVLTGKGSKRTLQEMENSLPEDEGH TRTLDTAKINEQITTEVPFGRIJDSSTQD RLIALKAVTNFGVVPVFPDSEBAIIFCK KLDDETRLLRELQEAQNERLSTRPPFNN ICLLGSPSYREMLAEQVTNNLKLAAQQV TFQDIVSTGVKRAKGISIFSPFMEHNF VLDLTDTEPKKTDVABQCPGOS
13496	27397	A	13644	1032	207	FADVTPKPKATKAVQSEHSIDAPWSTNIV ILASGACKLLDLSHSYCPSSRQNKSGOV CCLREQVBEKNGELKSLRQRVSRSDSQV RKLQEKLELRRVSVYPFSSLLSPSREP PKMNFVVEPLSNMMLGTWLSDFPAGATTY TLQPFQYLEEVHLSHVQPMNFSNFSF HPDTRKPMHRECGFIRLKPDITNKVAFVS AQNTGVVVEBEGEVNGQELCIASHSIAR ISPAKEPHVEQITRFRNLSEGLSQTV SMAITTPQMTQHLHVTYKKTVP
13497	27398	A	13646	148	380	RGSWREVTESASLPSRQAGKMRGLCCC CCCCCCCCCCCCCHCQHQGDGLKQADL WRSRGTQNGAQIQWQHQTLES
13498	27399	A	13647	2099	769	TRLAGRVSAKSPCRGPGAVGGLIVERSEK ARRPLLESRVAMAAVPELLQQEEDRSK LESYSVDLANVDSLEGLIDIPDLSEKRV KFTVHTKTLTLPQSEPSVTRCHDFV WLHDTLIETTDYAGLIIPAPTKPDFG PREKMQKIGEGEGSMTEKPAKMKQELE AEYLAVFYKCTVSSHVSFLQRLSSHPVLS KDRNFRVFLYEDQDLVSFRNTKTEHFGG FFKSVVKSADENVLFTGVKEVDDFFEQEK NFLINYNRIKDSCKVADKMTSRSHQVA DDYINTAACLSLALREPTVIKCYLLKV AELFEKLKRVGEVRSDEDEKLTELLRY YMLNI BAAKDLLYRRTKALIDYENSNA LDKARLKSCKDVKLAAHQAQCECCQKFEQL SESAKHELINIFKRRKVAAPRINLIENSE LEIKHARNNVSLQSCIDLPKNN
13499	27400	A	13648	1	1206	MSTSQSPCRSICHVYTSDEKSNFTDNLK LNLKRCVLLWYFAPQSGMLKAKKCCSC YTVSSGVTEOENACQKGVKLNADGARI RGTGPRGRRAEAEASSPAPAAVAACV AAAAASRQLASGNRTVSSGV/PAPAFILG TMNPNCARCGKIVVYPTKVNCLDKPHKK ACFHCETCKMTLAKNKNVGYEKKPYCNA HYPKQSFIMVADTPENIRLKKQSELSQ VRYKEEFTEKNGKGFSSVADTPELQRIK KTQDQISNLKYHEEFKSRNGPSQGBGM EPERRDSQDGSYRPLEQQQPHIPTS APVYQQPQQQPVQASQYGYKEPAAPVSI QRSAPGGGGRYRAVYDYSADDEVSF QDQDITVNVQIIDGMWYGTVERTGDTG MLFANYVEAI
13500	27401	A	13649	3	394	GDGQGHLSGSRNGGSGMNAFPAPESFLL FEGEKITINKLTKVPNACLFYTNKEDHT LGNILKSQLLKDPQVLPFGYKVPFPLEH KIIIRVQTTFDYSQBAFTNATDLSB

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13501	27402	A	13650	1	471	LSLLEERFRVRAGPGQAD SRPTGIRREAGSGPREAPRRSGCKSPGL GTVGMLRPKALTQVLSQANTGCVQSTLL LNNEGSLLAYSGYGDTRVTAATASN I WAAYDRNGNQAFNENLKFILMDCEGR VATTRVANLLCMYAKETVGFGLKAKA QALVQYLRPLTQVAAS
13502	27403	A	13651	1334	82	CYTGQTSLWPGSSCASSVARPSSIFRS ANSCEKSVRCARACTNSVPFIDISEED QAAELRAYLKSQAETISEENSEGGLKVD LAQIIEACDVCLKEDDKOVESVNSVVS LLLLPEPKQKRALISLCEKLVKFRAGE RPSLEQLLSNLFWGNDKATFVRYTVIC SLIKVAASCGAQIYIPTLEDVVRKVISD WNLTTEKHTLLRLLYEALVDCRKS DAA SKVNVLLGSYTEDNASQARVDAHRCIV RALKDPNAFLFDHLLLTKEPVKFLGELI HDLLTI FVSAKLASVVKFYQNNKDFIDS LGLLHEQNMAMKMLLTFFMGAVENKEIS FDTMQQLQIGADDVEAFVDAVRTKMV YCKIDQTKRKVVVSHSTRFTFGKQQWQ LYDTLANAKMKNLKNLSLSLSDT
13503	27404	A	13652	1	377	TTASGRSGVKGSTNSAEVPEASAEK EMEDKVTSPKEAEKALKARYPHLQKQ GGSDFLRKRLQKQKYFDSGDYNNAKAK MKNKQLPTAAPDKTEVTGDIPTPQDL QKPSLVASKLAG
13504	27405	A	13653	424	596	SLKNTYGLSCRKKKGAVKKILLVQAW LMPVITVLWEAEVGLLSARGLRPRAT W
13505	27406	A	13654	190	448	LRSYPAPHLGSPELRTRKGRGSHCLAG AAGPORTALGLSAPLCPPSPPTPGAGA PRYCSGSDAPFCLLRGAGPPIFMGWDE TS
13506	27407	A	13657	1612	563	SMPGWRLLTGVGAVLGRIDGLGALG PGRNTHINLTVRGLHGKSGTWNDEHLS ENVFPKQLVSDDEDAQLASKLCLPDE PWP IHPWEPGSFRVGLIALKLGMPLWT KDGQKHVVTLQVQDCHLVKYSKENCN GRMATLSVGKTVSRFRKATSLIFYSR LGLPPKQTVKIFNITDAAIKPGTPLYA AHRPGQTVDVDTAKTIGRGFGVMKRW FKQGPATHGQKTHRRKAVATGDI GRV WPGTDMPKRKNITRTEPGLKVRINTK INLIYVNSVPHKNCCLKVKDSKLEAY KDLGKNLFTPTTFDSDSESLFEDLYE NVCQPGASITFA
13507	27408	A	13658	128	2626	NSHRWVYVRAKRRRRGRQREOPEDRGV PMKRAAMALHSPQYIFGDFSPDEPTQFF VTPRSSVELPPYSGTVLGGTQAVDKLP GQEVRIEFGVDEVI EPSDITLERTPSYS ISSSTLNQPAPEFLGCTASKITPDGITK EASVGSIDCQYPGSALALDGSSNVEARV LENDGVSGGLGQREKKKKKRPPGYYSY LKDGGDDSI STEALVNGHANSAV PNSVS AKDAEPMGDMPPSVTPRTCNSPQNSIDS VSDIVPDSFPFGALGSDTRTAGQEQGP GADFGGSCFPASAGRDTLSRTAGAQPCV

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						GTDTTENLGVANGQILESSGGGTATNGV ELHTTSESIDLDPTKPSASPADGTGSA SGTLPVSPQPSWASLPHDSKPSSSSPVA YVETKYSPPAISPLVSEKQVEVKGLVLP VSEDPVAIKIARLEENVTILHKPVSLQP RGLINKGNWCYNATLQALVACPMMYEL MKFIPLYSKVQRPCSTSTRMDSFVRMLN EFTNMPVPPKPRQALQDKIVRIDRPGAA FEPTYIYRLLTVNKSLSSEKGRQSDASE YLGFILNGLHEMLNKKLLSPNEKLT ISNPKHUSVMEESQEQSQSSEDEBQ VSPRNKTSVTRQADPQVQPTITGI PGGHI RSVVYQSSSKESATLQPFPTLQLDIQSD KIRTVDQALLESVARESQQGYTTTKTKQE VEISRRVTLEKLPFVLVHLKRFVYEKT GGCQKLIKNIIEYVDLEISKELLSPGVK NKNFKCHRTYRLFAVVYHHGNSATGGHY TTDVFGIQLNGWLRIDDQTVKVINQYQV VKPTAERTAYLLVYRRVDLL
13508	27409	A	13659	42	382	TLWLKTIQTLYLTISGLGSDYGLAGFSA LGCHQAAYRMATAFILIQGLDLGRSHFQ AHSQCQWDSFPDCSRHOGCLLHLVQES PWFQSAERVSCITKCHRSIDTHLCSIL L
13509	27410	A	13660	178	349	DMGFCYVAQTVLKLGLSSDFPTSAQSEA GTTCHHAHLSEPFMLIMYRNFSPFQCLE T
13510	27411	A	13661	268	2	RQKQVILLSQSLSMEHRTVLPKSPG MNPSPLIASGGCNKSLAQGHIIFFSSP LLMNPSPLCVSVSSSLPWRKPLLLHLRS TLFO
13511	27412	A	13662	112	483	AGVGALRMVQRLTYRRRLSYNTASNKTR LSRTPGNRIYVLYTKKGVKAPKASACGVC PGRLEGVRAVRPKVLMRLSKTKGHVSRA YGGSMAKACVDRKRAFLEBQKIVVK VLKQAQSQKAK
13512	27413	A	13663	2	873	SVEEFDRGCTGRGQADAPGQJLVKIS FQPAVAGIKGDAKAKASAPAPASATE ILLTPAREQPPQHRSKRGSSVGGVCYL SHGMVLLMGLVFSVYIYRYFFLAQLA RDNFFRGVLYEDSLSSQVRTQMBELED VKIYLDENYERINVPVPQFGGGDPADII HDPQSGITAHVIDSLDEQYVIEANTIV LPRRFWILLMVKRTYLLPOTYLIQES MVVTEHVSDEKALGSETYHLGNGKDTYR LRERRATRRRINRGAGXNCNATRHFTENTF VVETLIGGVV
13513	27414	A	13664	118	3	AMSLIPTVPVREAKAGGLLEPRSLRPT WATNODPVST
13514	27415	A	13665	1	2876	IYRINRFSRKNKWSREGLDQGVSEELAT NQKLLVCGRYEGBIDSRVIOETIDEWS IGDYVLSGGELPAMTLIDGVSRFPGVL GHEASATEDSFAGLLDCHPHYTRPEVLE GHEVPPVLLSGNHAEIRRWRLKQSLGRT WLRPRPEILENLALTEQARILAEFKTEH AQQQKHGDMAADEAGRTFLRADPNMIE BGDRIWVCLSGGKDSYTMLEIRLNLOQS APINFSLVAVNLDOKQOPFPEIVLPEYL

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						EKLGVEYKIVBENTYGVKSKIPBGRIT CSLCSRLRRGILYRTATLGGATKIALGH HRDDILQTLPLMNFYGGKMGMPFKLMS DDGKHIVIRPLAYCREKDIQRPADAKAF PIIPCNLOSGSPNTQRQVIADMLRDNDK RYPGRLETMFSAQNQVVPSHLCDINLFD FKGITHGSEVNVGGDLAFDRREIFLQPA CWQPEEDENQDLRLNVVSPDFGRHRI AFDARFQCYLHRQARYLLSVVFNLDVA VTFPLANGDLNVLLEKRVAGGRANVVS KVGKQYKRVWPNWEPADLHKIRPHHPLN RNLDHFFPLDITNSTPSGGYVHVLKGV SDDLILKSPQKQGVYVRDRLMVTALP PACQVQVQALGCFALRLCEILGEVLAQ LQTSVLPAELLQARRASGDVASQRLA QDEEPFPLPFRGSPAAYRAPLDLYRDLQ EDEGSEDASLYGEPSPGPDSPASLAYR PPLWEQSAKLWGTGGRAWEPPEALPQA SSPPYGALEERLEPEPSAFSLIRREL SRPGDLATPSSAAASPRIRABGVFAS AYRVSSEPPQYQQTQLPVPWRPAHPLLR HLSPAACPLCSFARLPFRFLAACAMWR RPAALVATACTDGHSLAQPRGPALQQL GPRSRALGRQLPWCPSLLGRGLGLWLPC FKGSPHSGRGLSPGQPLLEVLGVYGR LOGQQA
13515	27416	A	13667	76	289	SSTPASFCLDENPNCSCSPFGSCACAGS CKCKECKCTCKKCCSCCPVGCACAKAQ GCICKGTSKCCSCCA
13516	27417	A	13669	2	667	GRVDARQSRIGATEFAAAAAAMPFYDY FKLLIGVDSPGVGKSCILLRFADDTYTES YISTIGVDYFKIRTIELDGKTIKLQINDT AGQERFRTITSSYYRGAHGIIVVYDVT QBSYANVKQNLQBEDRYASBNVNLVVG NKSDLITKVKVNDTITAKEFADSLGIPFL ETSAKINATNVEQAFPTMAASI KIRNGPG AASGGERPNLKIDSTPVPAGGGCC
13517	27418	A	13670	176	398	RILKTLQGRNNQPTTTTKRQKRTDTL PKGIYRRHISLNLQTLNLTFTVLPALCEA NAGGRLESRSRFPWATY
13518	27419	A	13671	149	247	RKGLALSPRLDCSGATTVCNLSNLQGLS NFI
13519	27420	A	13672	257	359	VASLHBAQWLTPVIPTLWKTIVGEGFE PKCSR
13520	27421	A	13673	142	1	HLKSGSLAKHQNLMPVITPALWEAEVGV LEVRSSRFPWATLQDPTSS
13521	27422	A	13674	619	168	MFTESSCTPKTYTSPVLRQSHSPQAQGV QWLDLGLSLQPLSGSSNPASACIQVL FVIYTSVKLGVGGR LGNKVMSNNKKFV CECRGWII LFPSPVSLRFDQGGDHGVS SAEKALQAGRTAGRVGVVPLPAGPCGA PCTTPPANS
13522	27423	A	13675	3	370	ARALTHPRTHQWQCLHQGTGGCQQS PSSEGRADLLSPALBEGYPPPASGCFIP HFLGCSIFNCLFPIMRHAKSPDALLE TLGCRANRLMPVITLNEAKVDRLLS RSSRPSWPTW
13523	27424	A	13676	3	281	IGTRPELSVSLGRQLTATRLQLFLPAR



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						TPOCFLEARVALALMADETDLPILPRLE YSGMITAYCSIDFLGSSDPPTLGSGVAG TTCNCCED
13524	27425	A	13677	272	389	YCRQIEKSKKKRCMLGTVAHACNPSTWG GRGGRIITRSRD
13525	27426	A	13678	261	363	NSSWGHWRLTSTVLPALWEAEVSGSPEV RSIRPV
13526	27427	A	13679	149	44	SCVMEVSVLKMYMLGAVAHACNPSTLG SQGGRTA
13527	27428	C	13680	118	267	NSHCTWLMQCVCCVCCVGYAYMYTYSF LRWDLPMLSRLSCSYSAQ*
13528	27429	A	13682	16	346	NHLLQDPHRLDINDFFFFFFFFFF FFFFFFFFFTFLKSPRPAKKKKKKKK KKKPPRFFFLGQAPPLFFFLINFFFFF LCKIISLVYNRGGPCLSKRFFLKERIS PL
13529	27430	A	13683	244	140	GRVDVFHHVQAQGLKLKLSGDLPAWPK ESRLQV
13530	27431	A	13684	191	777	NSDEHVYRCYGHKLSPFLSKYLRSGLA GVLLPLDAANDMEKIEEQFANLHVKCS LGTKEPTYLIGIDTSKTVQAQKBNLAV LCSNGSIRIYDKERLNVLRHPSGYGILL NGVRFANGCDSVYSACTDGTVKQMDARV AREKPVQLFKGYPSNIFISPDINCNDHI ICAGTEKVDLDALGGFGDARMEFLQN
13531	27432	A	13685	150	253	VGWGLMLVPVLPAPWEAKMSESLEDRNL LPCWAT
13532	27433	A	13686	500	321	IEWGSHYVAQAGLELLSSNNPPTSVSQS AGLVGMSHMLAAISKSSDASITSHHPN TTP
13533	27434	A	13687	6	424	MSLLQCGSIRCPKMPPEPAKAPAPKKGS KKAVTQAQKRDGKRRKRKRKESYSVVYV KVLQKVPDPTGTSKANGIMNSPVNDIF ERLAGEASRLAHYNKRSTTTSRETQTA VRLPLGELAKHVAESGTHKAVTKYTSK
13534	27435	A	13688	178	293	TGYSSQAQMLNTVLTATWEAEAGSGLQP RSIRPAAWQ
13535	27436	A	13689	663	144	KELSAVSAGIPHS CGSGCGGSSVAACV PAAPAAAGLCSGRQKVPFPFPLAGWPP GVNAPPPPVCSGVRRLHVQSDRLAVRLA ARRGILALLRSALKATLAGCSVRHVS RPSESLRPTSNRAASLRSSVPTVLSHV PLAASLGKRRACGGRHSAVAVYLSVCL SLPT
13536	27437	A	13690	125	3	FAHQGHAPGQAWRLPVPVLRASLGG RPEPRSSRTARA
13537	27438	A	13691	136	24	GGPPPPPPPPPPPPPPPPPPPPPPPPPP FPFGHLQDQFYVVK
13538	27439	A	13692	144	1	MLKIVQSGECLTKPKNFCLLSLCLP TLLALATLLAPTSPLILIL
13539	27440	A	13693	1476	380	NSNSTLASERTLWANTSADPERKSOAS ANMWATLPLCAGANLLGVVPGAAELC VNSLEKPHFKSNMSKHKTKYSTERYHHR LQTFASNWRKINAEHNGNHTFGNALNQF SDMSFAEIKHKYLWSEPCNCSATKSNYL RGTGPPYSPVDNRKKGNEFVSPVKNQGAC GSCNTPSTTGALESAIAIATGKMLSLAE OQILDCAQDPNNHSCGGGLPSQAFEYL

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						YNGKIMGEDTYPYQKDGCKPQPGKAI GFVKDVANITTYDEZAMVEAVALYNPVS FAFEVTDQFMMYRTGIIYSSTSCHKTPDK VNIHVLAVGYGKNGIPYNIWIKNSNGPQ WGMNGYFLIERGKNNMGLAACASYPIPLV
13540	27441	A	13694	87	2	PGNANWPTPVILALMWEAGSGPEPKSL
13541	27442	A	13696	130	2	CNLIILIIQVCRAWMLMPVIRALMWEAP GSGPEVSSRPALV
13542	27443	A	13697	282	107	GLTKCPGTIVCKSLKRVISYQLSIYCLSM MHSSTLTLMCSLKLGLSSDPPTSVSRV AS
13543	27444	A	13698	198	3	CSITVNNKVMTLPRSSMSLEIVCDIDL AVLRRLDGLSLQDPPRPPTPLSCLSLPSS WDYRRPLV
13544	27445	A	13699	2	120	ARGDGVSLNLERLAKNGAISAHNCRPT GSSDKNFKTRF
13545	27446	A	13700	60	341	PDWGLDERKMLTESGDPEEBEBOBEL VDPLTTVREQCQLQCKVKARERLELGD ERVSSRSHTDDDCPEELDFLHAKDHCV ALKLFNNLQ
13546	27447	A	13701	6	340	KNSRTLGCGGIRGSLCRPRKPGVGTO TRAVRPVACSADSRPHILRRADMKDS LVLLGRVPAHPDSRCWFLAMNPAGTLLA SOGGDRIRIRIWTGDSMWICKSVLSEGH QRTVRKVANSPCGNVLASASFATTICW KKLTLRINYILARKLEACIKPLCCALKYG CLEBKQLHS
13547	27448	A	13702	239	346	AKRGWLMHPVTPALWEAKVGSLEPRISR PLWATWQN
13548	27449	A	13703	210	300	LMPVISALWEAKANGLEPPTLRPAWAT W
13549	27450	A	13704	141	440	PSAFEHFEKINLYPLKFCISQGPFERQN NRDREIHRERYDRDREHRYERYERGLRE LAHVIVSAEKPHHRPPTITWETLGCNMSG SVQVQKPWEKGLMV
13550	27451	A	13705	204	438	LINVLITQLFFLFLSLRQSCSAQAARGQ WYNHGLQPSSTHGAANPTTASQSVGT GMSHDHGLFLHFTSLDIPSSL
13551	27452	A	13706	1707	1821	AKAGGSQRLTLANAVKPCLYWECKRAG PWWCAPVGG
13552	27453	A	13707	167	334	IRRANPKILTEIGTQWMLPVIPALNEA EGGGLLEPGSPSLVFLPFLITTLTILMRKK
13553	27454	A	13708	224	344	KDTAMEEIKDTERTGKPVILGAVAHACN PSTLGDQGRQLA
13554	27455	A	13709	1476	380	NSWSTLASELTLMWATSADPERKSKQAS AAMWATIPLLCAGAWLGVVPCGAELC VNSLEKPHFPSNWSKHKTSTSTETEHRR LQTFASNWRKILAINVNTITMALNQF SDMSFSLIKKILNSPEQNSATEKSNYLR RTGSGPYPSVNIWIKKNGIPSPVKNQAC GSCHTPTSTGALESAIALATGKMLSLAE QQLVDCAQDFNNHGCGGLPSQAPEYITL YNGKIMGEDTYPYQKDGCKPQPGKAI GFVKDVANITTYDEZAMVEAVALYNPVS FAFEVTDQFMMYRTGIIYSSTSCHKTPDK VNIHVLAVGYGKNGIPYNIWIKNSNGPQ WGMNGYFLIERGKNNMGLAACASYPIPL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						V
13555	27456	A	13710	763	257	YEKILKLTADAKPESQDVKATVAVLSFY LSSAAKHSVDGESLSSELQQGLPKEHA ASLCRCYEERQSPQLKHLRVCSLRMNL AGVGWRVDYTLSSSLQIRGKSPWCHG WKVATCPQGPAPACLPFPSSKTKFPR SSLARTESRPKTLMLKFNASEKGVPRPV
13556	27457	A	13711	133	401	VLSKSGNFYWLSTNHEIKQEGCAWQL TPVIPALWEAEAGGSLEPRSLRPAWATS WLPREIKLDDLKNGCGPSKITQGGPMVA GSLK
13557	27458	A	13712	212	74	RRINLADPRVFLKGPPIPPPPPPPPPP PFAMGNPLFLFNSTPGRK
13558	27459	A	13713	324	141	DRVLPRIECSGVITARYRHNLGSRDPP TSASLIAGSQTCHRAWLSFSYLFTTVF FIIL
13559	27460	A	13714	299	431	IRLIWLSAVDHAACNSSTLGGHGVQWTKG QDFETNLANTANPHFY
13560	27461	A	13715	133	1	ILVWAWMDMFAIPVLWEAETGSLERPS LRPMAWTKNTISTEN
13561	27462	A	13716	18	165	IPLHTHTHTHTHTHTGYLLASGTEPL SVLYMASERECRTYNMLNK
13562	27463	A	13717	119	1	KPNVSAQWGLAPVPALWEARVGULFKP RSILRPTWATQQ
13563	27464	A	13718	271	64	VLRISTNLNLTARTNRPFLOILMKPRK RWGTVAILRAPVGDQPDQHSPTSLIKI TKLSWVWNRTPVI
13564	27465	A	13719	21	209	KDGPFGTGGSETNESVEMTECCSVTQAG VQMHDLGSLQPPPPGFGFRFSCGLPSSW DYSRND
13565	27466	A	13720	391	151	KGFPLGEEKKGNFPPIILGKKTLGSPGK KGEKKKKKRGKIFFFACNPLGFFPKKIV LGEKNFYSGVWGGKKKGPPPHS
13566	27467	A	13721	109	2	RLRGVAHAQNPSTLGGVGGSQGFNC GOVTKVS
13567	27468	A	13722	69	369	RDILQADQNSLFPPTPSLNAYITPSSP IGPHTHRPYHATPTTYLPFYTNLLIKKKK KKKKKKKKKKKKKKKKKKKKGGGPP KKTGGAPIPGGGK
13568	27469	A	13723	58	1208	FWNENS PAS ELAPNGGGSVTSVPRLDY LTPQLYKLTGVBGFSRANGRDSFDRK TYKTPSANMVLKVEELVTGKNGNGEA GEPLFDPDROEYEAATLEQBDLKT LNAHPTVLGEQWNSKQREAELEKKKKLE QSKLENLELLETILQKKKKYKRTKV PVVKEPRPEIITRPVDVPTFLKALENK LPVVBKPLSDNNPDVCEYKRTALHRA CLBGHLAIVEKLEAGAGQISPRDMLST ALHWASRQKLDVLKLLMNAKISARD KLISDALHVAVTGTCABHLLACAD LNAKDREGDPTLHDAVRNRYMTLRLLI MYGADLNIKNMGKTPMULVLAHWQNTK AIFDSIRENSYKTSRIATF
13569	27470	A	13724	400	135	KWNGKELNGVDGIGWDRNEMYNKGLPH ETWNELEFNLNGLNNGMSWDGICKNGIK NNGIECSGMLNNGMEICMGECPLMENIR VEWN
13570	27471	A	13726	186	344	SASLGLWRCRDCRRSLVHSLVLAQAQV

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						VECDLSNMEITTELRQVFAETERHREER RRQQQLDAERLDSYVNAHDLYCNTRRS VEAPTERPGHRRQAENKRLYGDSSAKIQ AMEAAVLQSLDFDKHCDKQPKYWPVILPK F
13591	27492	A	13747	2	305	GRVGSFSVRDVELSDPAERGERGMPVAVG PYGQSQPSCFDRVYMGFVNGCAVGAAG ALFGTFSCLRGHGRGLMGIGIKTMNQ SGGTFGTFMAIGMGILIC
13592	27493	A	13748	2	305	GRVGSFSVRDVELSDPAERGERGMPVAVG PYGQSQPSCFDRVYMGFVNGCAVGAAG ALFGTFSCLRGHGRGLMGIGIKTMNQ SGGTFGTFMAIGMGILIC
13593	27494	A	13750	238	423	AVSNDQLTWGKGVQREKKQAQANGMLPV IPTLWGEVGSPEVKSSRPACPHGKTP FLLKMQ
13594	27495	A	13751	455	248	ISVGPGLFQNLFCFLPYGTFTLSKKFF IMETGSRFVIQAGVQMGYSYSPQQFFG FESSLKRPHSGVK
13595	27496	A	13752	2	98	IPTPTINTHTSHTHTHTHTHSTFLAMP PDLK
13596	27497	A	13753	196	2	INAPPKRIFLKKPPLFFFFFFFFFFFFFFF FFFFPFFIISFIPNPLTRKQKLERSMVF FKDSACSA
13597	27498	A	13754	917	379	KYKKSLLQKNLLVGCKYSLCYRRHKL HLVTHGERKKPAAVNSFFLFSSFFFLN LYRNTEITKKRVNLHETKADAESCNQDC TTSSETASELEQIRSGHSGMKWAGEGA AGQPRGEGEMWNTEMRRGARGRGGER EMERARVROGEREKEIDLYKKVTSKIE ETKLGNLLKG
13598	27499	A	13755	175	21	KKKNFFPPPRVLLGPKVFFKRAPLFFF FFFFFFFFFFFFFFFFLKKSNRPLAI
13599	27500	A	13757	234	341	EIGNVQMLMPVTPAVWEAEVGLLEPRS LRAARAI
13600	27501	A	13758	1	365	PAPNRRGGHIDRATSTELGANQCFFF SPRPSPSEKKTPEINKEPRPAPQSPNG NLGTREGGDSWAGTTRCLRDTSDGYR TEPPTALSWGQTRAFFFPALPAGKKRH RNLLKTQFF
13601	27502	A	13759	87	181	SHTHTHHTHTHTTFTYLVNVIHFDMEI LGL
13602	27503	A	13760	1	228	ARGRRRRRRRRRRRRRRRRRRRRRR RYREGGRLLLTMGEGETERATDLYHTPP PSIKAWRLCEPRPRAGILGCRNIF
13603	27504	A	13761	383	197	RCDDPAPWQSARITGVSTRAQPATSVL MGEDFLEDPVIAFVRLAPAVLLSKLSE VSVMT
13604	27505	A	13762	276	57	YAVLGSGGGRKNLFVVFVFLFFVFFFF FKKGGFLMLPEGRGNMGFFFPVMVG DKTKLFFKKKKRPR
13605	27506	A	13763	377	209	PEPAYGPAFLPYEGFGRNPPFFQWESR SVAQGVQWCYQLSLQPPPNPFCITLLN
13606	27507	A	13764	160	202	MEKYNVHPHSGTILHSEREQALPTIAK RNRQPSYSPSIDEWKINMISLHTVEYTTAK KRKNQLYSQ
13607	27508	A	13765	390	284	ESGGHFLSLSLSTIYIYIHIYITVVCVYI THTSHTI

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13608	27509	A	13766	350	41	YVVILQENRNTQNRKLLPKSTELCMLLQ MLLFILNTINYPLPLMQCYHRFCSPFLK TGSFYVTQAKVRWLF TGMITVHC SLKLL DSSHP PKLVLQELATVAS
13609		A	13767	330	156	KITQAMCVHVVPDNRREAVTVGIRLGR MRLFLBACTINCVPSEKEQDPVSHNRK K
13610	27511	A	13768	25	292	KCFFLSWRGGRSLQSQHFGRRPRADHLR PGVDPKPGQHGLFLVKGSDKPDLSSEVK FDRSKLKKNTTBKNTLPSKELFFPSLVG VNIQD
13611	27512	A	13769	585	680	KCLGSKTRWLTVPVITLWEAAGGSLRP RSS
13612	27513	A	13770	488	359	PSPRERKFLPFKKKKKGWPPPPKKNR GRG PQKEGPKPKP
13613	27514	A	13771	794	515	PDNGLEDQKMLTESGPREREEREEL VDPLTTVREQCEOLEKCKVARELELCD ERVSSRSHTBEDCTEELDFLHARDHCV AHKLNNLK
13614	27515	A	13772	130	397	VVGLTFLPCFMARSLPRHSKPOARKTK KKKKKKKKKKKKGGSLKKKIPGGAOKS GATKKKNFPKKRGQNKKNPGFFKNEIFF GGGAI
13615	27516	A	13773	376	145	TRVGGGCEQRCLCHCTPSWATEPNPVS NNKIPLELFPNQTFPHFVNKKGRNN WLSNYSISSTVTRHPTLPQF
13616	27517	A	13774	1	247	GLQSLADLLSGLLQKVCFLPSNGIMDLY LLYLYLTFVEGSGCSVAQARVQWCEHSL QPHTSASDDPPTSATTTTCHEARLLIIV
13617	27518	A	13775	376	145	TRVGGGCEQRCLCHCTPSWATEPNPVS NNKIPLELFPNQTFPHFVNKKGRNN WLSNYSISSTVTRHPTLPQF
13618	27519	A	13776	107	468	EIKARSFERARDCEGTTTDRDNREREKIL PKLREELFWVSGMRCFNPQGWSHWD NFGWG IPTGSPVSGWKEGKGPGEGRSHKY GTGRCKELGVSGNSAFTPLLHFYFKH RKRRKQI
13619	27520	A	13777	125	2	NIFFPLFELYFKCHWARWLTVPVIALW EAKEGGSPVRRSS
13620	27521	A	13778	166	74	GRICYSHSLSKTHTHTHTHTHSHISF IP
13621	27522	A	13779	1	341	ARGERERERERERERERERERERERE RERERERERERERERERERERERERE RERERLSFSLGGGALKKRIFLCVILE GKHLPLTHLTGFFGENTHTLSMKTRGG FCNGGDERRSASVMRAYIYRECEPHTH V
13622	27523	A	13780	614	337	RRCSSALCYRRHGNHKVIRSKQASVS PHEHLRLSLLEVRNVGLGHSIFPHSLR MYVCHVCHVCSITLYLSITLYLSITLY LSITSSR
13623	27524	A	13781	390	158	VLIRLSWGRICFOAHSGCWNGSGSCHK TEGLCLLAGSGSLWGLGALKGWSKEE FYTMQHSQSDTSLPLPYSIH
13624	27525	A	13782	308	163	TKFYLLFFFFFPLFLPFFFFFPLKKKF LFFIQGGGKIKTPGTLTLGL
13625	27526	A	13783	45	277	IASGRPPFFPIHLPPQAKAVFGGGGGT PPEYQNFVAYIKGQGNPFPLGCGDLFN



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						GOOFGGFFWSPFKGEIFFFFVFMAFOK KKKKKKPPFFIFWGGGPPFFFPFPFKQK KKKKKKKKKKKKKKKKKKKKKKRAAKWEA RSRSSA
13646	27547	A	13806	1	425	RLGGVALRSADGAPVSGEFGGKGLRW CLVTDFFPDSCTTCSYSRRSTPGCSGG SRGLSEGGSGSVSLQSRVLSAMKHVLN LYLLGVVLTLLSTFVRVMSLEGLLESP SPGTSWTRSQLANTEPTKGLDHPERSM
13647	27548	A	13807	5	313	EKPLQGITPTTSKTHLLYEFTPTTILIV KEYSTNYVLLIGTQIKTHIVFRKFS MTPILYKFDLAQWLPVPTLMEAKFGG LLEPRSLQGSYSLLTLL
13648	27549	A	13808	182	314	VITQLDKTERAQWTFVILVLYEAVGG LLEAMSGRPAAVATKTM
13649	27550	A	13809	219	1812	LPPPEGAGSGFNPFGGTGAPTGTPTGT AKTATTTTATGFSFSTSGTQGFNFGAPF QPATSTPTGLFSLATQTPATQTTGTFT GTATLASGGTGFLTGASKLNLNNTAA TPAMANPSGGLGASNLNTALSTVTSS QGTAPTGFVFGPSTTSVAPATTSGGFSF TGGSTAQSGFNIGSAGNSAQPTAPATL FLTPTATPATTAGATQPAAPTPTATITS TGPSLFAS IATAPTSSAUTGLSLCTPVT TAGAPTAGTQGFSLKAPGAAGSTSTTS TAATATATTTTSSITGFALNKLPLAFA GIPSTAAVATPFGGAGAGAAASAM TYAQLESLLNWSLELEDGERHTLQCAT QVNWADRTLIENGEKITSLHREVEKVL DQKRLDQRLDFILSQQKELEDLLSPLLE LVKESGTYLYQHAEEREKTYKLAENI DAQLRMAQDLKDIIEHNTSGAPADTS DPLQIQCKILNAHMDSLQWIDQNSALIQ RKVEEVTVKCBGRKQBQSRFTTFD
13650	27551	A	13810	134	263	KNSLEKKKNNRGPWMLPVPVLPALWEA GGLLEPRGLRPTWVT
13651	27552	A	13811	210	51	TLSHRKPTSFAYTARVGRGFTILEVSETR NPPIGWTRMLTPVLPALWEAAGG
13652	27553	A	13812	241	139	LHEAGLADPATPALMSKVGGLLEPRSPR PAWASW
13653	27554	A	13813	539	256	RTTQMSIAAGFTALNNKQPRCPWTEEQ TNKMSLHAMECASAMKONEVLQPAVR MARENSRRKPGDMHDINSVMSAGENLPG LGRSTGKGGD
13654	27555	A	13815	63	369	VRETPKXTHYLEEISSPASPTAIPQSLL PSFIFPSPSLAISGSGHGPVHLELHP PTEPSPSVCLMAGPKVPFGAAGKGSFD SNPLVIRSLALAPPASL
13655	27556	A	13817	258	3	AKSAPPSTNSLFTTHTHTHTHTHTH THSLRTTNAPSQVCRPQTSQROGECVG PTAFAPSPTLLKPHHPSHVHLPQPER
13656	27557	A	13818	516	665	WFKSGSPWIGWAVATCNSTLGGQSGNI TSGRSRTSVTTTTTSTQCAPA
13657	27558	A	13819	295	361	WLTPTVLPALLEAVTQSGLEPRS
13658	27559	A	13820	166	368	GWATQCSAQYVVSSSSIGALCLGBCS VTQAGVQWCDLSSPQPSHFGPKRFLCLS LPSWDHRRGDL



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, v=possible nucleotide insertion)
						TNVIGNYRTQMADKQEVFLPSTPGLGM HVEVKDPDKMLQVVLRSQYGSBGRPTF TSHTPGDHQICLHNSNTRMALFAGGKLR VHLDIQVGEHANNYPRIADKDKLTQL RARQLLDQVBOIQKEQDYQYRBERPRL TSESTNQRVLWWSIAQTVILILITGIWOM RHLKSPFFAKKLIV
13671	27572	A	13833	17	130	RLQEPGTRRRERERERERERERERERE RDTHSFLHG
13672	27573	A	13834	283	460	LVVRLAIKKNYSLKRETEPGSVAHVYNP SYLGGQGRRTARQGEFKTSGLDNIRPPS LKQ
13673	27574	A	13835	3	435	WPRFCTALQEPOTRRERERERERERERE RERERERERERERERERERATSLSRPSP LPFSACVSHPTTYVGERENLSLTKLKH TREKHSLSYTNASARDTRAPFSEGRAPP IYSVYLTHGVFFPPFFPSLCLSVRHAGL AHV
13674	27575	A	13837	351	57	RTLWHISKFPIGNLSLDLYVQSEWDLGT ADLSIMTSVLHCLPSPLESIKNTDWNPS VAHTCNPSITLGGRCRCRQGHQSKQPS LLKIQKIARCGG
13675	27576	A	13838	336	150	TPCYKRYLWGAHCPIFRITGLPIKNPYF GQAVCLLPVISARWEATGGSLERPSLR VAWAS
13676	27577	A	13839	310	454	HCSLGLFOVLLIILYKILLGWARNLTPV IPALWEVEAGGLLEARSRRP
13677	27578	A	13840	163	297	ITFFLLDLKLGQAMTIYVSYLYSLYSLI YLSIYLYTHRLMNTLQL
13678	27579	A	13841	33	316	LQHPPTPSPLCSHRLKTSSSQGGKEE LVKSLKKKPKLPGRFDAPEDSHLEKSP LEKFPDDVNBVTKEKGGPRGPEPTRYGD WERKGRCIDP
13679	27580	A	13842	4474	2586	DQSGCVKMEFPQGNINLYITIGPSHPF LSGAETPHFTPSLGEDEFEPPIPTSLSDP SLAVSDVVGHPDDLADPSSSQDGSFSAQ YGVQTLDMPVGMTHGLMBQGGGLSGGL TMDLHSGISGTQYSANPPVTIDVPMDDMT SGLMGHSQLTIDQSELSSQLGLSGGG TILPPAQSPEDRLSTTSPSTSSLHEDGV EDFRRLPSQKTVVVRAGKQKAPKRRK KKDPNPKQKPSAYALFPRDTQAIIKQ NPNATPGRVSKIVASMGWSLGESEKQIY KRKTEAAKKEYLKALAAAYKDNQECQATV ETVELDPAPPSPQTPSPPPMATVDPASPA PASIEPPALGPSIVNNTSLSSVYANQAS SGAGQSPNITKLITKQMLPSITMSGG GMVTVIPATVVVTSKGLQCTSTATIQP SQCAQIVTRSVLQAAAAAASQQLPP PRLOQPPPLQMPQPPPTQOQVTLTQQPPP LQAMQPPPKQKVRINLQOQPPPLQIKSV PLPLTKMQTTLVPPTVRSSPERPMNSP EAHTVSAPS PETICEMITDVVPEVESPS QMDVELVSGSPVALSPQPCVRVSGCENP PTVSKDWDNEYCSNCCVVKHCRDVFIAW VASRNSNTVVVFK
13680	27581	A	13843	54	251	EFYRMNSPSPLMLCVCVVCACLFMLCLC ALTCNCVNYKSLHLSNLTQVLSKFFYDS

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13681	27582	A	13844	154	26	ISPAENPGK DPHVPTTSSSSQARNLPFFVIFTLNRA EACGS PEVKSSNST
13682	27583	A	13845	475	225	GHTELYGALFQLLQALPEGGGOTSCLF NPSSDGGSSAAGVVGAGDLARSSRV SPTSSRPVSPDPSPPSLYLT PKETH
13683	27584	A	13846	479	319	RDCRRSLTHSVLSGAQGVQNRDLGSLQ PPPPSRLLPWPPKAPRNPQLIGHHPT
13684	27585	A	13847	182	499	LLCVKLCS CNENKALRBTQRAQVQGH SRAQVQVQGHSAINTVQIRSAASRRK AFSTCSSHLGMVLLFYTGSSSTYMRPTT RYSPLGRLLAAVPYSLLIPTLN
13685	27586	A	13848	388	494	RDSWERLEPLIPVLNRAQAGRLLEPRS LRLAWT
13686	27587	A	13849	198	63	HDATTNMLEIDIMFKRVSQTKQNKYMI PLIWKTKVLSHRBQK
13687	27588	A	13850	555	353	RCPPGAQAPLRAPSRAPVHLALSPLSQ GVSNPRELTAHPPEPPPPFFKIKHPKQ LSVGKRGQMTF
13688	27589	A	13851	169	66	LLAGSTGQARMLTPVTPELWKAIVGSL EIRSSR
13689	27590	A	13853	12	105	IASGLHDFPKKKKKKKKKKKKKKKGG AL
13690	27591	A	13854	256	363	ICLFIKDSDRGQTQWLTPVILLWKAEA GGSLPKS
13691	27592	A	13856	23	436	TDRLSDSHEERRERERERERERERERE RERERERERERERERERERERERERE RERESSLLCVRHCTFAPPTYI PLNETLR VCPTPCVNGALSVFSHTERARIFPYTCG GSVARAPVCMHTRIFSSRARARALCARP PLSRERRAHTRVFFI
13692	27593	A	13857	91	428	PPDTSPLTIDRGSTPLQATLPSQYGG QSPFEPKTKTTTQKKKKKKKPTPQKK NKPFPDPKPCPPGPRGNSQPKTKQQQ KKKKLLGGGAPAPNSPLGGGKQNSWAGF
13693	27594	A	13859	465	43	KRVITENPOHCSAETAIPNSLSCNCF HILNWHGHPNHPIYITTSIYIYIYIPHIY GMVYIYTRIOMCVCIYVHICINTHTIYI IYIHTHTIYIMERERETVSCSVAQAGVQ WCDLGLSLQPPNKRILKRFCLSLPSSWDY W
13694	27595	A	13860	290	52	WYKYLPGTRGLIWINYLKICIGRIELLV GYFPIYLSIYLSIYLSIYLSRSIAQP GVKRCNHSSILQPTPGLMILSNS
13695	27596	A	13861	108	22	IFFLFSAVKTRFSVAPKEFPYRMNHS I
13696	27597	A	13862	167	33	VPTVGTIYMCVSVRDLGQAWMLTPVIPA LWRAEAGGSLEFLRT
13697	27598	A	13863	448	355	FFFFFFFFFFFFFFFFFFFFFFFFFAKN PLN
13698	27599	A	13864	321	445	SQSTQAWCLMPVIALWETKSSSEFPR SLRPANATGHNPI
13699	27600	A	13865	380	80	MLLSPSPKPSPLFSLFSALLWCLLEL PFLSNVGKGMQNDPVLGSPSTSPDLSR IYLFPCFVCLVCFSTGFPSSVAQGVQ WCDPLGLKWLPPQSD
13700	27601	A	13866	372	264	KMENPEDKNFFIPMPPTIVLLFPFFFL FCLNQFF

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13701	27602	A	13867	161	304	LFIAEMTSHYLAQAGLELLASNPPTSA SEKTOITDGAETLLPOLRL
13702	27603	A	13868	230	348	VSPFIQNLVFCVERVYRVDPGVWVERGSK YNNGSTELHKK
13703	27604	A	13869	168	260	EVIASCYNGCFQLTSLCVCVCVCVCVCV CY
13704	27605	A	13870	140	16	LKYQQRNDLGLSQPPPPFKQFSCLSLL SSRNCTMTDRHE
13705	27606	A	13871	143	30	KILRVVVSQAWMLIPVIALMWEARVGG LEPRISRLA
13706	27607	A	13872	158	59	HLHGCHILLKLRLDAVSHAQNSSTLGGQ GKRIA
13707	27608	A	13873	232	115	APFFPKGADIFFFFFFFFFFFFPLIR GKPNWDVVRG
13708	27609	A	13874	1619	1375	KTTWRRLRLKQLMSLLRLRVVDSQGG LFFPQQRQQLPRLKNQNDIIPYCNLKL LGWNSPASAFRVARTTSLCRHTWL
13709	27610	A	13875	219	84	NPIQSTSTICNRAWRVTCLNSQILLRL RWEDHLSPOVNSCAL
13710	27611	A	13876	166	496	KKKKKKKKGGGGPLKKTTPGGAKIKNRK KKIFFQGGGQKTPGGILKKKPLGGGK KGNPPKKIKGLREKKKFKRGKGAQPAQ NPWKKLISPPOFFLKKFFRGRGFFI
13711	27612	A	13877	132	348	PSKKKKGGGPKKTPGGKPNNGGKQNS FPLMGGKIKNLGLGKNPYLGGGTNGN NPPTIKGGEKKKF
13712	27613	A	13878	287	134	QQGPPISPGPKCEENRGPESPGWGNPGI RSPPGAGNPDAFPQDGMFPSSKKQ
13713	27614	A	13879	333	480	VHPLRSAEGRPESNMHLTLKSKQQNL TPVIALMWEAAGGSGQQRTE
13714	27615	A	13880	1	227	PKTHCKIQTIVLVSEFFPSFFLSFFQSE SCSAQAQVQWHDLSLQAPPPGFKWFR FTLLGLGPHERRMNRDS
13715	27616	A	13881	276	378	GMPWNLTPVIALLEAVGSLLEPRSLR LALA*
13716	27617	A	13882	126	389	GSVIGTGCCGSLGTVCRGSLGTGLTLA SATPDYRLRLSSGSILRTTNSDLVPL TPVIALMWEAAGVSLERIPRIPARETW EDPH
13717	27618	A	13883	414	150	ARQAPKMGNPITGSPPKPLNPPPNPFL GPQKKKIFFPTPPPHFFFKGPPPPFF FFFFFSPHSGCILCHPCGRGIAVAQSW LTE
13718	27619	A	13884	197	363	DLGVVVVNTFMLKPKCLNVSRGHVQWLY IPVIPILMWEAAGSLKPRSLRPANAT
13719	27620	A	13885	101	236	NIHYANFPYFGLACPEYIVRALQKQYIQ THTHTHTHTHTTTHSL
13720	27621	A	13887	17	140	TVHLKMWKIGLHVAHACNPSTLGGRG PMRSGLGNFCL
13721	27622	A	13888	135	1	VLIAGLKLGGSTSPTSASKGAGTIVGIH YHTQLAPQFFLFCFLIR
13722	27623	A	13889	411	276	TLYFKHGMGFHHVGAQLELLASSDPP ALEFETSLHNKVRPL
13723	27624	A	13890	216	54	EPKCYTLFDBSYFFRELVSQGVWRRLR PAIPSPWAKRGKSLRPSKRETV
13724	27625	A	13891	3	149	SSDPRFSSSLAWVGLWSMVRVPPFL FILFLASHVGKSPSPSHF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
13725	27626	A	13892	166	1	LFSEKIPWMLLEVPVLPALREKAVGELLEPGSSRPAPAWATWKNPVYTKNTKISQAWQCT
13726	27627	A	13893	128	2	FSTTYPNPILKIPHPYLLTFLFESAILHPSEINSLVAQKKK
13727	27628	A	13894	225	391	HLSTHTLTTPFSLPESQWLVLPVLPWLEVKMGGLLEPRSSRPAPAWATQPPQVSRK
13728	27629	A	13895	192	1	TLVCVSSSPVKNYNNICLACAFMPLIFALWKEVSGSLLEKSSPEAWPTWVWPLESKNTKISLA
13729	27630	A	13896	152	245	DQSIADVLMYTHTHTHTHTHTHTHTLNQVPG
13730	27631	A	13897	270	406	ISTRFFLYDRASLCHPGWSAGVQSWLPSSNSQAQAILLPQFPE
13731	27632	A	13898	232	73	EMKGPMDVISTPFWRLTLQTTNYHECRWANGRLRLTPEGLLVITPWCDAH
13732	27633	A	13899	107	7	LQCAQMLPILPALWEAKAGGSLLEPRTSRPWA
13733	27634	A	13900	62	224	PTKPLLAHCNLCVLSUDEPAPASQASGVTGMSHCVAENLILHLPESSTAICTL
13734	27635	A	13901	450	194	KRQVKSHSGEVKTHVQWFGIDPSSFAWEARILPLNHLHQRSGTTPWRITKSNKDL ETVLSGGFFKRLKANKDIQTKCVFIQNFY
13735	27636	A	13902	300	404	AAPQRAFPQKKKKKKKKKKKKKKKAPFIKRGK
13736	27637	A	13903	131	29	ALGSLQPLSPRFKRFCSLSPSSWNSIALTVTTM
13737	27638	A	13904	267	74	VWVLVPPFTSYGVLEKPLLVNNIYVHV CVCLCMCVCCVCCCTVLRHCHWDMIIISQHDQ
13738	27639	A	13905	193	64	IRSHQIHLHFKFKFRLGWTWMLTFVIPAPWEAREGRSPPESS
13739	27640	A	13906	309	424	QSTDFLENRRVGAWMLTFVIPALWEAREVGLPEKNS
13740	27641	A	13907	404	251	SCLSLRSWYDRAVPPQANFVFFFFRMESCSVAGSGVQWQWBNISIKNK
13741	27642	A	13908	471	59	CPDQAKKGKRPPTPGPFQKGGQPKSGVLQSPPPPLGECPLGEPKGGWQGGFF FFFFPFKWHEHNEHLPFSKTEKPRAG EARKQSQSTKYAGLSRGRQASPTLRG HLAKASAGSNLQYTRWQGLPEFGN
13742	27643	A	13909	479	231	QRYCMLTFCEHFGDFDLNIVECLERKQVGVLDAPYLLSSFTGRQWLMFVITLWLRARVQGSLEAKSFPTPAWATQDPLSMF
13743	27644	A	13910	167	19	CIVLGIMLDSLWKEPQVFSWNRWFTFVIPALWRAEAGGSPVRSNSNS
13744	27645	A	13911	328	446	GSFSKTIITLDSQTWVVEVVLALQESRVGRSLAPRSSRLQ
13745	27646	A	13912	145	460	NAPMSTGCRVLSYSRLQRNLVWVLEVP IPATPQAREGRLLGPRSSRPWATKGVR ALSHKQNTKTKNLGSHSTGVSVFTTHIHSPTGLWRLSQWLLAMNLATN
13746	27647	A	13913	319	210	KLGFEGSPLEPFFFFFFFFFFFFFGFLTVSCNFTL
13747	27648	A	13914	372	10	PNTTCTPTTYGKKCCPGRISYYLCHRFIRILTFPDGESCYLQAGLLKLGSRSPPTSASGVAGNTDVCHHTQFLLFYILRTG

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						LALLFRLTINSWSQATLALFPQPLRSYPNFWLFFCLYN
13748	27649	A	13915	594	471	PSYIAYMCICMCVCVVVYINLCVCIYTHVHT PYNPVISK
13749	27650	A	13916	235	3	EANNLIRKTYTSGWFORSTKRPDAVRMKVLFFETESCSVAPGVGWHDHSLQPRPGLNRS SHLSF PSSDIYMA
13750	27651	A	13917	272	184	KTTAWAQNLTVPVISTLWEAKVGGSLGASQ
13751	27652	A	13918	46	321	SRVQGTGGHGRGCIQAGVGEAKRETGGPFWRLTVPVISKMEAKAGGSLEPVSRRATWNLLKRIYYTDEREYLIPLALNTSGSTSPF
13752	27653	A	13919	387	484	FTEITGWARMIMPVIPTLWEAAGGSPVRS
13753	27654	A	13920	142	321	FLFSIRPHLSCHGLPNNVQGLSIPSYLKVRLYGQANWPTPIIALWEDKAGGSLDPRSL
13754	27655	A	13921	270	412	IEDKKIYSILHPTETLERQAKNLTVPVIAFEVWKAGGSFEPRSLPV
13755	27656	A	13922	304	396	NFGWAQWLTVPVIALWESEAGGSLDFRGLRS
13756	27657	A	13923	305	387	VNWLTVPVIALWEAAGGSPFPRSRDP
13757	27658	A	13924	103	3	NKSPFELGWANWLPVLPALWEAAGGSPVRS
13758	27659	A	13925	195	400	CLLTLISGLVASCITERRHGKQAWMLMPV IPTLWEAKVGGSLERLNRSGWGTWRNRSISKYTEQLAAG
13759	27660	A	13926	294	489	KWARKQTLHKGRTACVCICVCVCVCVYTYTDIYIPYIHWPMNTKCSMLLVIGEMKILSRMWSNQ
13760	27661	A	13927	363	2	NMGFFGFFPPFLKIGPVFFITGAPKKKFFLSTPRALKFVLKKGGLFFFFFPLNVLVTKGSHCVAPDLLELSSNPVLVSGAGITKWS PQVQLDLFFTFSTETGSR SYAWADAN
13761	27662	A	13928	1	218	LRFRKKRKTTRKPMNVHMTHTSALKRREIRTKQTRNINLIDLGEIRVANTKORILYDGTOMRNLRESNL
13762	27663	A	13929	219	408	TFCHFIAPLHVYKPVVFFSFPIIMFFFLNCKNAFERKQKKKKQNNKKKKKKKISLSPPAPP
13763	27664	A	13930	161	22	WHFPASASHVAGTTGACHERLRQEDHFSIRVQGCSEPRLCCHTTPF
13764	27665	A	13931	116	1	INTGWARMLTVPVLPAPNRAAVGGSLERSTSQAWATNK
13765	27666	A	13932	181	38	PWPORATOPKISPLPPLAISALWEAAGGALPRSSRDPAWAKGDAMVD
13766	27667	A	13933	267	397	TVFDRTLFFPKKILNSWAPMLTPVPALWEAEVCGSPVRS
13767	27668	A	13934	129	12	NIGVGKALWLTSPVLPALWEAAGGPPKVRSSRTARPM
13768	27669	A	13935	179	1	KTYGGI PPPGPPPKKKKKPPFFFKKVP LFFISFFI PFFFFFLRQSLAQMSASVW KVS
13769	27670	A	13936	245	616	DEKKKBAQKATBQKIKVPEQLKPSV SQPQANSRNGTSTATSTNRNMRATAN

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop codon, / =possible nucleotide deletion, - =possible nucleotide insertion)
						WWLIPVIPALWEAKVOGSLSPSSSTPAW ATQGDLLILKKGDTLLQCHIVAKGSHSHS
13825	27726	A	13993	189	370	SRNALFKRRWESSQSSNSLGVFPQAA TKGNVRLWTLVIPALWEAKAGGSLEPRS SRPA
13826	27727	A	13994	179	25	SKHNKRNQICLLCSKRSMFVHVCIH ICVYVRYAYIYIGNCIHIYHS
13827	27728	A	13995	159	2	EDPLSPGVQDQGHHRKSLSGRGKISL QGQFKSSMAAYFGRRSGGCKLERR
13828	27729	A	13996	307	99	FIWEHFNVYNIFFTYKKFTSQAWMLMPV VPALWETAGSGSPVRSFRPPQGHDDVR PLGSLAWLQMD
13829	27730	A	13997	218	21	FQHFQRPFRVHLLSLQVQFQGHGETP SPLASSLIDLIPPPFPIDEPVLDAPQSV TLGVQDTTS
13830	27731	A	13998	227	404	GYSVTLLGLTLQTLQRIAHTRKRRRR ERERERERERVCCLMHELASHLLFFFL FRE
13831	27732	A	13999	400	668	PVGRNRELQGMGLGVRTWQSSLPFCQPT SSSVLSLGRGTPGISNTCLPPRSATBLG LFAQVPPFNQVQSQDQLSFLGCFRTY NRQTL
13832	27733	A	14000	225	414	NRVLLCHTGWSTVATLAYCSFKLLGSRD SPTLASRAARTIVKCRNVLLIKKKKKK KGRRL
13833	27734	A	14001	397	118	LFSGPFFDFSCBCEPQPTVFCLLLYNQ MQPYLLRSAPVDSYYMDSFLDRDVSFC QSGWSTVAPSRLLTAALNSLAQVILLQP LNVLCGLSR
13834	27735	A	14002	3	173	YFFRGRQWUCFYKIRIKMFMNRNLNL GQWCVIPVATQVRAQSGSEPTSLAPI
13835	27736	A	14003	440	290	YTHFLYIYIINTHTHTTYIYLCCTWVG QFDLLVLNKLKRYIYLSVFI
13836	27737	A	14004	2	116	ARLVAMPFKYBESIKDPLTARRKAKSV KIKKNKSAV
13837	27738	A	14005	279	422	SAIAPLSCLRTSLSLGLRQAWWIT PVIPTLWEAVEGSPDVTSP
13838	27739	A	14006	3	497	GGIGDSRCGSTKASSSPQLGRSSSVLP AAQPCPTPMDVFKKGSIAKEGVGVAV EKTQGVTEAAEKTKEGVMVGAKTKEN VVQGVTSVAEKTKEQANAVSEAVSSVN TVATKTVREANLAVTSGVVRKEDLRPS APQQRGRASKEKEBVAEQSGGD
13839	27740	A	14007	1	292	SLGGGGCNDPSTHCTFPAMATRODTVSL SLSIYMSVRVCIYMYMCVCVCI RIYTYI HTHHLIRVYIYIYIYIYIYIYIYIYIYI IYMGWCGCPPSI
13840	27741	A	14008	57	250	KIFFFLMNHITWGGVPVVLATWEASVGS LEPRSLGLQETMTSLLSRLPRQGEIL SLILKNTY
13841	27742	A	14009	184	2	AVFGRPQCOQVFGLLPSIQDTLKQKRTG QWLTFTFPMWEAAGSLDARSLRPAN ATGK
13842	27743	A	14010	123	3	KEPSRFGRLTSLIIPACWEAAGQPPPEA RSSTREFRTAK
13843	27744	A	14011	403	168	GTGLASFCISQPVMSGLLSPSEFPFPR IESHLVSRQRTAARLRDREREPAREKE RERRRGKASSGKPPGASASCVP

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13844	27745	A	14012	207	422	ETRRGSLAGPLSLNFIPLSVMSGSHSKYLR KVIGRAQWMPVVPALWEAEVGLHIELR RLGHTWAAW
13845	27746	A	14013	200	405	WLCVLGWSLLATSPLRECYGPISACNCL HLLRSSDSPASASQAQLEAWYQHLLIWM PQAASTQVGRKK
13846	27747	A	14014	319	176	KPSTITFLFLILFISRESRPVQTVEVK WLNHSSPCPTTPRFSLPSS
13847	27748	A	14015	63	401	EQRNHTLMSFGWDGHTHVLRLFLNTRM PLGHLISFSEGVSGSGSSGRRCQAGAGGR SATANARPQCCLLKGFLPAVPSCGLEG KAFERAGYSASHPIKGEYGVGHWILYVN
13848	27749	A	14016	416	63	VSKVYPRKINHQRVTHIEHTKILAMPKYI SNLCSILRFNRDLAPMRYHTKQCSR'S ITEYIAMFFVFLVFLKIGAHCHPQWTE VVLVCSQVTAASTSAQAILPPQPKIL GMQQA
13849	27750	A	14017	196	425	SLMFRPFLSPCCFCILYPTFTVTFSL CFAPSPWCSLLFFPHYLKFLILLTLTFF LPVLCLDCLFLVHDFLLSS
13850	27751	A	14018	3	233	SSRMGRGRTKTLADNRVSCVEDRAHRD RERERRERERRERENGAEPPQSFVSPW VDRPCLAGTLHLKCGCHRL
13851	27752	A	14019	163	1	AERHNDQICVEREITGWGQWMPVTPVL WEAKAKNLLLEPKNLQRNRRPONS
13852	27753	A	14020	203	83	LKKKINKSQAQHLTSVVLASQEAAGGS LEPRNSRPAAWAT
13853	27754	A	14021	179	3	VTWQRELRQMELRLLICRAWLTFVIP VWEAKAGGSPPEPRSSPAWETRNRDGP NS
13854	27755	A	14022	358	431	WHKKKQWHLGTGHAHCSFTSLGG
13855	27756	A	14023	98	3	GRFAGHLTPVAPTLWEAEMGSLSPRSL GHR
13856	27757	A	14024	254	385	RENNAEPSSSHSLNIPLOLQTVARACNP STLOGRGGWITRSGD
13857	27758	A	14025	140	1	KGVLGPGRLGVCFPCFPFLVCVCVCV CVCVMRRSLTSPRLQCI
13858	27759	A	14026	579	852	QREWVGWAGKEGWSHVDPASAQLPAN GQRGQPHSPGLGTGTSWAQEGAYVCLLS SCSHCCCCSCCCCCPPGCLPFLSGAI CHLVHL
13859	27760	A	14027	30	663	LRILALRELFASHIPGSLTTCVVRPPL PCSSSTKPDAGKYKPLAQKLGSRQTGPC LGHPACPSPLWELRGHGCSPYGPSPGSG VSLWQRAWKLPKNTPEEKDRTPALQEG LIRAVSVFLTLASTVASLWALQELARC GNLACKSILQVAAKALEMGVEGAYFVNL INLNDITDEAFKQDIIHNVSSLLQSAKT QNALVLDCLFETOR
13860	27761	A	14028	1	267	AYGVHIAHILPHCFPSNLSLSPVSRILA MDPNCSGAGVSCCTGASCKRCKRCKTS CKKSCCSCCPVGCCKAGGCVCKGASEK CSCCD
13861	27762	A	14029	46	1746	PARGAATMFPROEPFKLAGRGLKILHR ILEKROBGAETLELSADGRPVTTOTRDP PVVDCTCPGLPRRYTILMISGLGCISF GIRCNLGVATVSMVNNSTTHRGHVVVQ XAQFSWDPETVGLIHGSPFWGYVTQIP

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						GGPTQKFAANRVFGFAIVATSTINMLI PSAARVHYGCVIFVRILQGLVGVGYTPA CHGINSKWAPPLERSLATTAFGGSYAG AVVAMP LAGVLVQYSGWSSVYYVYSGPG IFWYLFWLLVSYESPALHPSISEERKY IEDAIGESAKLMNPLTKGSTPWRRFPPTS MPVYAIIVANFCRSWTFYLLLSQPAYF KEVFGFEISKVGLVLSALPHLWTLIVPI GQQLADFLRSRRIMSTTNVRKLMNCGGF GMKATLLLVGVYSHSKVALISFLYLVAG FSGFAISGFVNVNHLIDLPKRYASITLNGIS NVGVTLSGMVCPILVGVANTKEKTRERQW YVFLIASLVHYGGVILFYGVTFASGEKQP ASPEEMSEBEKCGFVQIDQLAGSDDSRHE DEAEPFGAPPAPPPSYGATHSTFTQPPRP PPPVVDY
13862	27763	A	14030	240	63	VPTAQSGNGGVELNRFPNEGPLSAVLKGRV AWAQWLTPTVPTLNEVKAGLLERSLSP PA
13863	27764	A	14031	289	414	HAENGRVQWLTPTALPACKABAGGPEP RSLRPAMATY
13864	27765	A	14032	386	1765	LGDARAPKESAIQAAPWSGTSCIAXYN FHGTABQDLPPFCBGDVLTIVAVTKDNNW YKAKNKVGRREGIIPANNVQRREKGVKAGT KLSLMPWFHOKITRQAEKLLYPPTGL FLVRESNYPGDYTLCVSGDQKVEHYRI NVHASKLSDERVYFENALQVNVHYTSD ADGLCTRLIKPKVMKGTVAQDEHYRSG WALNMKELKLLQTIQKRGQDVLQDYR GNKVAVKCIKNDATAQAFLAASVMTQL RHSNVLQGLGVIVEEKGGLYIVTEYMAK GSLVDYLRSGRSVLGGDCLLKFSIDVC EAMEYLEGNFVVERDLAARNVLSRDNV AKVSDPGLTKASSTQDTGKLPVKWTAP EALREKKTFSKSDVNSFGILLWEIYSFG RVPYPRILPKDVVPRVEKGYMDADPGC PPAVYEVMMKNCHLDAAMRPSFLQLREQ LEHIKTRHEL
13865	27766	A	14033	619	414	BQARCLBQHACTSPRQPRQLQCSLEKG HSLGMHGHGVPLCHDPCSPCPVVKASPA CWSNPAFLCPH
13866	27767	A	14034	2	614	LESRPDQKPSHPAPSPATSPAGKHP PSAKMSKRAKAKITKKPQRATSNVPA NWDQSQIQEFKRAFNMIDQNRDGFIDKE DLDHMLASLGKNNPTDYLEGMSRAPGP INFTMFLTMFGKELNGTDPEVDIRNAFA CFDREASGFIDHDLRELLITMGDRPTD EEVDENYREAPIDKKGNFNYVEFTRILK HGAKDKDD
13867	27768	A	14035	1	254	AVEFGPAGPGSLGRMAAMIIPVRCFTQ KIVGNKRAYILGLQASYTEGDALDALG LKRYCCRRMLAHVDLLEKLLNYPLEK
13868	27769	A	14036	494	148	FRFTSDCGVFAEGHIELQVESGVPTLGS TMARDNETKIKNYKTAFDSRFPNQNT RNCWNYLDFHRCQKAMTAGGDISVCE WYQRYQSLCPTSWYTDNDQRAEGTFF GKI
13869	27770	A	14037	130	3969	IMEDVKNFLYAWCGKRNKTPSYEIRAVG

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						NKNRQKFWCEVQVSGYNTGMGNSNKK DAQSNAAERDFNYLVIRINEIKSESVPAF GVASPPPLTDDTDTTANAEGLDPTMGG PLPPLHAKARNNSEVGASGYVGPPTW DRGANLKOYYSRKEEQEVOATLESEVD LNAGLHGNWILENAKARNLQYFQKEIKQ GEYKYTVQVQDHHRSFIABMTIYIKQLG RRIFAREHGSNKKLAAQSCALSLVRQLY HLGJVRAISGLTKKSGETVEPYKVNLS QQLSEHQNLILQELMLELPPPEPDSVP VVALNTGKLAQPEPSPQNGVGVVNSPP QSNMNPWTSSNIDEGPLAFATPEQISMD LKNSLMYQLSQMDLOAILQERELLVVK KFESEILEAISQNSVVIIRGATGQGKTT QVPQFILDFFIQNDRAECNIVVTQPRR ISAVSVAERVAFERGEEPGKSGYSVRF ESVLPRPHASIMFCTVGVLRLKLEAGIR GISHVIVDIEHEDINTSFLVLVLRDVV QAYPEVRIVFMSATIDTSMPCSYFFNCP SLKLWRTYPVQEYFLEDICQMTHTFPPP KDKKKKDDDDGGEDDANCNLIGDEY GPETRLMSQLNEKETPFELIEALLKYI ETIANVGAVLVFLQGNLLITMQKHLEF NPHQSHRYQLPLHMQPEBQAKVFD PVPVGVKVLSTNLAETSTINQVYV ISDCKQVKLFTAHNRNINXSVTNAKST NLEQRKGPRAGESTAGCFHLCSEARFER LETHMTPEMFRTPLHEIALSIXLRLGG IQGFLAKAIEPPPLDAVIEAHTIRELD ALDANDELTPLRILAKLPISPRFGKGM IMGCIFFYVGAICTIAATCFPEPFVNS GKQLGYTHRNFAGRNFSIHVALLSVFQA WDDARMGGESEAIRFCSEHRLNNATLRM TWKAVQIKRILINSFPEDCILLTVQFT NTGPDNNLDVVISLLAFGYVPIVCYHKE KRKILTTGRNALIHKSVCNCFSSQDM NTPSPFFVFGSKITRAISAKMTLVPP LQLLLFASKVQSGGQIVVDWIKLQKI SHRAACTNGLARAMEVAVYTKQPAI ISQLDVPVNRNLMIRQISESAGINL MGSTRYDGGRRPPKWAYRYNGSGYPRG GSSVSGGYGGGYSGGYSGGYGGSAT PSGRICAGVGGGYRGVSRGFRONSQGD YRPSGGYRGSGGPPQGGGGAGYGTOL DICEEVAAILKGYVSSVCRQ
13870	27771	A	14038	431	542	EGIPTGWARMLTPVIGTWEEAGGSPG REIDIGLAN
13871	27772	A	14010	238	362	ERCTFLSFRMLAPRVYSVGRKAFSPSV CVRAHGKCDYSYS
13872	27773	A	14041	6290	3514	FRAAGSSSTNSGRICPLSGALLQYSEG LLARPHRGSGFGVGRQHQAVRVGSAHA SSAGYVCVSAPPFVFLRCVGGGGISIR VYALFYGKCNPTREWAVSSELSPSFQEQ NCMKNVBQKQBSVSDVTVGFTQBEW QHLDPQRALRYRUVLENSNLSVSGYC VIKRPIVIRHLQGGEPWKQSEFPSPSGF PEVWDMLKBSQBNQSKHLEWVETIN NEMLITKEQSDVIGIPFWVSSFPSRM

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, N=Methionine, Q=Asparagine, P=Proline, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
						FOQCDSCGSEFNTVSELSVSKINYLGRK SDEPNACGKLLNLT KHEHTHREKNEVL KNRNTLSHRENTLQHEKIQTLDEHPEYS IQETLLERKAVFNTKRENAEENNDYD EPGRTPCDSSSLFHQIQSPSRDNYHPEFS DCEKFLCVKSTLSKPGHVSMMKRYDCGS GNVFRKLCLSHLQKQDGEKHFECNEC GKAFWEKSHLTQHQRVHTGQKPPQCNBC EKAFWKSNLTKEQRSHTEKPFECNEC GKAFSHKSAITLHQRTHTGEEKPYQCNAC GRTFYQKSDLTIKHQRTHTGQKPYECYEC GKSFCMNSHLTVHQRTHTGKPFECLEAC GKSPQKSHLTQHQRTHIGCKPYECNAC GKTFYHKSVLTRHQIHTGLKPYECYEC GKTFCLKSDLTIHQRTHIGKPFACPEC GKGFSSHKSTLSQHYRTHIGKPYECHEC GKIFYNKSYLTKEHRTHTGKPYECNEC GRTFOKQSOLTQHQRTHIGKPYECNEC GKAPCHKGALIVHQRTHTGKPYKNEC GKSPFCVKGSLTHERKHTGKPYECNEC GKFFRHKGSILTVMHRAHTGKSCQCNBC GKIFYRKESLAHQHRSHTGKPYECNCTC RKTFSQKSNLIVHQRRHIGENIMNEMDI RNFQFQVSLHNASYSYHSGSSFDILNVO Q
13873	27774	A	14043	187	422	LTTPKLHSAQEPDAGFVSPPFFSTPTQT GGRSRAEPDQNYCQPAVPAVLRGCLPL SPGEPPHDTSSPEHLTOGGIVF
13874	27775	A	14044	340	442	NKFLSNVRLLEPVIPTFNEAKVGNLEA RSLRMQ
13875	27776	A	14045	3	1240	LVEGAAGQGVSDGARLERCGTRSPQSE EVLSSMARGSAFFAALNINSLILCLLA LRABAGFPQESLYLWIDAHQARVLIGF EEDILIVSEBGHAFPTHDFRKAQQRMAF ISVNIHSMNFTWMAQAQAEYFYEFLSLR SLDKGINADPTVNVPLGTVPKASVVQ VGFPCLGKQDGVAAFEVDVTVMSSEGIT LIQTQONAIFFRTQQACPCPGGCRNGGF CNEKRICECFDGFHGPBCEKALCTFRCM NGGLCTVGFQFCICFPFGVFNCDKANGS TTCFNGOCTFYQKCLCEPGLSGQCELI SKCQPCRNQKCKIGSKCKCKGKQGD LCSKPVCEPGGGAHGTCEHPNCKQCGG WHGRHCKRYEASLTHALRPAGAQLRQH TPSLKAKEKRRDPPESNTYIN
13876	27777	A	14046	18	274	YSORVLCENRNSGVSNKRGWANNQLT TTPAINAEAEVGGILLPSRLASQPP QHEPYSMSYCAQPRFSLCIRGFIFYSLN F
13877	27778	A	14047	177	441	GGSHYANFNITFTFKLIAQFFCFPFEMQ SCS VARLECRGAI SAHCNHLHGGSSNSP VMAQILKNQKSNFDEATLLGLSYTLL GEI
13878	27779	A	14048	136	319	DVFI.LL.FHSNYFLFFETGSHSVSQGVK NCDLSSLOPPPLGSSDPPTSASRVLPALF FFLEF
13879	27780	A	14049	388	128	ELKLPSTYRGQSQGLSKRYFADLIATVS NRFLCPSANHLAVYLLEDLPMRDRDISI

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						QQIHLVALSCILLASKYVSDLHDKFLMFI
13880	27781	A	14050	262	3	VIYNYISVREFFENIYRTFYTLSLFLYLS THTHHTHTHTHTQRTGHVVCVCIYTYM YMCYAKNNYKPTFLISGKARHTHLHP CI
13881	27782	A	14051	149	423	YPHLCAFLILPSSISSFRAGVFFPFSYLSL TAYPLTWKPEPPATQPTNPPPPGHPA TRGPKSALLDHSYACASAPPLGTGTAT SPSFALI
13882	27783	A	14052	2	1440	FVAVIAMAAPCLLRQGRGALKTMQLQA QVPRGLASTVLSAEQSKSEKQGPQNSK KQSPKNVVPKRRGKGLAQTAELS NLSSPSSVPPAVNKGKVASPSPSGV FTDGGVPKFLSRKTIIVEFPQKVLSPPRK QQSDSEARQVGRKVTSPSSSSSSSSDS ESDDEADVSEVTPRVVSKRGGLRKPEA SHSFENRAFRVTVSAKETLLQKPHVDI TDPEKPHQPKKKGSPAKPSEGRENARPK TTMPRSQVDEEFLQSLKEKQLQKTPRL NEIDKTSQKPFIEVKGPIPVHTKSGLSAP PKGSPAPAVLAEEARAEQGLQASPPGAA EGHLEKVPPEPQRKAAPPLPRKETSQTQ GIBGHLKGGQAVEDQIPPSNLETVPVE NNHGFHEKTAALKLEAGEAMEADAAPG NDRGGTQEPAPVPAEPFDNTTYNQLQH DYSTYTFLDINLELSKFRMPQPSSGRES PRH
13883	27784	A	14053	177	1253	EKKRTLPVRSVTGELQKSKLSLDAAGTN DSEKKRFTETATKYPERVSPVHLQALL TNNEANKRFPVTAELPRDEADALYEALK KLRTYAAIEDEVVQKDEQFREWFLKEF PQVKRKIQIESIEKLRALANGIEVHRC TISNVSSSTGAASGIMSLAGLVLPAPT AGTSLALTAAGVGLGAASAVTGITTSIV EHSYTSSAENSRLTATSIDRLKVPKE VMRDIIPNLLSLNNYYEATQITGSEIR AIRQAPARLPVTTWRISAGSGGQAE TIAGTTRAVSRGARILSATTSIGIFLAD VYNLVYESKHLHBGAKSASAEELRRQAQ ELBENLWELTYQRIINPCHT
13884	27785	A	14054	1585	2099	ICVRTFFPLALQVRAAAEHHHSSGLPY WYILTAETLKNRNGHQPPEPTQHSITD NSLAKTSEELLPLPSPAPSPDML KTPPECLITPLPPSALPSADNLKTPAE CLLYPIPPSADNMLKTPPECLITPLPS APPSVDMLKTPPECVCSLPPHPRQMI SRN
13885	27786	A	14055	2	2865	ALPDGGAASVADRAEGRPAKPSKTAARE KTEGAVAAVGGGSPSRCCYGCCHEARL GRSLPRGVIMLTASLSIWNGSLGIV LFLITFGPFVIFYLTFYILCFVGGGLVV TLFPGKTINSEKYLEQCEHSPLPPTSFGV PKCLBEMKREARTIKIDRRLTGANIIDE PLQQVIQFSLRDYVQYNYTISDDESFL LEIROTTLQNALIQFATRSKIDWQPYPT TRIVDDFGTHLRVFRGAQKKITEKDDQV KGTABLDVDTPEVEVEMEKRCRDLVC

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Yrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TSPKDEGFLRLDLCRVLLVLLLPFQDFQ NKIMRYFVREILARGILLPLINQLSDPD YINQYVIMKIRDSNKNYSAFNNIILKSD NIGLEAVRDGAEEQLYLRSLDTAGDD INTIKNQINSLFVFKVCDSEIRIQRIGSG KEINTVKLAANFGKLCITVPLDSILVDNV ALQFFMDYMQQTGGQHLFFMITVEGVR VIAQQQLVLLSRQRDGHKQNTQTEGLL RAAAVGIYEQYLSSEKASRVTVDDYLVA KLADLNHEDPTSEIFDIQRKVLEKL RDERFYDSFRQNALVBNLAELNMLKDP SFRGSDDGDSFNGSPGSGINLSLDDL SNVSSDDSVQLHAYISDITVADYDVPYAV AGVCNDHGKTYALVATVHRRNLNSEEM WKTYRRYSDFDHPHVRITETQFESLSIL KLPEKKTENNMDRDFLEKRRKDLNAYLQ LLLAPEMMKASPALAHYVDFLENKAYS KKGGLDFARKMDTFVNPLRNSMNVNNAV KSLPDSLAEGMTKMSDNMGKMSERLQGD IKQSFPPKVPPLIPKTDSDPEHRRVSAQL DDNVDDNIPLRVLLLDDEVDLKERNQ WLRRNIKNLLQQLIRATYGDITNRIKIVD HVDNHTSPQVADS VKGRFDAPFNPGLIL AEAVPCKDKSIRMRTRVAGKTKLLAIMP GE
13886	27787	A	14057	311	150	FLCFTRRGPTATISGLKLGLSSDDPSS TSQIPGITGTSKCPQTHLPFLALS
13887	27788	A	14058	53	211	RGHITCLDIPFTHENYKYYINITYLSIY LSIYLSIYLSISHSYITERA
13888	27789	A	14059	1	1642	RDGRKMATATIALQVNGQGGSEPAALA AAVVAAGDKWPKPGQDTSIGENQGSTA AKLGLPPLTPEQENLQKAKKYAMEQSI KSVLVEQTIAHQQQQLTNLQMAQGRQA LAIMCRVYVGSIIYELGEBDTRQAFAPF GPIKSIDMSWDSVTMHGKGFAPVEYVVP EAVQALALBQMSVMLGRNITKVGPRSNII GOAQPIIDQLAEEARAFNRIYVASVHQD LSDDDIKSVFEAPFGIKSCTIARDPTTG KHGKGFIIEYKAQSSQDAVSMNLFDL GGQYLRLVGKAVTPIMPLLTATPQGLPP AAVVAATAAKITAKQAVAGAVLGLT CTPGLVSDALTLAQPLTLTPQAVPMQA PGVITGVTPARPPITVTPISGVVNPIL ASPPTLGLLEPKKKEKKEKLEPESERPE MLSEQHMSISGSSARHVMVQKLLRQKE STVMVLRNMVDPKDIIDDLGEVTERCKG KRGAVNRVITYQKQGEEDAEIIVKIF VEFISIASETHKAIQALNGRWFAGRKVVA EVIDQERFDNSDLA
13889	27790	A	14060	1238	1474	VLAQEGRPWRPEASTDACRLNFORLR RKGFSNVLPGLAQALYSGGYHLKPAD ELMGGLNKKSTADASGSRGHQL
13890	27791	A	14061	266	400	GQWARPVTPALWEAKAGGSLRPSMLRPA GQHIKTPSVLITSKKT
13891	27792	A	14062	2178	1881	VLAQPSILLDAPRTDGGDMGRAMVARLG LNLLLALLLPQTQIYSSETTTGTSSNSS QSTNTGLAPNPTNATTKAAGGALQSTA SLFPVLSLLHLYS



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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, Y=Valine, W=Tryptophan, X=Unknown, *Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
13892	27793	A	14063	261	1	NSVLTALLFSLMIVHLPFPPPSGVTDTAG ALSTOGPPSPSTSVTGRGPAHSHASQLPP APGEFAPLNESSCRGWAGRAFLERFPDAW VDP
13893	27794	A	14064	2384	1115	QHFSRERGLCVQRESSVTSWTSWGAWS PCPPSNASCNTLHTRDNASDPGGQSL GRSPGPAPPQGLHLLDTDLHSLAQIGK SPVAGVNGGSLWPRESPGTANGHSPH TPPGPGPPGPCPTKRRLLPAGEAPDVSS ESEGPAFRRRRGLGHPTAANSSDAKAT PFWSHLLPGPESPVLDPDCCPMGRRLK GARRLKLPRLSLRKPGLSPPEASPV PTTAVSRTLLGNFESLRLGRFAPSHT EGFTARIASGSYCPQHVTLFVTVTFD VSEONAPAPFLGIVDLNPLGRKGYSPVK VGTVQVTLFNPQTVVMFLVTFDFSDM PAAHMTFLRRLFLVLPVGEENANPTHR LLCYLLKLRFSSRSRGLSLHGDRIYLF SRRLSLELDTGLPYELQAVTEAPHNPRYS PLP
13894	27795	A	14065	232	416	GMVQLGIGTTEGKRGTSRSSRRQREGRO GNRKTGRRRRGRSTKTDAPSYPDAERP RSKLI
13895	27796	A	14067	238	45	IQTCGSHSPCIPSIWEAKAGLLEPRL SPACPTQKDPISHLGSELPQSFLLLRL VPLFLSAC
13896	27797	A	14068	3	1705	SCSEKATPWRAVNASQELQHPQGGQRP LQGLTPARPNPAPLTVBCQRS CSRVP PAPLPSTHTPPQSSCPYSSPFTTADA PGAQRRAVTPQSRGRGFLDTGTWLV VLPTQAPPKPGSQSDKSLNREL SAERP LNEQIARAEDKIKKTYPPENKPGQSNY SFVDNINLLKAITEKKIEKREQSIRSS PLDNKLNVEDVDSTENRKLIDDYDSTKS GLDHKQDDPDGLHQLDGTPLTAEDIVH KIAARIYEENDRAVPDKIVSKLLNLGLI TESQANTLEUEVAEVQLKLSKEANNYE EDPINKPTSWTENQAGRIPEKVTMPMAIY DGLAKGENDETUSNTLTITNGLERRTKT YSEDNFEELQYFPNPFYALLKS IDSEKEA KEIGETLITIMETLIDFVRMAVYGTISF REGVSVLENLDEMIALQYTNKLEKNATD NISKLPAPESEKSHSTOSTKEBAARKE KSYGSLKASTKODNSNPGCTDEKERT EAYLEAIRKNIWELKCHDKGKNEEDYL SKMRDPINKQADAVVEKGLDKEBAZAI KRIYSSL
13897	27798	A	14069	1	140	NTSVAIQTIIEYSAFRRGKGLTHVPLM NLKDTMLREISOSOKDTV
13898	27799	A	14071	212	104	HTNHOCOTVLPAQQAALATPQGLAPSVPF PQSCLRNV
13899	27800	A	14072	358	112	FPLTVMHLVPLWNLKIFPCWFIQEBOL FFFFFLRTGSHYVQAGLELLGSTNLPL ASVSRAVGTGIHCTQPNPLHTLHL
13900	27801	A	14073	3	151	YMGFHHVGYAGLELLTSSDLPWPWPKCW DYRHEPSCLAMFFYFALIAPE
13901	27802	A	14074	8	1493	VTIHLFVGGQAVRADFLKKS SCCLLCI VFLDVPRIDLITINDQAVIYFKSHPPVGR

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						GDAVLKTNAPACQLCSRXGPAWLWLLGT GILASVHCQPLLHNGDESLQGQP PPRHQ LSEPA PAYHRI TPTITNFALRLYKELAA DAPGNIFFS PVSISTTLLALLSLGAQANT SALILEGLGFNLTRTPEADIHQGFRLSL HTLALPSKLELKVGNLSFLDLKRLKPRQ HVLDSIKELYGATAPSANFTDSVTTGRQ INDYLRRTQYQQVVDCLPEFSQDTFMVL ANYIFPKAKWHPFSRYGTQKQESFFVD ERTSLGVMMHQKMERFLDQDLACTV ICIITYGNALALLVLPQKHKQVEAL QPQTARKNGQLLPSLLDLHLPREISG QYNLEDILPQIGLVNTLNLEADFSGVTG QLNKTIKXVSHKANVDMSEKGTETAGAS GLLSQPPSLNIMSDPHAFNRPFLLLLN EVITQSLFLFLGKVVNPVAG

## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-13901, a mature protein coding portion of SEQ ID NO: 1-13901, an active domain of SEQ ID NO: 1-13901, and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 25 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
  - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
  - 30 (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NOS: 1-13901.
11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

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13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
  - 5 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with
  - 10 nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
  - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
  - c) detecting said product and thereby the polynucleotide of claim 1 in the
  - 15 sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 20 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
  - b) detecting formation of the complex, so that if a complex formation is
  - 25 detected, the polypeptide of claim 10 is detected.
17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under
  - conditions sufficient to form a polypeptide/compound complex; and
  - 30 b) detecting the complex, so that if the polypeptide/compound complex is
  - detected, a compound that binds to the polypeptide of claim 10 is identified.
18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

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a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

- b) detecting the complex by detecting reporter gene sequence expression, so  
5 that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

- a) culturing a host cell comprising a polynucleotide sequence selected from  
10 the group consisting of a polynucleotide sequence of SEQ ID NO: 1-13901, a mature protein coding portion of SEQ ID NO: 1-13901, an active domain of SEQ ID NO: 1-13901, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-13901, under conditions sufficient to express the polypeptide in said cell; and  
15 b) isolating the polypeptide from the cell culture or cells of step (a).
20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 13902-27802, the mature protein portion thereof, or the active domain thereof.
- 20 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
22. A collection of polynucleotides, wherein the collection comprises the  
25 sequence information of at least one of SEQ ID NOS: 1-13901.
23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 30 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

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26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
- 5 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 10 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.